



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 210734

TO: Manjunath N Rao
Location: REM-2A01/2C70
Art Unit: 1652
Wednesday, December 20, 2006
Case Serial Number: 10/616101

From: Usha Shrestha
Location: Biotech-Chem Library
REM-1A64
Phone: (571)272-3519

Usha.shrestha@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Usha Shrestha
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-3519

*Please do not
change the order of pages
when scanning.
Thanks*

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12-759
STIC-Biotech/ChemLib

210734

From: Chan, Christina
Sent: 77025 Monday, December 18, 2006 8:56 AM
To: Rao, Manjunath N.; STIC-Biotech/ChemLib
Subject: RE: REquest for RUSH sequeunce search for case No. 10/616101

CRFE

~~Please Rush. Thanks. Chris~~

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Rao, Manjunath N.
Sent: Friday, December 15, 2006 2:23 PM
To: Chan, Christina
Subject: REquest for RUSH sequeunce search for case No. 10/616101

12/18
✓

Hello Christina,

Please authorize the search request below as RUSH. The reason being this is an amended case and applicants have now included SEQ ID NO for the claimed polypeptides.

Many Thanks
-Manjunath

Manjunath N. Rao, Ph.D.
Primary Examiner, Art Unit 1652
Room 2A01, Remsen Bldg.
United States Patent and Trademark Office
400, Dulany St.
Alexandria, VA 22314
Phone: 571-272-0939
Fax: 571-273-0939

2C70

1-3797na
2-3816na
3-1065aa
4-1240aa
LB

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 12-22-06
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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--
From: Manjunath N. Rao
Art Unit 1652, Room 2A01
Mail Box in Room 2C70
Phone: 272-0939

Date: 12-15-06

Please search the following as soon as possible for application with serial number 10/616101

1. SEQ ID NO: 1, 2 against all commercial nucleic acid sequence databases, issued patents/published applications nucleic acid sequence database and pending application nucleic acid sequence database. Please provide a print of results

2. SEQ ID NO: 3 and 4 against all commercial amino acid sequence databases, issued patents/published applications amino acid sequence database and pending application amino acid sequence database. Please provide a print of results.

If you have any questions please call me at the above phone number.

Thanks

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 12:06:29 ; Search time 20529.6 Seconds
(without alignments)
11827.212 Million cell updates/sec

Title: US-10-616-101-1
Perfect score: 3797
Sequence: 1 ctttgaagacactggatttc.....cctttgctgaaaaa 3797

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb env.*
- 2: gb_pat.*
- 3: gb_ph.*
- 4: gb_pi.*
- 5: gb_pr.*
- 6: gb_ro.*
- 7: gb_sts.*
- 8: gb_sv.*
- 9: gb_un.*
- 10: gb_vi.*
- 11: gb_ov.*
- 12: gb_htg.*
- 13: gb_in.*
- 14: gb_on.*
- 15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3797	100.0	3797	2	AR392872 Sequence
2	3797	100.0	3797	2	AR653623 Sequence
3	3393.4	89.4	3816	2	AR392873 Sequence
4	3393.4	89.4	3816	2	AR653624 Sequence
5	3388.8	89.2	4275	2	AR361486 Sequence
6	3388.8	89.2	6028	5	AF309033 Homo sapi
7	3388.8	89.2	6123	2	AX057579 Sequence
8	3387.2	89.2	3815	5	AF329696 Homo sapi
9	3387.2	89.2	4127	2	AX062241 Sequence
10	3387.2	89.2	4406	2	AX062247 Sequence
11	3387.2	89.2	4992	2	AX062275 Sequence
12	3387.2	89.2	5002	2	AX062273 Sequence
13	3387.2	89.2	5075	2	AR578380 Sequence
14	3387.2	89.2	5810	5	AF264912 Homo sapi
15	3387.2	89.2	6018	2	AR584137 Sequence
16	3387.2	89.2	6189	2	CQ896544 Sequence
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18	3387.2	89.2	6189	2	CS023798 Sequence

19	3387.2	89.2	6189	5	AF438201 Homo sapi
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21	3386	89.2	3394	2	AX133694 Sequence
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23	3382.8	89.1	4512	2	AX076213 Sequence
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25	3300.4	86.9	3501	5	AF342982 Homo sapi
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29	3291.8	86.7	3498	2	AX062142 Sequence
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33	2774.6	73.1	5005	2	AR361485 Sequence
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36	2403.2	63.3	3930	11	AX062229 Sequence
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44	1813.4	47.8	4134	2	AR361487 Sequence
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				5	AF082556 Homo sapi

ALIGNMENTS

RESULT 1
AR392872
LOCUS AR392872 3797 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6617102.
ACCESSION AR392872
VERSION AR392872.1 GI:40118097
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3797)
AUTHORS Luo, Y., Chan, E., Xu, X., Huang, B. and Ososovskaya, V.
TITLE Tankyrase H, compositions involved in the cell cycle and methods of use
JOURNAL Patent: US 6617102-A 1 09-SEP-2003;
Rigel Pharmaceuticals, Inc.; South San Francisco, CA
FEATURES
source
1. 3797
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN	Query Match	Best Local Similarity	Score	DB 2;	Length	3797;
		100.0%;	100.0%;	0;	Mismatches	0;
		Matches 3797;	Conservative	0;	Indels	0;
Qy	1	CTTTGAAGACACTGGATTTTCATCTTTTGGCTGGGGTTATCTCTGTGTCTCACTACAT	60			
Db	1	CTTTGAAGACACTGGATTTTCATCTTTTGGCTGGGGTTATCTCTGTGTCTCACTACAT	60			
Qy	61	AGACAAATATTAGCTGTGAGCAGATCTTTTGTGCTTCTTGTAGTCCCTGAGTTTGTCTGTA	120			
Db	61	AGACAAATATTAGCTGTGAGCAGATCTTTTGTGCTTCTTGTAGTCCCTGAGTTTGTCTGTA	120			
Qy	121	CAGAAACATCTGTGAGATAGATGTGGAAAGGAATCTAGCAAGAGTTTGTCTCACTGTA	180			
Db	121	CAGAAACATCTGTGAGATAGATGTGGAAAGGAATCTAGCAAGAGTTTGTCTCACTGTA	180			
Qy	181	TCATAAGGTTGTGATTTACATATTTAAGTTTATCTTTTGAACATCTGAAATGATATACA	240			
Db	181	TCATAAGGTTGTGATTTACATATTTAAGTTTATCTTTTGAACATCTGAAATGATATACA	240			

Qy 241 TACTAAATATGCGAGAACTCTATTGTAGAGTGAGAGAAACATTTGAACTTTGAGCTTTCAAGTC 300
Db 241 TACTAAATATGCGAGAACTCTATTGTAGAGTGAGAGAAACATTTGAACTTTGAGCTTTCAAGTC 300
Qy 301 ACTTATTTTGTATTTCTTTTCTTTGAGGTTAGCAGTAGTACCAACCCAGGCACTGTTAGGT 360
Db 301 ACTTATTTTGTATTTCTTTTCTTTGAGGTTAGCAGTAGTACCAACCCAGGCACTGTTAGGT 360
Qy 361 ACCACTGCTGTAGTGAGAGTCCCTCTGGCTTTTATCATTTAAGGTTTGGCCGGAAGA 420
Db 361 ACCACTGCTGTAGTGAGAGTCCCTCTGGCTTTTATCATTTAAGGTTTGGCCGGAAGA 420
Qy 421 CGTAGTGAATATTTGCTTTCAGAAATGCTGCAAGTGTCCAAGCAGTGATGATGGGGCCT 480
Db 421 CGTAGTGAATATTTGCTTTCAGAAATGCTGCAAGTGTCCAAGCAGTGATGATGGGGCCT 480
Qy 481 TATTCTCTTTCATTAATGATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGGC 540
Db 481 TATTCTCTTTCATTAATGATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGGC 540
Qy 541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATCTCTCTCCATGAAGCTGC 600
Db 541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATCTCTCTCCATGAAGCTGC 600
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Db 721 TACTGGTGAATATAAGAAAGATGAACCTCTAGAAAGTCCAGGAGTGCAATGAAGAAA 780
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Db 781 AATGATGCTCTACTCAACCATTAATTAATGTCAACCTGCCACGCAAGTGATGGCAAGAGTC 840
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Db 841 AACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTTTACTGCA 900
Qy 901 ACATGGAGCTGATGCTCAATGCTAAAGATAAAGGTTGATCTGGTACCATTTACACAATGCTG 960
Db 901 ACATGGAGCTGATGCTCAATGCTAAAGATAAAGGTTGATCTGGTACCATTTACACAATGCTG 960
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Qy 1081 ATGTTCTCTTCTTTAAGTTATGGTGAGACCCCAACACTGCTCAATTTGTCACAATAAAG 1140
Db 1081 ATGTTCTCTTCTTTAAGTTATGGTGAGACCCCAACACTGCTCAATTTGTCACAATAAAG 1140
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Db 1141 TGCTATAGACTTGGCTCCCAACACAGTTTAAAGAAAGATTTAGCATATGAATTTAAAG 1200
Qy 1201 CCACTCGTGTGCAAGCTGACAGAGCTGTACTCTGCAATCAAAAACATCTCTC 1260
Db 1201 CCACTCGTGTGCAAGCTGACAGAGCTGTACTCTGCAATCAAAAACATCTCTC 1260
Qy 1261 TCTGGAATGGTGAATTTCAAGCACTCTCAAAACACATGAACAGCATTTGCTGCTGC 1320
Db 1261 TCTGGAATGGTGAATTTCAAGCACTCTCAAAACACATGAACAGCATTTGCTGCTGC 1320

Qy 1321 TGCATCTCATATCCCAAAAGAGCAAAATATGTGAACCTGTTGCTTAAGAAAGAGGCAAA 1380
Db 1321 TGCATCTCATATCCCAAAAGAGCAAAATATGTGAACCTGTTGCTTAAGAAAGAGGCAAA 1380
Qy 1381 CATCAATGAAGAACTAAAGAAATTTCTTGACTCTCTGCACTGCGTGCATCTGAGAAAGCTCA 1440
Db 1381 CATCAATGAAGAACTAAAGAAATTTCTTGACTCTCTGCACTGCGTGCATCTGAGAAAGCTCA 1440
Qy 1441 TAAATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGGTTAATGCTCTGGATAATCT 1500
Db 1441 TAAATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGGTTAATGCTCTGGATAATCT 1500
Qy 1501 TGCTCAGACTTCTCTACAGAGCTGATATTTGGTCACTCAAAAACCTGCCCTACT 1560
Db 1501 TGCTCAGACTTCTCTACAGAGCTGATATTTGGTCACTCAAAAACCTGCCCTACT 1560
Qy 1561 CTTGAGCTATGGGTGTCATCTCTAACAATTTATCCCTTCAGGCTTTACTGCTTTACAGAT 1620
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Qy 1621 GGGAAATGAAGATGTACAGCAACTCTCCAAGAGGGTATCTCATTTAGGTAAATCAGAGGC 1680
Db 1621 GGGAAATGAAGATGTACAGCAACTCTCCAAGAGGGTATCTCATTTAGGTAAATCAGAGGC 1680
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Qy 2341 ACTTATTTCTTTACATTAATGCGACATCTTACGGGCACTGTAGATGTAGCAGCTCTACTAAT 2400
Db 2341 ACTTATTTCTTTACATTAATGCGACATCTTACGGGCACTGTAGATGTAGCAGCTCTACTAAT 2400
Qy 2401 AAGTATAATGCAATGCTCAATGCGCAAGCAAAATGGGCTTTTCAACCTTTTGCAAGAGC 2460

Db	2401		AAAGTATAATGTCATGTGTCAATGCGCAGCAAAATGGGCTTTTTCACACTTTGCGCAAGC	2460
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Qy	2521	TCCTTAAAAATCAGGAAGCAAAACACCTTTAGATTAGTTTTCAGCGGATGATGTCAGCGC	2580	
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Qy	2581	TCCTTCGACAGCGCATGCCCCCATCTGCTCTGCCCCCTTGTGTACAGGCTCAAGTGCT	2640	
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Qy	2701	ATCAAGCCTTTCTCGAGCCAGCAGCTTTGACAACTTATCTGGGAGTTTTTTCAGAACTGTC	2760	
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Qy	3181	CAATATTTCTCAAGATTCAAGGTTTGTACAGAAACTATGGGAAGATACACTCACCG	3240	
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Db	3481	CCACAGCAGCTGCTCTTTTCCGGGGTAACCTTGGGGAAGTCTTTCTCGAGCTTCAGTGC	3543
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Qy	3781	TTGCTGAAAAAATAAAAA 3797	
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RESULT 2			
AR653623	AR653623	3797 bp	linear
LOCUS	Sequence 1 from patent US 6887675.		
DEFINITION	Sequence 1 from patent US 6887675.		
ACCESSION	AR653623		
VERSION	AR653623.1	GI:67584112	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 3797)		
AUTHORS	Luo, Y., Chan, E., Xu, X., Huang, B. and Ososovskaya, V.		
TITLE	Tankyrase H, compositions involved in the cell cycle and methods of use		
JOURNAL	Patent: US 6887675-A 1 03-MAY-2005;		
FEATURES	Rigel Pharmaceuticals, Inc.; South San Francisco, CA		
source	Location/Qualifiers		
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ORIGIN	/mol_type="genomic DNA"		
Query Match	100.0%;	Score 3797;	DB 2; Length 3797;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 3797;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
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Qy	61	AGACAAATATTAGCTGTGACACAGATCTTTTGTGTGCTTCTGTAGTCCCCCAGTTTAAAG	120
Db	61	AGACAAATATTAGCTGTGACACAGATCTTTTGTGTGCTTCTGTAGTCCCCCAGTTTAAAG	120
Qy	121	CAGAAACATTTCTGTGAGATAGATGTGGGAAAGAAATTTCTAGCAAGAGTTTTGTGCACGTGA	180
Db	121	CAGAAACATTTCTGTGAGATAGATGTGGGAAAGAAATTTCTAGCAAGAGTTTTGTGCACGTGA	180
Qy	181	TCATAGGTTGTGATTTTACATATTTAAGTTTTATCTTTGAAATCTGAAAATGTATACA	240
Db	181	TCATAGGTTGTGATTTTACATATTTAAGTTTTATCTTTGAAATCTGAAAATGTATACA	240
Qy	241	TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTTGAACCTTTTGAGCTTTTCAGTC	300
Db	241	TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTTGAACCTTTTGAGCTTTTCAGTC	300
Qy	301	ACTTATTTTGTATTTCTTTTGGAGTTAGCAGTAGTACACCCAGGCACTGCTTAGGT	360
Db	301	ACTTATTTTGTATTTCTTTTGGAGTTAGCAGTAGTACACCCAGGCACTGCTTAGGT	360

QY 361 ACCACTGCTGCTTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTGGCGGAAGA 420
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QY 481 TATTCCTCTTCATTAATGCATGCTCTTTTGGTGCATGCTGGAAGTAGTCAATCTCCTTTTGG 540
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QY 541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTATATCTCCTCCATGAAGCTGC 600
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QY 1201 CCACTCGTGTGCAAGTGCACGAGAGTGTATGTAATCAAAACATCTCTC 1260
Db 1201 CCACTCGTGTGCAAGTGCACGAGAGTGTATGTAATCAAAACATCTCTC 1260
QY 1261 TCTGGAATGGTGAATTTCAAGCATCTCAACACATGAAACAGCATTTGCTGCTGC 1320
Db 1261 TCTGGAATGGTGAATTTCAAGCATCTCAACACATGAAACAGCATTTGCTGCTGC 1320
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Db 1321 TGCAATCTCCATATCCCAAGAAAGCAAAATATGTAATGTAAGAAAGGAGCAAA 1380
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RESULT 3
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LOCUS AR392873 3816 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6617102.
ACCESSION AR392873
VERSION AR392873.1 GI:40118098
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3816)
AUTHORS Luo, Y., Chan, E., Xu, X., Huang, B. and Ossofskaya, V.
TITLE Tankyrase H, compositions involved in the cell cycle and methods of use
JOURNAL Patent: US 6617102-A 2 09-SEP-2003;
Rigel Pharmaceuticals, Inc.; South San Francisco, CA
FEATURES
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1. 3816
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ORIGIN

Query Match 89.4%; Score 3393.4; DB 2; Length 3816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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[illegible][illegible]

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Qy	3163	TGGAATCTTCAACAGATACAATATCTCAAGATTCAGAGTTTGTAACAAGAACTATG	3222
Db	3182	TGGAATCTTCAACAGATACAATATCTCAAGATTCAGAGTTTGTAACAAGAACTATG	3241
Qy	3223	GGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAACACACACCATGCCAATGA	3282
Db	3242	GGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAACACACACCATGCCAATGA	3301
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Qy	3343	AAGCATGCGTACATAGTGGTATGTTTGGAGCTGGGCATTTATTTTGTGAAACTCTTC	3402
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Qy	3463	CAGATCTTGTACATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACCTTTGGGAAAGTC	3522
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Qy	3703	ATAAATAGTTATTTAAGAACTAATCCACTGAACCTTAAATCATCAAGCAGCAGTGG	3762
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DEFINITION	Sequence 2 from patent US 6887675.		
ACCESSION	AR653624		
VERSION	AR653624.1 GI:67584113		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 3816)		
AUTHORS	Luo, Y., Chan, E., Xu, X., Huang, B. and Ossoskovakaya, V.		
TITLE	Tankyrase H, compositions involved in the cell cycle and methods of use		
JOURNAL	Patent: US 6887675-A 2 03-MAY-2005;		
FEATURES	Rigel Pharmaceuticals, Inc.; South San Francisco, CA		
source	1. 3816		
	/organism="unknown"		
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Query Match	89.4%	Score 3393.4;	DB 2; Length 3816;

Best Local Similarity 99.9%; Pred. No. 0;			
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	403	AGGTTTGGGCGGAAGACGCTAGTTGAATATTTCTCTCAGATGCTGCTCAAGTGTCCAGC	462
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Db	1322	AGCATTCATGCTGCTGCTGCTATCCATATCCCAAGAAAGCAATATGCTGACTGTT	1381
Qy	1363	GCTAAGAAAGGAGCAACATCAATGAAAGACTTAAAGAAATTTCTGACTCTCTGACGT	1422
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Db 1982 TGTAGCTGATTTATGGAATTTTACACCTTTACATGAAAGCAGACAGCAAAAGGAAATATGA 2041
Qy 2023 AATTTGCAAACTCTGCTTCCAGCATGCTGTCAGAGCCCTACCAAAAAAAGAGGGATGGAAA 2082
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Qy 2983 AATTTAAAGGAGTGCAGAGACTTATCTCCGACAAACAGGCTTAAACCATATTTAACTTT 3042
Db 3002 AATTTAAAGGAGTGCAGAGACTTATCTCCGACAAACAGGCTTAAACCATATTTAACTTT 3061
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Db 3062 GAACACCTCTGGTAGTGGAAACAATTTCTTATAGATCTGCTCTCTGATGATAAAGAGTTTCA 3121
Qy 3103 GTCTGTGGAGAGAGATGCAAAAGTACAGTTCTGAGAGCAGAGATGGAGTCTATGAGG 3162
Db 3122 GTCTGTGGAGAGAGATGCAAAAGTACAGTTCTGAGAGCAGAGATGGAGTCTATGAGG 3181
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Qy	2143	TGCAGCTTTGCTAGATGCTGCAAGAGGGTGTGTTAGCAGAGTGAAGAAGTTGTCTTC	2202
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Qy	2203	TCCTGATAATGTAATTTGCCCGATACCAAGGCAGACATTTCAACACTTTTACATTTAGC	2262
Db	2249	TCCTGATAATGTAATTTGCCCGATACCAAGGCAGACATTTCAACACTTTTACATTTAGC	2308
Qy	2263	AGCTGGTTATTAATTTAGAAAGTTGCAGAGTATTTGTTACAACACGGAGCTGATGAA	2322
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Qy	2323	TGCCCAAGACAAGGAGGACTTATCTTTTACATAATGCAGCATCTTACGGGCATGTAGA	2382
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Qy	2383	TGTAGCAGCTCTACTAATAAAGTATATGCAATGTCATGCCACGACAAATGGGCTTT	2442
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Db	2909	ACTTGAGCCTAATGGATATATTGAGAGAGAGACAGATCACTTTGGATGTATTAGTTGA	2968
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Qy	3463	CAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTC	3522
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DEFINITION	Sequence 2 from Patent WO0077225.		
ACCESSION	AX057579		
VERSION	AX057579.1 GI:12310301		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
REFERENCE	1		
AUTHORS	Chi, N.W. and Lodish, H.F.		
TITLE	A novel insulin signaling molecule		
JOURNAL	Patent: WO 0077225-A 2 21-DEC-2000;		
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; THE GENERAL			
HOSPITAL CORPORATION (US)			
FEATURES	Location/Qualifiers		
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ORIGIN

Query Match 89.2%; Score 3388.8; DB 2; Length 6123;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 449 AGGTTTGGCGGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAGATGCCAAGC 508
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Qy 463 ACGTGATGATGGGGCCCTATTCTCTTCATAATGCATGCTCTTTTGGTCAATGCTGAAGT 522
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ACCESSION AF329696
VERSION AF329696.1 GI:13161041
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REFERENCE
1 (bases 1 to 3815)
Lyons,R.J., Deane,R., Lynch,D.K., Ye,Z.S., Sanderson,G.M.,
Eyre,H.J., Sutherland,G.R. and Daly,R.J.
Identification of a novel human tankyrase through its interaction
with the adaptor protein Grb14
J. Biol. Chem. 276 (20), 17172-17180 (2001)
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2 (bases 1 to 3815)
Lyons,R.J., Deane,R., Lynch,D.K., Ye,Z.-S.J., Sanderson,G.M.,
Eyre,H.J., Sutherland,G.R. and Daly,R.J.
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VERSION AX062241.1 GI:12540142
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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AUTHORS Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.
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Query Match 89.2%; Score 3387.2; DB 2; Length 4127;
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Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
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Db	1228	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTGTGTTGAAGCAATGAAAGCAAGGT	1287

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KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.
TITLE Tankyrase2 materials and methods
JOURNAL Patent: WO 0100849-A 106 04-JAN-2001;
ICOS CORPORATION (US)
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LOCUS Sequence 134 from Patent WO0100849.
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ACCESSION AX062275
VERSION AX062275.1 GI:12540176
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Christenson, E., Denaggio, A. J., Goldman, P. S. and Mcelligott, D. L.
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JOURNAL Patent: WO 0100849-A 134 04-JAN-2001;
ICOS CORPORATION (US)
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DEFINITION	

ACCESSION	AX062273
VERSION	AX062273.1 GI:12540174
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	Hominidae; Homo.
REFERENCE	1
AUTHORS	Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.
TITLE	Tankyrase2 materials and methods
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DEFINITION Sequence 556 from patent US 6783969.
ACCESSION AR578380
VERSION AR578380.1 GI:56581176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 5075)
AUTHORS Tang,Y.T., Goodrich,R.W., Asundi,V. and Drmanac,R.T.
TITLE Cathepsin V-like polypeptides
JOURNAL Patent: US 6783969-A 556 31-AUG-2004;
Nuvelo, Inc.; Sunnyvale, CA
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DEFINITION AF264912
ACCESSION AF264912.1 GI:12005975
VERSION
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Hominidae; Homo.
1 (bases 1 to 5810)
Kulmov, A.N., Kuprash, D.V., Petrov, V.N., Vdovichenko, K.K.,
Scanlan, M.J., Jongeneel, C.V., Lagarkova, M.A. and Nedospasov, S.A.
Cloning and characterization of TNKL, a member of tankyrase gene
family
Genes Immun. 2 (1), 52-55 (2001)
11294570
PUBMED
2 (bases 1 to 5810)
Kulmov, A.N., Kuprash, D.V., Petrov, V.N., Vdovichenko, K.K.,
Kashkarova, U.A., Boltchenko, V.E., Nedospasov, S.A. and
Lagarkova, M.A.
Direct Submission
Submitted (08-MAY-2000) Laboratory of Molecular Immunology, A.N.
Belozersky Institute of Physico-Chemical Biology, Moscow State
University, Moscow 119899, Russia
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DEFINITION Sequence 11 from patent US 6794501.
ACCESSION AR584137
VERSION AR584137.1 GI:56622263
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
AUTHORS Chen, Y.-I., Old, L.J., Scanlan, M.J. and Stockert, E.
TITLE Colon cancer antigen panel
JOURNAL Patent: US 6794501-A 11 21-SEP-2004;
Ludwig Institute for Cancer Research and Cornell Research
Foundation, Inc.; New York, NY
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Best Local Similarity 99.9%; Pred. No. 0;
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC

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Searched: 5244920 seqs, 3486124231 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1

AAA91487

ID AAA91487 standard; DNA; 3797 BP.

XX

AC AAA91487;

XX

DT 06-AUG-2001 (first entry)

XX

DE Tankyrase homologue isotype 1 coding sequence.

XX

Tankyrase homologue isotype 1; TaHo-1; TaHo-2; cell proliferation;

KW cell cycle protein; cell cycle associated disorder; cancer; gene mapping;

KX chromosome mapping; gene therapy; vaccine; ds.

XX

OS Unidentified.

XX

PH Key Location/Qualifiers

CDS 404..3706

FT /*tag= a

FT /partial

FT /product= "TaHo1"

FT /note= "Tankyrase homologue isotype 1; No start codon

FT given"

XX

PN WO200130987-A2.

XX

PD 03-MAY-2001.

 XX || PF | 25-OCT-2000; 2000WO-US041528. |
PR	25-OCT-1999; 99US-00427154.
XX	(RIGE-) RIGEL PHARM INC.
PA	Luo Y, Chan E, Xu X, Huang B;
PI	WPI; 2001-300503/31.
XX	P-PSDB; AAY97748.
DR	Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing
XX	or preventing cell proliferation in cells, and for diagnosing, treating

PT or preventing cell cycle associated disorders such as cancer.

XX Claim 13; Fig 1; 63pp; English.

XX This sequence encodes the Tankyrase homologue isoform 1 (TaHo-1) protein
CC of the invention. The invention also relates to the TaHo-2 protein. The
CC TaHo proteins are useful for inducing or preventing cell proliferation in
CC cells, and in the study or treatment of conditions mediated by the cell
CC cycle proteins, such as to diagnose, treat or prevent cell cycle
CC associated disorders, preferably cancer. The TaHo coding sequences are
CC useful as hybridisation probes, in chromosome and gene mapping and in the
CC generation of anti-sense DNA and RNA. The coding sequences are also
CC useful for the preparation of TaHo, for generating either transgenic
CC animals or knock out animals which, in turn, are useful in a development
CC and screening of therapeutically useful agents, in gene therapy, as
CC vaccine, and for construction of hybridisation probes for mapping the
CC gene which encodes TaHo and for the genetic analysis of individuals with
CC genetic disorders. The TaHo proteins, and their coding sequences are
CC useful in screening assays

XX SQ Sequence 3797 BP; 1153 A; 732 C; 850 G; 1062 T; 0 U; 0 Other;

Query Match 100.0%; Score 3797; DB 4; Length 3797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 AGACAAATATTAGCTGTGAGCAGATCTTTTGTGCTTCTGTAGTCCCGAGTTTAG 120
Qy 121 CAGAAACATCTGTGAGATAGATGTGGGAAGGAATTTCTAGCAAGAGTTTGTGACATGTA 180
Db 121 CAGAAACATCTGTGAGATAGATGTGGGAAGGAATTTCTAGCAAGAGTTTGTGACATGTA 180
Qy 181 TCATAAGGTTGTGATTACATATTAAAGTTTATATCTTTGAAACATCTGAAATGTATACA 240
Db 181 TCATAAGGTTGTGATTACATATTAAAGTTTATATCTTTGAAACATCTGAAATGTATACA 240
Qy 241 TACTAAATATGCAGACTCTATTGTAGATGAGAAACATTTGAACTTTGAGCTTTCAGTC 300
Db 241 TACTAAATATGCAGACTCTATTGTAGATGAGAAACATTTGAACTTTGAGCTTTCAGTC 300
Qy 301 ACTTATTTTGTATTCTTTCTTTGAGGTTAGCAGTAGTACACCCAGGCAGCTGCTTAGGT 360
Db 301 ACTTATTTTGTATTCTTTCTTTGAGGTTAGCAGTAGTACACCCAGGCAGCTGCTTAGGT 360
Qy 361 ACCACTGCTGTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTGGCGGGAAGA 420
Db 361 ACCACTGCTGTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTGGCGGGAAGA 420
Qy 421 CGTAGTTGAAATATTTGCTTCAGATGTGCAAGTGTCCNAGCAGCTGATGATGGGGCCT 480
Db 421 CGTAGTTGAAATATTTGCTTCAGATGTGCAAGTGTCCNAGCAGCTGATGATGGGGCCT 480
Qy 481 TATTCCCTCTTCATTAATGATGCTCTTTTGGTCATGCTGAGTAGTCAATCTCTTTTGGC 540
Db 481 TATTCCCTCTTCATTAATGATGCTCTTTTGGTCATGCTGAGTAGTCAATCTCTTTTGGC 540
Qy 541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATCTCTCTCCATGAAGCTGC 600
Db 541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATCTCTCTCCATGAAGCTGC 600
Qy 601 AATTAAAGGAAGATTGATTTGCTTGCATGCTGTTACAGCAGTGGAGCTGAGCCAAACAT 660
Db 601 AATTAAAGGAAGATTGATTTGCTTGCATGCTGTTACAGCAGTGGAGCTGAGCCAAACAT 660
Qy 661 CCGAAATACAGATGGAAGGACGAGATTTGGATTTTGTAGCAGATCCATCTGCCAAGGAGTGT 720
Db 661 CCGAAATACAGATGGAAGGACGAGATTTGGATTTTGTAGCAGATCCATCTGCCAAGGAGTGT 720

Qy 721 TACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCACGAGAGTGGCAATGAAGAAA 780
Db 721 TACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCACGAGAGTGGCAATGAAGAAA 780
Qy 781 AATGATGGCTCTACTACACCATTTAAATGTCAACTGCCACGCAAGTGTATGCGAAGATGC 840
Db 781 AATGATGGCTCTACTACACCATTTAAATGTCAACTGCCACGCAAGTGTATGCGAAGATGC 840
Qy 841 AACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTTACTGCA 900
Db 841 AACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTTACTGCA 900
Qy 901 ACATGAGAGCTGATGTCATGCTTAAAGTAAAGTGTGCTGCTGATCATTAACAATGCTG 960
Db 901 ACATGAGAGCTGATGTCATGCTTAAAGTAAAGTGTGCTGCTGATCATTAACAATGCTG 960
Qy 961 TTCTTATGGTCAATTTATGAAGTAACTGAACCTTTTGGTCAAGCATGGTCTGTGTAATGC 1020
Db 961 TTCTTATGGTCAATTTATGAAGTAACTGAACCTTTTGGTCAAGCATGGTCTGTGTAATGC 1020
Qy 1021 AATGGACTTTGTGGCAATTTCACTCTCTTCATGAGGCAAGTCTTAAAGAACAGGGTTGAAGT 1080
Db 1021 AATGGACTTTGTGGCAATTTCACTCTCTTCATGAGGCAAGTCTTAAAGAACAGGGTTGAAGT 1080
Qy 1081 ATGTTCTCTCTCTTAAAGTTATGCTGAGAGCCCAACTGCTCAATTTGTCAATATAAAG 1140
Db 1081 ATGTTCTCTCTCTTAAAGTTATGCTGAGAGCCCAACTGCTCAATTTGTCAATATAAAG 1140
Qy 1141 TGCTATAGACTGGCTCCACACCCACAGTAAAGAAAGATTAGCATATGAATTTAAAGG 1200
Db 1141 TGCTATAGACTGGCTCCACACCCACAGTAAAGAAAGATTAGCATATGAATTTAAAGG 1200
Qy 1201 CCATCTGCTGCTGCAAGCTGCAAGAGAGCTGATGTTTACTCGAATCAAAAACATCTCTC 1260
Db 1201 CCATCTGCTGCTGCAAGCTGCAAGAGAGCTGATGTTTACTCGAATCAAAAACATCTCTC 1260
Qy 1261 TCTGGAATGGTGAATTTCAAGCATCTCTCAACACATGAAACAGCATTTGCTGCTGTC 1320
Db 1261 TCTGGAATGGTGAATTTCAAGCATCTCTCAACACATGAAACAGCATTTGCTGCTGTC 1320
Qy 1321 TGCAATCTCCATATCCCAAGAAAGCAAAATATGTGAACTGTTGCTTAAGAAAGAGCATA 1380
Db 1321 TGCAATCTCCATATCCCAAGAAAGCAAAATATGTGAACTGTTGCTTAAGAAAGAGCATA 1380
Qy 1381 CATCAATGAAAGACTAAAGAAATTTCTTGAATCTCTCTGCAAGTGGCATCTGAGAAAGCTCA 1440
Db 1381 CATCAATGAAAGACTAAAGAAATTTCTTGAATCTCTCTGCAAGTGGCATCTGAGAAAGCTCA 1440
Qy 1441 TAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGATAATCT 1500
Db 1441 TAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGATAATCT 1500
Qy 1501 TGGTCAGACTTCTCTACACAGAGCTGATATTTGGTGTCTCATCAAACTGCGCCCTACT 1560
Db 1501 TGGTCAGACTTCTCTACACAGAGCTGATATTTGGTGTCTCATCAAACTGCGCCCTACT 1560
Qy 1561 CCTGAGCTATGGGTGATCCTTAAATTTATCCCTTCAAGGCTTTTACTGCTTTACAGAT 1620
Db 1561 CCTGAGCTATGGGTGATCCTTAAATTTATCCCTTCAAGGCTTTTACTGCTTTACAGAT 1620
Qy 1621 GGGAAATGAAATGTACAGCAATCTCTCAAGAGGATATCTCATTTAGGTAATTCAGAGGC 1680
Db 1621 GGGAAATGAAATGTACAGCAATCTCTCAAGAGGATATCTCATTTAGGTAATTCAGAGGC 1680
Qy 1681 AGACAGACAAATTTGCTGGAAGCTGCAAGAGTGTGAAACTGTGAAAAAATCTGTG 1740
Db 1681 AGACAGACAAATTTGCTGGAAGCTGCAAGAGTGTGAAACTGTGAAAAAATCTGTG 1740
Qy 1741 TACTGTTTCAAGATGTCAGAGACATTTGAAGGGGCTGAGTCTACACACCTTCATTT 1800
Db 1741 TACTGTTTCAAGATGTCAGAGACATTTGAAGGGGCTGAGTCTACACACCTTCATTT 1800

QY 1801 TGCAGCTGGGTATACAGAGTGTCCGTGGTGGAAATATCTGTACAGCATGGAGCTGATGT 1860
DB 1801 TGCAGCTGGGTATACAGAGTGTCCGTGGTGGAAATATCTGTACAGCATGGAGCTGATGT 1860
QY 1861 GCATGCTAAAGATAAAGGAGGCTTGTACCTTTTGCACAATGATGTTCTTTATGGACATTA 1920
DB 1861 GCATGCTAAAGATAAAGGAGGCTTGTACCTTTTGCACAATGATGTTCTTTATGGACATTA 1920
QY 1921 TGAAGTTCGAGAACTTCTTTGTAAACATGGAGCAGTAGTAAATGATGAGCTGATTTATGGAA 1980
DB 1921 TGAAGTTCGAGAACTTCTTTGTAAACATGGAGCAGTAGTAAATGATGAGCTGATTTATGGAA 1980
QY 1981 ATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTTGCACAACTTCTGCT 2040
DB 1981 ATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTTGCACAACTTCTGCT 2040
QY 2041 CCAGCATGGTGAGACCCCTACCAAAAAAACAAGGATGGAATATCTCTTTGGATCTTGT 2100
DB 2041 CCAGCATGGTGAGACCCCTACCAAAAAAACAAGGATGGAATATCTCTTTGGATCTTGT 2100
QY 2101 TAAAGATGGAGATACAGATATTTCAAGATCTCTTAGGGGAGATGAGCTTTGCTAGATGC 2160
DB 2101 TAAAGATGGAGATACAGATATTTCAAGATCTCTTAGGGGAGATGAGCTTTGCTAGATGC 2160
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DB 2161 TGCCAAAGAGGGTGTGTTAGCCAGAGTGAAGAGTTGTCTCTCTGATAATGTAAATTTG 2220
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DB 2221 CCGGATACCCAAAGCAGACATTTCAACCTTTTACATTTAGCAGCTGTTTATAATTT 2280
QY 2281 AGAAGTTCGAGATATTTGTTTACACCGAGCTGATGTAATGCCAAGCAAGGAGG 2340
DB 2281 AGAAGTTCGAGATATTTGTTTACACCGAGCTGATGTAATGCCAAGCAAGGAGG 2340
QY 2341 ACTTATTCCTTTACATATGAGCATCTTACGGGATGATGATGAGCAGCTCTACTAAT 2400
DB 2341 ACTTATTCCTTTACATATGAGCATCTTACGGGATGATGATGAGCAGCTCTACTAAT 2400
QY 2401 AAAGTATATGATGTGTCATATGCCAGCAAAATGGGCTTTTACACCTTTTGCACGAAGC 2460
DB 2401 AAAGTATATGATGTGTCATATGCCAGCAAAATGGGCTTTTACACCTTTTGCACGAAGC 2460
QY 2461 AGCCCAAGAGGAGCAACACAGCTTTGCTGCTTGTGCTAGCCCATGAGCTGACCCGAC 2520
DB 2461 AGCCCAAGAGGAGCAACACAGCTTTGCTGCTTGTGCTAGCCCATGAGCTGACCCGAC 2520
QY 2521 TCTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTTACGGGATGATGTCAGGCG 2580
DB 2521 TCTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTTACGGGATGATGTCAGGCG 2580
QY 2581 TCTTCTGACAGAGCATGCCCCCATCTGCTCTGCTTGTGCTTGTGCTAGCCCATGAGCTGCT 2640
DB 2581 TCTTCTGACAGAGCATGCCCCCATCTGCTCTGCTTGTGCTTGTGCTAGCCCATGAGCTGCT 2640
QY 2641 CAATGGTGTGAGAGCCAGGAGCACTGAGATGCTCTCTCTTTCAGGTCATCTAGGCC 2700
DB 2641 CAATGGTGTGAGAGCCAGGAGCACTGAGATGCTCTCTCTTTCAGGTCATCTAGGCC 2700
QY 2701 ATCAAGCCTTTCTGAGCAGCAGCTTCTTGACAACTTATCTGGAGTGTGTTTTCAGAACTGTC 2760
DB 2701 ATCAAGCCTTTCTGAGCAGCAGCTTCTTGACAACTTATCTGGAGTGTGTTTTCAGAACTGTC 2760
QY 2761 TTCAGTAGTATGTTCAAGTGAAACAGAGGGTCTTCCAGTTTGGAGAAAAAGGAGTTCC 2820
DB 2761 TTCAGTAGTATGTTCAAGTGAAACAGAGGGTCTTCCAGTTTGGAGAAAAAGGAGTTCC 2820
QY 2821 AGGAGTAGATTTAGCATTAATCAATTCGTAAGGATCTTGGACTTGGACCTTAATGGA 2880
DB 2821 AGGAGTAGATTTAGCATTAATCAATTCGTAAGGATCTTGGACTTGGACCTTAATGGA 2880
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DB 2881 TATATTTGAGAGAGAAACAGATCACTTTTGGATGTATTAGTTGAGATGGGGCACAGGAGCT 2940
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DB 2941 GAAGGAGATTGGAAATCAATGCTTATGACATAGGCACAACTAATTAAGAGATCGAGAG 3000
QY 3001 ACTTATCTCCGGACAAACAAAGTCTTAAACCCATATTTAACTTTGAACACCTCTGGTAGTGG 3060
DB 3001 ACTTATCTCCGGACAAACAAAGTCTTAAACCCATATTTAACTTTGAACACCTCTGGTAGTGG 3060
QY 3061 AACAAATTTATAGATCTGCTCTCTGATGATTAAGAGTTTCAGTCTGTGGAGGAAGAGAT 3120
DB 3061 AACAAATTTATAGATCTGCTCTCTGATGATTAAGAGTTTCAGTCTGTGGAGGAAGAGAT 3120
QY 3121 GCAAAAGTACAGTTCCGAGACACAGAGATGGAGTGCATGCGAGGTGGAATCTTCAACAGATA 3180
DB 3121 GCAAAAGTACAGTTCCGAGACACAGAGATGGAGTGCATGCGAGGTGGAATCTTCAACAGATA 3180
QY 3181 CAATATTTCTCAAGATTCAGAAAGTGTGTAACAAAGAACTATGGGAAAGATACACTCACCG 3240
DB 3181 CAATATTTCTCAAGATTCAGAAAGTGTGTAACAAAGAACTATGGGAAAGATACACTCACCG 3240
QY 3241 GAGAAAAAGAGTTTCTCAAGAAAAACCAACCATGCCAATGAAACGAATGCTTATTTATGG 3300
DB 3241 GAGAAAAAGAGTTTCTCAAGAAAAACCAACCATGCCAATGAAACGAATGCTTATTTATGG 3300
QY 3301 GTCTCTCTTTGTGAATGCAATTTATCCAAAGGCTTTGATGAAAGGCGATGCTACATAGG 3360
DB 3301 GTCTCTCTTTGTGAATGCAATTTATCCAAAGGCTTTGATGAAAGGCGATGCTACATAGG 3360
QY 3361 TGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACTCTTCCAAAGCAATCAATATGT 3420
DB 3361 TGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACTCTTCCAAAGCAATCAATATGT 3420
QY 3421 ATATGGAATTTGGAGAGGTAATGCTGCTTCCAGTTTCAAAAGACAGATCTTCTTACATTTG 3480
DB 3421 ATATGGAATTTGGAGAGGTAATGCTGCTTCCAGTTTCAAAAGACAGATCTTCTTACATTTG 3480
QY 3481 CCACAGCAGCTGCTCTTTTGGCGGGTAACTTGGGAAAGTCTTCTGCGAGTTTCAGTGC 3540
DB 3481 CCACAGCAGCTGCTCTTTTGGCGGGTAACTTGGGAAAGTCTTCTGCGAGTTTCAGTGC 3540
QY 3541 AATGAAATGSCAATCTCTCTCCAGGTCATCACTCAGTCACTGCTAGGCCCCAGTGTAAA 3600
DB 3541 AATGAAATGSCAATCTCTCTCCAGGTCATCACTCAGTCACTGCTAGGCCCCAGTGTAAA 3600
QY 3601 TGGCCTAGCAATTAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCTGAGTATTT 3660
DB 3601 TGGCCTAGCAATTAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCTGAGTATTT 3660
QY 3661 AATTACTTACAGATTATGAGGCTGAAAGTATGCTGATGATGATTAATAGTATTTTAAAG 3720
DB 3661 AATTACTTACAGATTATGAGGCTGAAAGTATGCTGATGATGATTAATAGTATTTTAAAG 3720
QY 3721 AAACCTAATTCACCTGAACCTTAAATATCAAAAGCAGAGTGGCTCTACGTTTTTACTCCT 3780
DB 3721 AAACCTAATTCACCTGAACCTTAAATATCAAAAGCAGAGTGGCTCTACGTTTTTACTCCT 3780
QY 3781 TTGCTGAAAAAATAA 3797
DB 3781 TTGCTGAAAAAATAA 3797

RESULT 2

ABQ77066

ID ABQ77066 standard; DNA; 3797 BP.

XX ABQ77066;

AC ABQ77066;

XX 08-APR-2003 (first entry)

DT 08-APR-2003 (first entry)

XX Tankyrase H isotype 1 TaHo-1 DNA from clone TH-1.

DE

XX Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-1;
KW TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
KW cell cycle related disorder; poly ADP-ribose polymerase; PARP; ds.
XX Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 404..3706
FT /*tag= a
FT /product= "TaHo-1"
FT /partial
FT /note= "No start codon given"
XX
FN WO200286170-A1.
XX
XX 31-OCT-2002.
XX
XX 25-APR-2002; 2002WO-US013185.
XX
XX 25-APR-2001; 2001US-00843159.
XX (RIGE-) RIGEL PHARM INC.
XX
XX Luo Y, Chan E, Xu X, Huang B, Ososovskaya V;
XX
XX WPI; 2003-093158/08.
DR P-PSDB; ABG73730.
XX
XX New recombinant nucleic acid encoding a cell cycle protein, useful for
PT diagnosing and treating a cell cycle related disorder, e.g. cancer.
XX
XX Claim 13; Fig 1A-B; 90pp; English.
XX
XX This invention describes a novel recombinant nucleic acid encoding the
CC cell cycle protein TaHo, a tankyrase H isoform. The products of the
CC invention have cytostatic and immunostimulant activity and can be used
CC for gene therapy and in vaccines. The cell cycle protein TaHo and the
CC nucleic acid encoding the protein are useful for diagnosing and treating
CC a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
CC tumour cell. The methods are useful for screening for a bioactive agent
CC capable of binding to a cell cycle protein tankyrase H, or a bioactive
CC agent capable of modulating a cell cycle protein tankyrase H or PARP
CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
CC inducing an immune response against the cell cycle proteins. This
CC sequence encodes the tankyrase H isoform 1, TaHo-1, isolated from clone
CC TH-1 which is described in the disclosure of the invention
XX
XX Sequence 3797 BP; 1153 A; 732 C; 850 G; 1062 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 3797; DB 8; Length 3797;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CTTTGAGACACTGGATTTCATCTTTTGGCTGGGGTAACTCTCTGTGCTCACTACAT 60
XX
XX 1 CTTTGAGACACTGGATTTCATCTTTTGGCTGGGGTAACTCTCTGTGCTCACTACAT 60
XX
XX 61 AGACAAATATTAGCTGTGAGCAGATCTTTTGTGCTTCTGTAGTCCCGCAGTTTAG 120
XX
XX 61 AGACAAATATTAGCTGTGAGCAGATCTTTTGTGCTTCTGTAGTCCCGCAGTTTAG 120
XX
XX 121 CAGAAACATTCTGTGAGATAGATGGGAAAGGAATCTAGCAAGAGTTTTGTGCACGTGA 180
XX
XX 121 CAGAAACATTCTGTGAGATAGATGGGAAAGGAATCTAGCAAGAGTTTTGTGCACGTGA 180
XX
XX 181 TCATAAGGTTGTGATTACATATTAGTTTTATCTTTTATCTTGAACATCTGAAATGTATACA 240
XX
XX 181 TCATAAGGTTGTGATTACATATTAGTTTTATCTTTTATCTTGAACATCTGAAATGTATACA 240
XX
XX 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTGAACTTTTGAGCTTTTCAGTC 300
XX
XX 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTGAACTTTTGAGCTTTTCAGTC 300

Qy 301 ACTTATTTTGTATCTTTCTTTGAGGTTAGCAGTAGTACCAACCAAGGCACCTGCTAGGT 360
Db 301 ACTTATTTTGTATCTTTCTTTGAGGTTAGCAGTAGTACCAACCAAGGCACCTGCTAGGT 360
Qy 361 ACCACTGCTGCTTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAAGGTTTGGCGGGAAGA 420
Db 361 ACCACTGCTGCTTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAAGGTTTGGCGGGAAGA 420
Qy 421 CGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGTCCAAAGCAGCTGATGATGGGGCCT 480
Db 421 CGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGTCCAAAGCAGCTGATGATGGGGCCT 480
Qy 481 TATTCCTCTTCATTAATGCTATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCTTTTGGC 540
Db 481 TATTCCTCTTCATTAATGCTATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCTTTTGGC 540
Qy 541 ACATGGTGACAGACCCCAATGCTCGAGATAATGGAAATTAATCTCTCTCCATGAAGCTGC 600
Db 541 ACATGGTGACAGACCCCAATGCTCGAGATAATGGAAATTAATCTCTCTCCATGAAGCTGC 600
Qy 601 AATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTTACAGCATGAGCTGAGCCAAACCAT 660
Db 601 AATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTTACAGCATGAGCTGAGCCAAACCAT 660
Qy 661 CCGAAATACAGATGGAAAGGACAGCATTTGGATTTTAGCAGATCCATCTGCCAAGCAGTGT 720
Db 661 CCGAAATACAGATGGAAAGGACAGCATTTGGATTTTAGCAGATCCATCTGCCAAGCAGTGT 720
Qy 721 TACTGGTGAATATAAGAAAGATGAACCTCTTAGAAAGTGCCAGGAGTGGCAATGAAGAAA 780
Db 721 TACTGGTGAATATAAGAAAGATGAACCTCTTAGAAAGTGCCAGGAGTGGCAATGAAGAAA 780
Qy 781 AATGATGGCTTACTCACACCATTTAAATGTCACTGCCACGCAAGTAGTGACGAAAGTGC 840
Db 781 AATGATGGCTTACTCACACCATTTAAATGTCACTGCCACGCAAGTAGTGACGAAAGTGC 840
Qy 841 AACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGTTGTACAGCTGTTTACTGCA 900
Db 841 AACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGTTGTACAGCTGTTTACTGCA 900
Qy 901 ACATGAGAGCTGATGCTCCATCTAAAGATAAAGGTGATCTGTGTACCATTTACACAATGCC 960
Db 901 ACATGAGAGCTGATGCTCCATCTAAAGATAAAGGTGATCTGTGTACCATTTACACAATGCC 960
Qy 961 TTCTTTATGGTCAATTTATGAAGTAACTGAACTTTTGGTCAAGCATGGTGTGCTGTAAATGC 1020
Db 961 TTCTTTATGGTCAATTTATGAAGTAACTGAACTTTTGGTCAAGCATGGTGTGCTGTAAATGC 1020
Qy 1021 AATGGACTTGTGGCAATTTCACTCTCTTCATGAGGAGCTTCTAAGAACAGGGTTGAGT 1080
Db 1021 AATGGACTTGTGGCAATTTCACTCTCTTCATGAGGAGCTTCTAAGAACAGGGTTGAGT 1080
Qy 1081 ATGTTCTCTTCTCTTAAGTTATGGTGCAGACCCCAACACTGCTCAATTTGTCAATATAAAG 1140
Db 1081 ATGTTCTCTTCTCTTAAGTTATGGTGCAGACCCCAACACTGCTCAATTTGTCAATATAAAG 1140
Qy 1141 TGCTATAGACTTGGCTCCACACCACTGTTAAAGAAAGATTAGCATATGAATTTAAAGG 1200
Db 1141 TGCTATAGACTTGGCTCCACACCACTGTTAAAGAAAGATTAGCATATGAATTTAAAGG 1200
Qy 1201 CCATCTGTTGTCAGAGCTGCAAGAGAGCTGATGTTTACTCGAATCAAAAACATCTCTC 1260
Db 1201 CCATCTGTTGTCAGAGCTGCAAGAGAGCTGATGTTTACTCGAATCAAAAACATCTCTC 1260
Qy 1261 TCTGGAATGGTGAATTTCAAGCATCTCAAAACATGAACACAGCATTTGCAATTTGTGCTGC 1320
Db 1261 TCTGGAATGGTGAATTTCAAGCATCTCAAAACATGAACACAGCATTTGCAATTTGTGCTGC 1320
Qy 1321 TGCAATCTCCATATCCCAAGAAAGCAAAATATGTGAATCTGTGTAAAGAAAGGAGCAAA 1380
Db 1321 TGCAATCTCCATATCCCAAGAAAGCAAAATATGTGAATCTGTGTAAAGAAAGGAGCAAA 1380

Qy	1381	CATCAATGAAAGACTAAAGAAATCTTTGACCTCTCTGCACTGTGCATCTGAGAAAGCTCA	1440
Db	1381	CATCAATGAAAGACTAAAGAAATCTTTGACCTCTCTGCACTGTGCATCTGAGAAAGCTCA	1440
Qy	1441	TAATGATGTTCTTGAAGTAGTGGTGAACACATGAAGCAAGAGTTAACTCTCTGGATATCT	1500
Db	1441	TAATGATGTTCTTGAAGTAGTGGTGAACACATGAAGCAAGAGTTAACTCTCTGGATATCT	1500
Qy	1501	TGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCATCTACAAACCTGCCGCCTACT	1560
Db	1501	TGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCATCTACAAACCTGCCGCCTACT	1560
Qy	1561	CCTGAGCTATGGGTGTGATCCTTAACATTTATATCCCTTACAGGGCTTTACTGCTTTACAGAT	1620
Db	1561	CCTGAGCTATGGGTGTGATCCTTAACATTTATATCCCTTACAGGGCTTTACTGCTTTACAGAT	1620
Qy	1621	GGGAAATGAAATGCTACAGCAACTCTCCAAAGAGGGTATCTCATTAGTGGTAAATTCAGAGGC	1680
Db	1621	GGGAAATGAAATGCTACAGCAACTCTCCAAAGAGGGTATCTCATTAGTGGTAAATTCAGAGGC	1680
Qy	1681	AGACAGACAATTTGCTTGGAAAGCTGCAAAAGGCTGGAGATGTGCAAACTGTAAAAAACTGTG	1740
Db	1681	AGACAGACAATTTGCTTGGAAAGCTGCAAAAGGCTGGAGATGTGCAAACTGTAAAAAACTGTG	1740
Qy	1741	TACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCAGTCTACACACTTCAATTT	1800
Db	1741	TACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCAGTCTACACACTTCAATTT	1800
Qy	1801	TGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGATATCTGCTACAGCATGGAGCTGATGT	1860
Db	1801	TGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGATATCTGCTACAGCATGGAGCTGATGT	1860
Qy	1861	GCATGCTAAAGATAAAGAGAGCCTTGTACCTTTGCACAAATGCATGTTCTTTATGGACAATTA	1920
Db	1861	GCATGCTAAAGATAAAGAGAGCCTTGTACCTTTGCACAAATGCATGTTCTTTATGGACAATTA	1920
Qy	1921	TGAAGTTGCAGAACTTTCTTGTAAACATGAGAGCAGTAGTAAATGTAGCTGANTTATGGAA	1980
Db	1921	TGAAGTTGCAGAACTTTCTTGTAAACATGAGAGCAGTAGTAAATGTAGCTGANTTATGGAA	1980
Qy	1981	ATTATACACCTTTTACATGAAGCAGCAGCAAAAGGAATAATGCAATTTTGGCAAACTTCGTCT	2040
Db	1981	ATTATACACCTTTTACATGAAGCAGCAGCAAAAGGAATAATGCAATTTTGGCAAACTTCGTCT	2040
Qy	2041	CCAGCATGGTGCAGACCTTACCAAAAAAACAAGGGATGGAAATACTCCTTTGGATCTTGT	2100
Db	2041	CCAGCATGGTGCAGACCTTACCAAAAAAACAAGGGATGGAAATACTCCTTTGGATCTTGT	2100
Qy	2101	TAAAGATGGAGATACAGATATTTCAAGATCTGCTTTAGGGAGATGCACTTTGTAGATGC	2160
Db	2101	TAAAGATGGAGATACAGATATTTCAAGATCTGCTTTAGGGAGATGCACTTTGTAGATGC	2160
Qy	2161	TGCCAAGNAGGGTTGTTTAGCCAGAGTGAAGAAGTTGTCTTCTCCTGATTAATGTAAATTG	2220
Db	2161	TGCCAAGNAGGGTTGTTTAGCCAGAGTGAAGAAGTTGTCTTCTCCTGATTAATGTAAATTG	2220
Qy	2221	CCGCGATACCCAAGSGCAGACATTCAAACACCTTTACATTTAGCAGCTGGTTATAATAATTT	2280
Db	2221	CCGCGATACCCAAGSGCAGACATTCAAACACCTTTACATTTAGCAGCTGGTTATAATAATTT	2280
Qy	2281	AGAAAGTTGCAGAGTATTTGTTTAAACAACGGAGCTGTGAATGCCCAAGCAAAAGSAGG	2340
Db	2281	AGAAAGTTGCAGAGTATTTGTTTAAACAACGGAGCTGTGAATGCCCAAGCAAAAGSAGG	2340
Qy	2341	ACTTATTTCCCTTTTACATAATGCAGCATCTTACGGGCATGTAGATGTAGCAGCTCTACTAAT	2400
Db	2341	ACTTATTTCCCTTTTACATAATGCAGCATCTTACGGGCATGTAGATGTAGCAGCTCTACTAAT	2400
Qy	2401	AAAGTATAAATGCATGTGTCAATGCACGGAATAATGGCTTTTACACCTTTTGACCGAAGC	2460
Db	2401	AAAGTATAAATGCATGTGTCAATGCACGGAATAATGGCTTTTACACCTTTTGACCGAAGC	2460
Qy	2461	AGCCCAAAAGGGAGCAACACAGCTTTTGTGCTTTTGTGCTAGCCCATGGAGCTGACCCGAC	2520

Db	2461		AGCCAAAGGGACGAACA	CAGCTTTGCTTTGCTTTGCTTAGCCCATGGAGCTGACCCGAC	2520
Qy	2521	TC	TTAAAAATCAGGAAGGACAAAC	CACTTTTAGATTTTAGTTTCAGCGGATGATGTCAAGCGC	2580
Db	2521	TC	TTAAAAATCAGGAAGGACAAAC	CACTTTTAGATTTTAGTTTCAGCGGATGATGTCAAGCGC	2580
Qy	2581	TC	TTTGACAGCAGCCATGCCCCCA	CTGTCTGCGCCCTCTTTGTATACAAGCCTCAAGTGCT	2640
Db	2581	TC	TTTGACAGCAGCCATGCCCCCA	CTGTCTGCGCCCTCTTTGTATACAAGCCTCAAGTGCT	2640
Qy	2641	CAATGGTGTGAGAGCCAGGAGCC	CTGAGATGCTCTCTTCAGGTCCATCTAGCC	2700	
Db	2641	CAATGGTGTGAGAGCCAGGAGCC	CTGAGATGCTCTCTTCAGGTCCATCTAGCC	2700	
Qy	2701	ATCAAGCCTTTCTGCAGCCAGCAGT	CTTGACAACCTATCTGGGAGTTTTTCAGAACTGTC	2760	
Db	2701	ATCAAGCCTTTCTGCAGCCAGCAGT	CTTGACAACCTATCTGGGAGTTTTTCAGAACTGTC	2760	
Qy	2761	TTCAAGTATGTTCAAGTGGAA	CAGAGGTGCTTCAGTTGGAGAAAAGGAGTTCC	2820	
Db	2761	TTCAAGTATGTTCAAGTGGAA	CAGAGGTGCTTCAGTTGGAGAAAAGGAGTTCC	2820	
Qy	2821	AGGAGTAGATTTTAGCATAACT	CAATTCGTAAGGAATCTTTGGACTTGAGCACCTAATGGA	2880	
Db	2821	AGGAGTAGATTTTAGCATAACT	CAATTCGTAAGGAATCTTTGGACTTGAGCACCTAATGGA	2880	
Qy	2881	TATATTTGAGAGAGAACAGAT	CACCTTTGGATGTATTAGTTGAGATGGGCAACAAGGAGCT	2940	
Db	2881	TATATTTGAGAGAGAACAGAT	CACCTTTGGATGTATTAGTTGAGATGGGCAACAAGGAGCT	2940	
Qy	2941	GAAGGAGATGGAAATCAATGCT	TATGACATAGGCACAAACTAATTAAGAGGATCGAGAG	3000	
Db	2941	GAAGGAGATGGAAATCAATGCT	TATGACATAGGCACAAACTAATTAAGAGGATCGAGAG	3000	
Qy	3001	ACTTATCTCCGGACAAAGGTCT	TAAACCATTTAACTTTGAACACCTCTGCTAGTGG	3060	
Db	3001	ACTTATCTCCGGACAAAGGTCT	TAAACCATTTAACTTTGAACACCTCTGCTAGTGG	3060	
Qy	3061	AACAATTTTATAGATCTGTCT	CTGATGATAAGAGTTTCAGTCTGTGAGGAAGAGAT	3120	
Db	3061	AACAATTTTATAGATCTGTCT	CTGATGATAAGAGTTTCAGTCTGTGAGGAAGAGAT	3120	
Qy	3121	GCAAAGTACAGTTTCGAGAGC	ACAGAGATGAGGTCTATGAGGTGGAATCTTCAACAGATA	3180	
Db	3121	GCAAAGTACAGTTTCGAGAGC	ACAGAGATGAGGTCTATGAGGTGGAATCTTCAACAGATA	3180	
Qy	3181	CAATATTTCTCAAGATTCAGAA	GGTTTGTAACAAGAAACTATGGGAAAGATACACTCACCG	3240	
Db	3181	CAATATTTCTCAAGATTCAGAA	GGTTTGTAACAAGAAACTATGGGAAAGATACACTCACCG	3240	
Qy	3241	GAGAAAAGAAAGTTTCTCAAG	AAACCAACCATGCCAATGAAAGATGCTATTTCAATGG	3300	
Db	3241	GAGAAAAGAAAGTTTCTCAAG	AAACCAACCATGCCAATGAAAGATGCTATTTCAATGG	3300	
Qy	3301	GTCTCCTTTTGTGAATCAAT	TATCCAAAGGCTTTGATGAAAGGCATGCTACATAGG	3360	
Db	3301	GTCTCCTTTTGTGAATCAAT	TATCCAAAGGCTTTGATGAAAGGCATGCTACATAGG	3360	
Qy	3361	TGGTATGTTTGGAGCTGGCA	TTTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGT	3420	
Db	3361	TGGTATGTTTGGAGCTGGCA	TTTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGT	3420	
Qy	3421	ATATGGAATTTGGAGGAGT	ACTGGGTCCAGTTCAAAAGACAGATCTTGTGTACATTTG	3480	
Db	3421	ATATGGAATTTGGAGGAGT	ACTGGGTCCAGTTCAAAAGACAGATCTTGTGTACATTTG	3480	
Qy	3481	CCACAGGCAGCTGCTCTTTT	TCGGGGTAACTTTCTGAGTAAAGTCTTTCTCGAGTTCACTGC	3540	
Db	3481	CCACAGGCAGCTGCTCTTTT	TCGGGGTAACTTTCTGAGTAAAGTCTTTCTCGAGTTCACTGC	3540	
Qy	3541	AATGAAAATGGCAATTTCT	CTCTCCTCAGGTCACTCAGTCACTGGTAGGCCAGTGTAAT	3600	

Db 3541 AATGAAATGACACATCTCTCCAGGTCATCACTCACTCACTGAGGCCAGCTGTAAA 3600
 Qy 3601 TGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCTCGAGTATTT 3660
 Db 3601 TGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCTCGAGTATTT 3660
 Qy 3661 AATTACTTACAGATATGAGGCCCTGAAGGTATGTCGATGGATAAATAGTATTTTAAAG 3720
 Db 3661 AATTACTTACAGATATGAGGCCCTGAAGGTATGTCGATGGATAAATAGTATTTTAAAG 3720
 Qy 3721 AAATCAATTCACATGAACCTAAATCATCAAAAGCAGAGTGGCTCTACGTTTACTCCT 3780
 Db 3721 AAATCAATTCACATGAACCTAAATCATCAAAAGCAGAGTGGCTCTACGTTTACTCCT 3780
 Qy 3781 TTGCTGAAAAAANA 3797
 Db 3781 TTGCTGAAAAAANA 3797

RESULT 3
 ADH69414
 ID ADH69414 standard; DNA; 3797 BP.
 XX AC ADH69414;
 XX DT 25-MAR-2004 (first entry)
 XX DE Human tankyrase homologue isotype 1 (TaHo-1) DNA.
 XX KW Tankyrase H cell cycle protein; p21; gene therapy;
 XX KW bioactive agent screening; cancer; cytostatic; gene; human; ds.
 XX OS Homo sapiens.
 XX FH Key
 XX CDS Location/Qualifiers
 FT 404..3706
 FT /*tag= a
 FT /product= "Human tankyrase homologue isotype 1"
 FT /partial
 FT /note= "no start codon given"

US6617102-B1.
 09-SEP-2003.
 25-OCT-2000; 2000US-00696668.
 25-OCT-1999; 99US-00427154.
 (RIGE-) RIGEL PHARM INC.
 Luo Y, Chan E, Xu X, Huang B, Ossovekaya V;
 WPI: 2003-895391/82.
 P-PSDB; ADH69405.

Screening for a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21 for diagnosing or treating cancer by combining a tankyrase H cell cycle protein, a candidate bioactive agent and p21.

Disclosure; SEQ ID NO 1; 39pp; English.

The invention relates to a method for screening a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21. The invention is useful in gene therapy. The method is useful for screening for a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21 for preparing a composition for diagnosing or treating cancer. The present sequence is human tankyrase homologue isotype 1 (TaHo-1) DNA.

Sequence 3797 BP; 1153 A; 732 C; 850 G; 1062 T; 0 U; 0 Other;

Query Match 100.0%; Score 3797; DB 10; Length 3797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGAAGACACTGGATTTTCATATCTTTTGGCTGGGGTTATCTCTCTGTCTCTCACTACAT 60
 Db 1 CTTTGAAGACACTGGATTTTCATATCTTTTGGCTGGGGTTATCTCTCTGTCTCTCACTACAT 60
 Qy 61 AGACAAATATTAGCTGTGACAGATCTTTTGTGTTCTCTGTAGTCCCCAGTTTAAAG 120
 Db 61 AGACAAATATTAGCTGTGACAGATCTTTTGTGTTCTCTGTAGTCCCCAGTTTAAAG 120
 Qy 121 CAGAAACATTTCTGTGAGATAGATGTGGAAAGGAATTTCTAGCAAGAGTTTGTCACTGTA 180
 Db 121 CAGAAACATTTCTGTGAGATAGATGTGGAAAGGAATTTCTAGCAAGAGTTTGTCACTGTA 180
 Qy 181 TCATAAGGTTGTGATTTACATATTTAAGTTTATCTTTTGAAACATCTGAAATGTATACA 240
 Db 181 TCATAAGGTTGTGATTTACATATTTAAGTTTATCTTTTGAAACATCTGAAATGTATACA 240
 Qy 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTGAACTTTGAGCTTTCAGTC 300
 Db 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTGAACTTTGAGCTTTCAGTC 300
 Qy 301 ACTATTTTCTATTTCTTTCTTTGAGGTTAGCAGTAGTACCACCAAGCAGCTCTTAGGT 360
 Db 301 ACTATTTTCTATTTCTTTCTTTGAGGTTAGCAGTAGTACCACCAAGCAGCTCTTAGGT 360
 Qy 361 ACCACTGCTGCTTAGTGGAGAGTCCCTCTGCTGCTTTATCATTAAGGTTTGGCGCGAAAGA 420
 Db 361 ACCACTGCTGCTTAGTGGAGAGTCCCTCTGCTGCTTTATCATTAAGGTTTGGCGCGAAAGA 420
 Qy 421 CGTAGTTGAATATTTGCTTTCAGAAATGTGTGCAAGTGTCCAAAGCAGCTGATGATGAGGGCCT 480
 Db 421 CGTAGTTGAATATTTGCTTTCAGAAATGTGTGCAAGTGTCCAAAGCAGCTGATGATGAGGGCCT 480
 Qy 481 TATTCCTCTTCATTAATGCATGCTCTTTTGGCTCATGCTGAGTAGTCAATCTCTCTTTTGGC 540
 Db 481 TATTCCTCTTCATTAATGCATGCTCTTTTGGCTCATGCTGAGTAGTCAATCTCTCTTTTGGC 540
 Qy 541 ACATGTTGCAGACCCCAATGCTCGAGATAATTGGAATTTATCTCTCTCCATGAAGTGC 600
 Db 541 ACATGTTGCAGACCCCAATGCTCGAGATAATTGGAATTTATCTCTCTCCATGAAGTGC 600
 Qy 601 AATTAAGGAAAGATTTGATGTTTGCATTTGCTGTTTACAGATGGAGTGAGCCAAACCAT 660
 Db 601 AATTAAGGAAAGATTTGATGTTTGCATTTGCTGTTTACAGATGGAGTGAGCCAAACCAT 660
 Qy 661 CCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCCATCTGCCAAAGCAGTGT 720
 Db 661 CCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCCATCTGCCAAAGCAGTGT 720
 Qy 721 TACTGTTGAATATAAGAAAGATGAACCTCTTAGAAAGTCCAGGAGTGGCAATGAAGAAA 780
 Db 721 TACTGTTGAATATAAGAAAGATGAACCTCTTAGAAAGTCCAGGAGTGGCAATGAAGAAA 780
 Qy 781 AATGATGGCTCTACTACACATTAATGTCAACTGCCAGCAAGTAGTATGCGCAAGATGC 840
 Db 781 AATGATGGCTCTACTACACATTAATGTCAACTGCCAGCAAGTAGTATGCGCAAGATGC 840
 Qy 841 AACTCCATTACATTTGGCAGCAGGATATACAGAGTAAAGATTTCTACAGCTGTTTACTGCA 900
 Db 841 AACTCCATTACATTTGGCAGCAGGATATACAGAGTAAAGATTTCTACAGCTGTTTACTGCA 900
 Qy 901 ACATGGAGCTGATGTCCTCACTAAAGATAAAGGTGATCTGGTACCATTTACAAATGCCTG 960
 Db 901 ACATGGAGCTGATGTCCTCACTAAAGATAAAGGTGATCTGGTACCATTTACAAATGCCTG 960
 Qy 961 TTCTTATGGTCATTATGAAGTAACTGAACCTTTTGGTCAAGCATGGTCTGTGTAATGTC 1020
 Db 961 TTCTTATGGTCATTATGAAGTAACTGAACCTTTTGGTCAAGCATGGTCTGTGTAATGTC 1020
 Qy 1021 AATGCACTTTGTGGCAATTCACCTCTCTTCATGAGGAGCTTCTTAAGAACAGGGTTGAAGT 1080

Db 1021 AATGACCTTGCGCAATTCACCTCTCTTCATGAGCAGCTTCTAAGAACAGGGTTGAAGT 1080
Qy 1081 ATGTTCTCTTCTTAAGTTATGTTGTCAGACCCAAACACATGCTCAATTTGTCAATAAAG 1140
Db 1081 ATGTTCTCTTCTTAAGTTATGTTGTCAGACCCAAACACATGCTCAATTTGTCAATAAAG 1140
Qy 1141 TGCTATAGACTTGGCTCCACACACACAGTTAAAGAAAGATTAGCATATGAATTTAAAGG 1200
Db 1141 TGCTATAGACTTGGCTCCACACACACAGTTAAAGAAAGATTAGCATATGAATTTAAAGG 1200
Qy 1201 CCACTCGTTGTCGAAGCTGCGAGAGCTGATGTTACTCGAATCAAAAAACATCTCTC 1260
Db 1201 CCACTCGTTGTCGAAGCTGCGAGAGCTGATGTTACTCGAATCAAAAAACATCTCTC 1260
Qy 1261 TCTGAAATGTTGAATTTCAAGCATCTCTCAACACATGAACAGCATGTCATTGCTGTC 1320
Db 1261 TCTGAAATGTTGAATTTCAAGCATCTCTCAACACATGAACAGCATGTCATTGCTGTC 1320
Qy 1321 TGCACTCTCCATATCCAAAGAAAGCAAAATATGTGAATGTTGCTAAAGAAAGAGCAAA 1380
Db 1321 TGCACTCTCCATATCCAAAGAAAGCAAAATATGTGAATGTTGCTAAAGAAAGAGCAAA 1380
Qy 1381 CATCAATGAAAGACTAAAGAAATCTTGACTCTCTGCAAGTGGCATCTGAGAAAGCTCA 1440
Db 1381 CATCAATGAAAGACTAAAGAAATCTTGACTCTCTGCAAGTGGCATCTGAGAAAGCTCA 1440
Qy 1441 TAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGATAATCT 1500
Db 1441 TAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGATAATCT 1500
Qy 1501 TGGTCAGACTCTCTACACAGAGCTGCAATATGTTGTCATCTACAAACCTGCGGCTACT 1560
Db 1501 TGGTCAGACTCTCTACACAGAGCTGCAATATGTTGTCATCTACAAACCTGCGGCTACT 1560
Qy 1561 CCGTAGCTATGTTGATGCTTAAACATTAATATATATATATATATATATATATATATAT 1620
Db 1561 CCGTAGCTATGTTGATGCTTAAACATTAATATATATATATATATATATATATATATAT 1620
Qy 1621 GGGAAATGAAATGTTGAGTGTCTTAAAGAGGTTATCTCAATGAGGTTATCTCAATGAGG 1680
Db 1621 GGGAAATGAAATGTTGAGTGTCTTAAAGAGGTTATCTCAATGAGGTTATCTCAATGAGG 1680
Qy 1681 AGACAGACAAATGCTGGAAGCTGCAAGAGCTGAGATGTCGAAACCTGTAAAGAAACCTGTG 1740
Db 1681 AGACAGACAAATGCTGGAAGCTGCAAGAGCTGAGATGTCGAAACCTGTGTAAAGAAACCTGTG 1740
Qy 1741 TACTGTTTCAAGTGTCAATGTCAGAGACATTTGAAGGGGCTCAGTCTACACCACTTCATTT 1800
Db 1741 TACTGTTTCAAGTGTCAATGTCAGAGACATTTGAAGGGGCTCAGTCTACACCACTTCATTT 1800
Qy 1801 TGCAGCTGGTATAACAGAGTGTCCGTGGTGAATATCTGTCAGAGATGAGAGCTGATGT 1860
Db 1801 TGCAGCTGGTATAACAGAGTGTCCGTGGTGAATATCTGTCAGAGATGAGAGCTGATGT 1860
Qy 1861 GCATCTAAAGATAAAGAGGCTTGTACTCTTTGCAATGATGTCATCTTATGACATTTA 1920
Db 1861 GCATCTAAAGATAAAGAGGCTTGTACTCTTTGCAATGATGTCATCTTATGACATTTA 1920
Qy 1921 TGAAGTTGAGAACTTCTTTGTTAAACATGAGCAGTATGTTAATGAGCTGATTTATGGAA 1980
Db 1921 TGAAGTTGAGAACTTCTTTGTTAAACATGAGCAGTATGTTAATGAGCTGATTTATGGAA 1980
Qy 1981 ATTTACCTTTTACATGAAGCAGAGCAAGAAATATGAATTTTGAACCTTCTGCT 2040
Db 1981 ATTTACCTTTTACATGAAGCAGAGCAAGAAATATGAATTTTGAACCTTCTGCT 2040
Qy 2041 CCAGATGTTGAGACCTTACCAAAAACAGAGGATGGAATATCTCTTTGGATCTGT 2100
Db 2041 CCAGATGTTGAGACCTTACCAAAAACAGAGGATGGAATATCTCTTTGGATCTGT 2100
Qy 2101 TAAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGGAGATGAGCTTTGCTAGATGC 2160

Db 2101 TAAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGGAGATGAGCTTTGCTAGATGC 2160
Qy 2161 TGCCAAAGAGGGTTGTTTAGCCAGAGTGAAGAGTGTCTTCTCTCTGATATGTAATG 2220
Db 2161 TGCCAAAGAGGGTTGTTTAGCCAGAGTGAAGAGTGTCTTCTCTCTGATATGTAATG 2220
Qy 2221 CCGGATACCCAAAGCAGACATTTCAACACCTTTTACATTTAGCAGCTGTTATAAATTT 2280
Db 2221 CCGGATACCCAAAGCAGACATTTCAACACCTTTTACATTTAGCAGCTGTTATAAATTT 2280
Qy 2281 AGAAGTTGACAGATTTGTTTAAACACGAGCTGATGTGAATGCCAAGACAAAGAGG 2340
Db 2281 AGAAGTTGACAGATTTGTTTAAACACGAGCTGATGTGAATGCCAAGACAAAGAGG 2340
Qy 2341 ACTTATTCCTTTACATATGAGCATCTTACGCGCATGTAGATGTAGCAGCTCTACTAAT 2400
Db 2341 ACTTATTCCTTTACATATGAGCATCTTACGCGCATGTAGATGTAGCAGCTCTACTAAT 2400
Qy 2401 AAAGTATAATGCATGTGTCAATGCGACGACAAATGGGCTTTTCACACCTTTGACGAAAGC 2460
Db 2401 AAAGTATAATGCATGTGTCAATGCGACGACAAATGGGCTTTTCACACCTTTGACGAAAGC 2460
Qy 2461 AGCCCAAAAGGAGCAACACAGCTTTGTGCTTTGTGTAGCCCATGAGCTGACCCGAC 2520
Db 2461 AGCCCAAAAGGAGCAACACAGCTTTGTGCTTTGTGTAGCCCATGAGCTGACCCGAC 2520
Qy 2521 TCTTAAATCAGNAGGAGCAACACCTTTAGATTTAGTTTTCAGCGGATGATGTCAGCGC 2580
Db 2521 TCTTAAATCAGNAGGAGCAACACCTTTAGATTTAGTTTTCAGCGGATGATGTCAGCGC 2580
Qy 2581 TCTTCTGACAGCCATGCCCCCATCTGCTCTGCTCTTGTTCACAGCCCTCAAGTGTCT 2640
Db 2581 TCTTCTGACAGCCATGCCCCCATCTGCTCTGCTCTTGTTCACAGCCCTCAAGTGTCT 2640
Qy 2641 CAATGTTGTGAGAGCCAGAGGACCTGACAGATGCTCTCTTTCAGGTCATCTAGGCC 2700
Db 2641 CAATGTTGTGAGAGCCAGAGGACCTGACAGATGCTCTCTTTCAGGTCATCTAGGCC 2700
Qy 2701 ATCAAGCTTTCTCCAGCCAGCAGTCTTGACAACTTATCTGGAGTTTTCAGAACTGTC 2760
Db 2701 ATCAAGCTTTCTCCAGCCAGCAGTCTTGACAACTTATCTGGAGTTTTCAGAACTGTC 2760
Qy 2761 TTTCACTAGTTAGTTCAAGTGGAAACAGAGGCTGCTTCCAGTTTGGAGAAAAGAGGTTCC 2820
Db 2761 TTTCACTAGTTAGTTCAAGTGGAAACAGAGGCTGCTTCCAGTTTGGAGAAAAGAGGTTCC 2820
Qy 2821 AGGAGTAGATTTAGCATFAACTCAATTCGTAAGGAATCTTGGACCTTGAGACCTAATGGA 2880
Db 2821 AGGAGTAGATTTAGCATFAACTCAATTCGTAAGGAATCTTGGACCTTGAGACCTAATGGA 2880
Qy 2881 TATATTTGAGAGAGACAGATCACTTTTGGATGATTTAGTTGAGATGGGGCACAAGAGCT 2940
Db 2881 TATATTTGAGAGAGACAGATCACTTTTGGATGATTTAGTTGAGATGGGGCACAAGAGCT 2940
Qy 2941 GAAGGAGATTGGAATCAATGCTTATGGAATAGGACATAGGACAAACTAATTAAGGAGTCCAGAG 3000
Db 2941 GAAGGAGATTGGAATCAATGCTTATGGAATAGGACATAGGACAAACTAATTAAGGAGTCCAGAG 3000
Qy 3001 ACTTATCTCCGACAAAGGCTTTAAACCCATATTTAACTTTTGAACACCTCTGTTAGTGG 3060
Db 3001 ACTTATCTCCGACAAAGGCTTTAAACCCATATTTAACTTTTGAACACCTCTGTTAGTGG 3060
Qy 3061 AACAAATCTTATAGATCTGCTCTGATGATAAGAGTTTTCAGTCTGTTGGAGGAGAGAT 3120
Db 3061 AACAAATCTTATAGATCTGCTCTGATGATAAGAGTTTTCAGTCTGTTGGAGGAGAGAT 3120
Qy 3121 GCAAGTAGCAGTCTGAGAGACAGAGATGAGGTCATGCAAGTGGAACTTTCAACAGATA 3180
Db 3121 GCAAGTAGCAGTCTGAGAGACAGAGATGAGGTCATGCAAGTGGAACTTTCAACAGATA 3180
Qy 3181 CAATATCTCAAGATTTCAAGAGGTTTGTAAACAGAAACTATATGGGAAAGATACACTCACCG 3240
Db 3181 CAATATCTCAAGATTTCAAGAGGTTTGTAAACAGAAACTATATGGGAAAGATACACTCACCG 3240

QY 3241 CAGAAAAGAGTCTTCTGAAGAAAACCAACATGCCCAATGAAGATGCTATTTCATGG 3300
DB 3241 CAGAAAAGAGTCTTCTGAAGAAAACCAACATGCCCAATGAAGATGCTATTTCATGG 3300
QY 3301 GTCTCCCTTTCTGGAATCAATATATCCACAAAGGCTTTGATGAAAGGATGCTACATAGG 3360
DB 3301 GTCTCCCTTTCTGGAATCAATATATCCACAAAGGCTTTGATGAAAGGATGCTACATAGG 3360
QY 3361 TGGTATGTTTGGAGCTGCAATTTATTTTGTCTGAAAACTCTTCCAAAAGCAATCAATATGT 3420
DB 3361 TGGTATGTTTGGAGCTGCAATTTATTTTGTCTGAAAACTCTTCCAAAAGCAATCAATATGT 3420
QY 3421 ATATGGAATTCGAGAGGATCTAGGCTGTCAGTTCAAAAAGCAATCTTCTGTTTACATTTG 3480
DB 3421 ATATGGAATTCGAGAGGATCTAGGCTGTCAGTTCAAAAAGCAATCTTCTGTTTACATTTG 3480
QY 3481 CCACAGGAGCTGCTCTTTTCCCGGTTAACTTGGGAAAGTCTTCTGCAAGTTCAGTGC 3540
DB 3481 CCACAGGAGCTGCTCTTTTCCCGGTTAACTTGGGAAAGTCTTCTGCAAGTTCAGTGC 3540
QY 3541 AATGAAAATGCAATCTCTCTCCAGGTCACTCACTCACTGAGTGGCCCAAGTAA 3600
DB 3541 AATGAAAATGCAATCTCTCTCCAGGTCACTCACTCACTGAGTGGCCCAAGTAA 3600
QY 3601 TGGCTAGCATAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCTGAGTATTT 3660
DB 3601 TGGCTAGCATAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCTGAGTATTT 3660
QY 3661 AATTACTTACAGATTTAGGCGCTGAGGTATGCTGATGATAAATAGTATTTTAA 3720
DB 3661 AATTACTTACAGATTTAGGCGCTGAGGTATGCTGATGATAAATAGTATTTTAA 3720
QY 3721 AAATCTAATTCACCTGAACCTAAATCAATCAAGAGAGAGTGGCTCTACGTTTACTCCT 3780
DB 3721 AAATCTAATTCACCTGAACCTAAATCAATCAAGAGAGAGTGGCTCTACGTTTACTCCT 3780
QY 3781 TTGCTGAAAAA 3797
DB 3781 TTGCTGAAAAA 3797

RESULT 4
ID ADY97759 standard; cDNA; 3797 BP.
XX
XX AC ADY97759;
XX
XX DT 16-JUN-2005 (first entry)
XX

DE Human tankyrase homologue isotype 1 encoding cDNA SEQ ID NO:1.
XX
XX KW cell cycle; cancer; cytosolic; tankyrase homologue isotype 1; gene; ss.
XX

OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 404..3706
XX FT /*tag= a
XX FT /product= "tankyrase homologue isotype 1"
XX

PN US2005074825-A1.
XX
XX PD 07-APR-2005.
XX
XX PF 08-JUL-2003; 2003US-00616101.
XX
XX XX 25-OCT-1999; 99US-00427154.
PR 25-OCT-2000; 2000US-00696668.
PR 25-APR-2001; 2001US-00843159.
XX
XX PA (LUOY/) LUO Y.
XX (CHAN/) CHAN E.

PA (XUX/) XU X.
PA (HUAN/) HUANG B.
XX (OSSO/) OSSOVSKAYA V.
PI Luo Y, Chan E, Xu X, Huang B, Ossovsckaya V;
XX
XX WPI: 2005-294737/30.
DR P-PSDB; ADY97761.
XX
XX Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase
PT homololog, useful for screening its modulator.
XX
XX Claim 10; SEQ ID NO 1; 75pp; English.

XX The invention relates to a recombinant polypeptide (I) such as cell cycle
CC protein e.g. tankyrase homologue (TaHo), comprising an amino acid
CC sequence having 85% or more sequence identity to the 1065 amino acid
CC sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also
CC described: (1) diagnosing cancer, which involves determining the activity
CC of (I) from a test sample of an individual and comparing the level with a
CC control with a control; (2) treating (M1) an individual with a cell cycle
CC inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I),
CC comprising a nucleic acid that hybridizes under high stringent conditions
CC to a sequence complementary to the 3797 base pair sequence of ADY97760,
CC the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
CC more sequence identity to ADY97759 or ADY97760; (4) an expression vector
CC (III) comprising (II) operably linked to regulatory sequences recognized
CC by a host cell (IV) transformed with the nucleic acid; (5) a host cell
CC comprising (II) or (III); (6) producing (I); (7) a polypeptide that
CC specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
CC cell, involves contacting the tumor with a bioactive agent capable of
CC inhibiting TaHo activity. (I) is useful for screening a bioactive agent
CC capable of modulating (I), or screening for agents capable of interfering
CC with the binding of (I) and P21. (M1) is useful for treating an
CC individual with a cell cycle related disorder. (M2) is useful for
CC inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
CC oligonucleotide. The present sequence encodes the human tankyrase
CC homologue isotype 1.

XX Sequence 3797 BP; 1153 A; 732 C; 850 G; 1062 T; 0 U; 0 Other;

Query Match 100.0%; Score 3797; DB 14; Length 3797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTGAAGACACTGGATTTTCATACCTTTTGGCTGGGGTTATCTCTGTGTCTCACTACAT 60
DB 1 CTTTGAAGACACTGGATTTTCATACCTTTTGGCTGGGGTTATCTCTGTGTCTCACTACAT 60
QY 61 AGACAAATATAGCTGTGAGCAGATCTTTTGTGCTTCTTGTAGTCCCCAGTTTAG 120
DB 61 AGACAAATATAGCTGTGAGCAGATCTTTTGTGCTTCTTGTAGTCCCCAGTTTAG 120
QY 121 CAGAAACATTTCTGAGATAGATGTGGAAAGGAATTTCTAGCAAGAGTTTGTCACTGTA 180
DB 121 CAGAAACATTTCTGAGATAGATGTGGAAAGGAATTTCTAGCAAGAGTTTGTCACTGTA 180
QY 181 TCATAAGGTTGTGATTTTACATATTTTAAAGTTTATATCTTTGAACATCTGAAATGTATACA 240
DB 181 TCATAAGGTTGTGATTTTACATATTTTAAAGTTTATATCTTTGAACATCTGAAATGTATACA 240
QY 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTGAACCTTTGAGCTTCAGTC 300
DB 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTGAACCTTTGAGCTTCAGTC 300
QY 301 ACTTATTTTGTATTCTTTTCTTTGAGGTTTAGCAGTAGTACCACCAAGGCACTGCTTAGGT 360
DB 301 ACTTATTTTGTATTCTTTTCTTTGAGGTTTAGCAGTAGTACCACCAAGGCACTGCTTAGGT 360
QY 361 ACCACTGCTGTTAGTGGAGAGTCCCTCTGCTTTTATCATTAAGGTTTGGCGGAAAGA 420
DB 361 ACCACTGCTGTTAGTGGAGAGTCCCTCTGCTTTTATCATTAAGGTTTGGCGGAAAGA 420

QY 421 CCGTGTGAAATATTTGGCTTCAAGTGGTCAAGTGTCCAAAGCACGTGATGATGGGGCT 480
DB 421 CCGTGTGAAATATTTGGCTTCAAGTGGTCAAGTGTCCAAAGCACGTGATGATGGGGCT 480
QY 481 TATTCCTCTTCAATATGATGCTCTTTTGGTCAATCTGAAGTGTCAATCTCTTTTGG 540
DB 481 TATTCCTCTTCAATATGATGCTCTTTTGGTCAATCTGAAGTGTCAATCTCTTTTGG 540
QY 541 ACATGGTGCAGACCCCAATGCTCGAGATTAATTTGGAATATATCTCTCTCCATGAAGCTGC 600
DB 541 ACATGGTGCAGACCCCAATGCTCGAGATTAATTTGGAATATATCTCTCTCCATGAAGCTGC 600
QY 601 AATTTAAAGGAAGATTTGATTTGTTGCTGCTGTTTACAGCATGAGCTGAGCCCAACAT 660
DB 601 AATTTAAAGGAAGATTTGATTTGTTGCTGCTGTTTACAGCATGAGCTGAGCCCAACAT 660
QY 661 CCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCCATCTGCCAAGCAGTGT 720
DB 661 CCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCCATCTGCCAAGCAGTGT 720
QY 721 TACTGGTGAATATAGAAAGATGAATCTTAGAAAGTGCAGGAGTGGCAATGAAGAAA 780
DB 721 TACTGGTGAATATAGAAAGATGAATCTTAGAAAGTGCAGGAGTGGCAATGAAGAAA 780
QY 781 AATGATGGCTCTACTCACACCATTAATGTCTCAACTGCCACGCAAGTGTGCGAAGATC 840
DB 781 AATGATGGCTCTACTCACACCATTAATGTCTCAACTGCCACGCAAGTGTGCGAAGATC 840
QY 841 AATCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTTGACAGCTGTACTGCA 900
DB 841 AATCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTTGACAGCTGTACTGCA 900
QY 901 ACATGGAGCTGATGTCATCTTAAGATTAAGGTGATCTGTACCATTTACACATGGCCTG 960
DB 901 ACATGGAGCTGATGTCATCTTAAGATTAAGGTGATCTGTACCATTTACACATGGCCTG 960
QY 961 TTCCTATGCTCAATTAAGTAACTGAACTTTTGGTCAAGCATGCTGTGTAATGTC 1020
DB 961 TTCCTATGCTCAATTAAGTAACTGAACTTTTGGTCAAGCATGCTGTGTAATGTC 1020
QY 1021 AATGACTTTGGCAATTCACCTCTTTCATGAGCAGCTTCTAAGAACAGGTTGAAAT 1080
DB 1021 AATGACTTTGGCAATTCACCTCTTTCATGAGCAGCTTCTAAGAACAGGTTGAAAT 1080
QY 1081 ATGTTCTCTTCTTAAGTATATGTTGTCAGACCCCAACA CTGCTCAATTTGTCAATATAAAG 1140
DB 1081 ATGTTCTCTTCTTAAGTATATGTTGTCAGACCCCAACA CTGCTCAATTTGTCAATATAAAG 1140
QY 1141 TGCTATAGACTTGGCTCCACACACAGTTAAAGAAAGATTTAGCATATGAATTTAAAGG 1200
DB 1141 TGCTATAGACTTGGCTCCACACACAGTTAAAGAAAGATTTAGCATATGAATTTAAAGG 1200
QY 1201 CCACCTCGTTGCTGCAAGCTGACAGAGAGCTGATGTTACTCGAATCAAAAACATCTCTC 1260
DB 1201 CCACCTCGTTGCTGCAAGCTGACAGAGAGCTGATGTTACTCGAATCAAAAACATCTCTC 1260
QY 1261 TCTGAAATGTTGAATTTCAAGCATCTTCAAAACA CATGAAA CAGCATTTGCTATGTTGCTGC 1320
DB 1261 TCTGAAATGTTGAATTTCAAGCATCTTCAAAACA CATGAAA CAGCATTTGCTATGTTGCTGC 1320
QY 1321 TGCACTCCATATCCAAAGAAAGCAATATGTAAGTGTGCTAAGAAAGGAGCAAA 1380
DB 1321 TGCACTCCATATCCAAAGAAAGCAATATGTAAGTGTGCTAAGAAAGGAGCAAA 1380
QY 1381 CATCAATGAAGAAGATTTCTTGACTCTCTGACGCTGGCATCTGAGAAAGCTCA 1440
DB 1381 CATCAATGAAGAAGATTTCTTGACTCTCTGACGCTGGCATCTGAGAAAGCTCA 1440
QY 1441 TAAATGATGTTGTTGAAGTGTGTTGAACATGAAGCAAGGTTAATGCTCTGGAATACT 1500
DB 1441 TAAATGATGTTGTTGAAGTGTGTTGAACATGAAGCAAGGTTAATGCTCTGGAATACT 1500

QY 1501 TGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCAATCTCAAAACCTGCGGCTACT 1560
DB 1501 TGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCAATCTCAAAACCTGCGGCTACT 1560
QY 1561 CCGTGAAGCTATGGGTGTGATCTTAACATTTATATCCCTTCAGGGCTTTATCTGCTTTACAGAT 1620
DB 1561 CCGTGAAGCTATGGGTGTGATCTTAACATTTATATCCCTTCAGGGCTTTATCTGCTTTACAGAT 1620
QY 1621 GGGAAATGAAATGTTACAGCAACTCTCCAGAGGGGTATCTCAATAGGTAATTTACAGAGC 1680
DB 1621 GGGAAATGAAATGTTACAGCAACTCTCCAGAGGGGTATCTCAATAGGTAATTTACAGAGC 1680
QY 1681 AGACAGCAATTTGCTGGAAGCTGCAAAAGCTGGAGATGTCGAAAACCTGTAAGAAAACCTGTG 1740
DB 1681 AGACAGCAATTTGCTGGAAGCTGCAAAAGCTGGAGATGTCGAAAACCTGTAAGAAAACCTGTG 1740
QY 1741 TACTGTTTCAAGAGTGTCAACTGCGAGAGATTTGACCTTTGCAATGCAATGCTTTATGGAACATTT 1800
DB 1741 TACTGTTTCAAGAGTGTCAACTGCGAGAGATTTGACCTTTGCAATGCAATGCTTTATGGAACATTT 1800
QY 1801 TGCAGCTGGGTATACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGT 1860
DB 1801 TGCAGCTGGGTATACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGT 1860
QY 1861 GCATGCTAAAGATAAAGGAGGCTTTGTACCTTTGCAATGCAATGCTTTATGGAACATTT 1920
DB 1861 GCATGCTAAAGATAAAGGAGGCTTTGTACCTTTGCAATGCAATGCTTTATGGAACATTT 1920
QY 1921 TGAAGTTGCAAACTTTCTTTGTTAAACATGGAAGCAGTGTAAATGATGCTGATTTATGGA 1980
DB 1921 TGAAGTTGCAAACTTTCTTTGTTAAACATGGAAGCAGTGTAAATGATGCTGATTTATGGA 1980
QY 1981 ATTTACACCTTTTACATGAAGCAGCAGCAAGGAAATATGAAATTTGCAAACTTTCTGCT 2040
DB 1981 ATTTACACCTTTTACATGAAGCAGCAGCAAGGAAATATGAAATTTGCAAACTTTCTGCT 2040
QY 2041 CCAGCATGGTGCAGACCTTACCAAAAAACAGGGATGGAATATCTCTTTGGATCTTGT 2100
DB 2041 CCAGCATGGTGCAGACCTTACCAAAAAACAGGGATGGAATATCTCTTTGGATCTTGT 2100
QY 2101 TAAAGATGGAATACAGATTTCAAGATCTGCTTAGGGAGATGAGCTTTGCTAGATGC 2160
DB 2101 TAAAGATGGAATACAGATTTCAAGATCTGCTTAGGGAGATGAGCTTTGCTAGATGC 2160
QY 2161 TGCCAAAGAGGTTGTTTAGCCAGAGTGAAGTGTCTCTCTGATATGTAATTTG 2220
DB 2161 TGCCAAAGAGGTTGTTTAGCCAGAGTGAAGTGTCTCTCTGATATGTAATTTG 2220
QY 2221 CCGCATACCCCAAGCAGACATTCACACCTTTTACATTTAGCAGCTGGTTATAATTT 2280
DB 2221 CCGCATACCCCAAGCAGACATTCACACCTTTTACATTTAGCAGCTGGTTATAATTT 2280
QY 2281 AGAAGTTGACAGATTTTGTTCACACCGAGCTGATGTAATGCCAAGACAAAGGAGG 2340
DB 2281 AGAAGTTGACAGATTTTGTTCACACCGAGCTGATGTAATGCCAAGACAAAGGAGG 2340
QY 2341 ACTTATTTCTTTATATATGAGCATCTTACGGGCTGATGTAAGTGTAGCAGCTCTACTAT 2400
DB 2341 ACTTATTTCTTTATATATGAGCATCTTACGGGCTGATGTAAGTGTAGCAGCTCTACTAT 2400
QY 2401 AAAGTATATGATGTGTCAATGCGACAAATAGGGCTTTTACACCTTTGACAGAGC 2460
DB 2401 AAAGTATATGATGTGTCAATGCGACAAATAGGGCTTTTACACCTTTGACAGAGC 2460
QY 2461 AGCCCAAGGAGCGAACA CAGCTTTGCTTTGTTGCTAGCCCATGAGGCTGACCCGAC 2520
DB 2461 AGCCCAAGGAGCGAACA CAGCTTTGCTTTGTTGCTAGCCCATGAGGCTGACCCGAC 2520
QY 2521 TCTTAAATCAGGAGGAGCAACACCTTTAGTATTTTACGGGATGATGTCAGGCG 2580
DB 2521 TCTTAAATCAGGAGGAGCAACACCTTTAGTATTTTACGGGATGATGTCAGGCG 2580
QY 2581 TCTTCTGACAGCAGCCTATGCCCCCATCTGCTCTGCCCCCTTTGTTTACAAGCCTCAAGTGTCT 2640

Db 2581 TCCTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTTGTTACAGGCTCAAGTGCT 2640
Qy 2641 CAATGGTGTGAGAGCCAGAGCAGCACTGCGAGATGCTCTCTCTTCAGGTCCATCTAGCCCC 2700
Db 2641 CAATGGTGTGAGAGCCAGAGCAGCACTGCGAGATGCTCTCTCTTCAGGTCCATCTAGCCCC 2700
Qy 2701 ATCAAGCCTTTCTGACGACAGCAGCTCTTGACAACTTATCTGGGAGTTTTCAGAACTGTG 2760
Db 2701 ATCAAGCCTTTCTGACGACAGCAGCTCTTGACAACTTATCTGGGAGTTTTCAGAACTGTG 2760
Qy 2761 TTCAGTAGTGTGAGTGAAGTGAAGAGAGGCTCTTCCAGTTTGAGAGAAAGAGAGGTTC 2820
Db 2761 TTCAGTAGTGTGAGTGAAGTGAAGAGAGGCTCTTCCAGTTTGAGAGAAAGAGAGGTTC 2820
Qy 2821 AGAGTAGATTTTACGATACTCAATTCGTAAGGAATCTTGGACTTGAGCACCTTAATGGA 2880
Db 2821 AGAGTAGATTTTACGATACTCAATTCGTAAGGAATCTTGGACTTGAGCACCTTAATGGA 2880
Qy 2881 TATATTTGAGAGAAACAGATCACTTTGGATGATATTAGTTGAGATGGGGCACAAGGAGCT 2940
Db 2881 TATATTTGAGAGAAACAGATCACTTTGGATGATATTAGTTGAGATGGGGCACAAGGAGCT 2940
Qy 2941 GAAGGAGATTTGGAATCAATCTTATGACATAGGCACAACTAATTAAGGAGTCCGAGAG 3000
Db 2941 GAAGGAGATTTGGAATCAATCTTATGACATAGGCACAACTAATTAAGGAGTCCGAGAG 3000
Qy 3001 ACTTATCTCCGGACAACAGGCTTTAAACCCATATTTAACTTTGAACACCTCTGCTAGTGG 3060
Db 3001 ACTTATCTCCGGACAACAGGCTTTAAACCCATATTTAACTTTGAACACCTCTGCTAGTGG 3060
Qy 3061 AACAAATCTTATAGATCTGCTCTGATGATAAAGAGTTTCAGTCTGTGGAGGAGAGAT 3120
Db 3061 AACAAATCTTATAGATCTGCTCTGATGATAAAGAGTTTCAGTCTGTGGAGGAGAGAT 3120
Qy 3121 GCAAGTACAGTTCGAGGACAGAGATGGAGGTCATGCGAGTGGAACTTTCACAGATA 3180
Db 3121 GCAAGTACAGTTCGAGGACAGAGATGGAGGTCATGCGAGTGGAACTTTCACAGATA 3180
Qy 3181 CAATATTTCTCAAGATTCAGAGGTTTGTAAACAAAGAACTATGGAAAGATACACTACCG 3240
Db 3181 CAATATTTCTCAAGATTCAGAGGTTTGTAAACAAAGAACTATGGAAAGATACACTACCG 3240
Qy 3241 GAGAAAGAGTTCGAGAGAAACCAACACCATGCGCAATGAACGAATGCTATTTCATGG 3300
Db 3241 GAGAAAGAGTTCGAGAGAAACCAACACCATGCGCAATGAACGAATGCTATTTCATGG 3300
Qy 3301 GTCTCCTTTGTGAATGCAATTTATCCCAAGGCTTTGATGAAGGCGATCGTACATAGG 3360
Db 3301 GTCTCCTTTGTGAATGCAATTTATCCCAAGGCTTTGATGAAGGCGATCGTACATAGG 3360
Qy 3361 TGGTATGTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGT 3420
Db 3361 TGGTATGTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGT 3420
Qy 3421 ATATGGAATTTGGAGGAGTACTGGGTGTCAGTTTCACAAAGACAGATCTTGTTACATTTG 3480
Db 3421 ATATGGAATTTGGAGGAGTACTGGGTGTCAGTTTCACAAAGACAGATCTTGTTACATTTG 3480
Qy 3481 CCACAGGCGCTGCTCTTTTGGCGGGTAACTTCTGGGAAAGTCTTCTCGCAGTTTCAGTGC 3540
Db 3481 CCACAGGCGCTGCTCTTTTGGCGGGTAACTTCTGGGAAAGTCTTCTCGCAGTTTCAGTGC 3540
Qy 3541 AATGAAATGGCAATTTCTCTCCAGGTTCATCACTCAGTCACTGGTAGGCCAGGTGAAA 3600
Db 3541 AATGAAATGGCAATTTCTCTCCAGGTTCATCACTCAGTCACTGGTAGGCCAGGTGAAA 3600
Qy 3601 TGGCTTAGCATAGCTGAATATGTTATTACAGAGGAGAACAGGCTTATCTCGAGTATTT 3660
Db 3601 TGGCTTAGCATAGCTGAATATGTTATTACAGAGGAGAACAGGCTTATCTCGAGTATTT 3660
Qy 3661 AATTACTTACCAGATTTAGGCGCTGAGGCTGATGCTGATGATAAATAGTTATTTTAAAG 3720
Db 3661 AATTACTTACCAGATTTAGGCGCTGAGGCTGATGCTGATGATAAATAGTTATTTTAAAG 3720

Db 3661 AATTACTTACCAGATTTAGGCGCTGAGGCTGATGCTGATGATAAATAGTTATTTTAAAG 3720
Qy 3721 AACTAATTTCCACTGAACCTTAAATCATCAAGCAGAGTGCGCTCTACGTTTACTCCT 3780
Db 3721 AACTAATTTCCACTGAACCTTAAATCATCAAGCAGAGTGCGCTCTACGTTTACTCCT 3780
Qy 3781 TTGCTGAAAAAANA 3797
Db 3781 TTGCTGAAAAAANA 3797
RESULT 5
AA91488
ID AA91488 standard; DNA; 3816 BP.
XX AA91488;
XX AC
XX 06-AUG-2001 (first entry)
XX Tankyrase homologue isotype 2 coding sequence.
DE Tankyrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation;
XX cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
KW chromosome mapping; gene therapy; vaccine; ds.
KW
XX Unidentified.
XX
FH Key Location/Qualifiers
CDS 2..3726
FT /*tag= a
FT /partial
FT /product= "TaHo2"
FT /note= "Tankyrase homologue isotype 2; No start codon given"
XX
XX WO200130987-A2.
XX
XX 03-MAY-2001.
XX
XX 25-OCT-2000; 2000WO-US041528.
XX
XX 25-OCT-1999; 99US-00427154.
XX
XX (RIGE-) RIGEL PHARM INC.
XX
XX Luo Y, Chan E, Xu X, Huang B;
PI
PI WPI: 2001-300503/31.
PI P-PSDB; AAY97749.
XX
XX Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing or preventing cell proliferation in cells, and for diagnosing, treating or preventing cell cycle associated disorders such as cancer.
PS Claim 13; Fig 2; 63pp; English.
XX
XX This sequence encodes the Tankyrase homologue isotype 2 (TaHo-2) protein of the invention. The invention also relates to the TaHo-1 protein. The TaHo proteins are useful for inducing or preventing cell proliferation in cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also useful for the preparation of TaHo, for generating either transgenic animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents, in gene therapy, as vaccine, and for construction of hybridisation probes for mapping the gene which encodes TaHo and for the genetic analysis of individuals with genetic disorders. The TaHo proteins, and their coding sequences are useful in screening assays
XX
XX Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;

Query Match		89.4%	Score 3933.4;	DB 4;	Length 3816;	
Best Local Similarity		99.9%	Pred. No. 0;			
Matches 3394;		Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
Qy	403	AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGGTTCAGAAATGGTGCAGTGTCCAAAGC	462			
Db	422	AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGGTTCAGAAATGGTGCAGTGTCCAAAGC	481			
Qy	463	ACGTGATGATGGGGCCCTTATCTCTTCATATGCGATGCTCTTTGGTGCATGCTGAAGT	522			
Db	482	ACGTGATGATGGGGCCCTTATCTCTTCATATGCGATGCTCTTTGGTGCATGCTGAAGT	541			
Qy	523	AGTCAATCTCTTTTGGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTTATAC	582			
Db	542	AGTCAATCTCTTTTGGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTTATAC	601			
Qy	583	TCCTCTCATGAGTGCATTTAAAGGAAAGATTGATGTTTGGATGCTGCTGTTACAGCA	642			
Db	602	TCCTCTCATGAGTGCATTTAAAGGAAAGATTGATGTTTGGATGCTGCTGTTACAGCA	661			
Qy	643	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCC	702			
Db	662	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCC	721			
Qy	703	ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG	762			
Db	722	ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG	781			
Qy	763	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACATTTAAATGTCACATGCCACGC	822			
Db	782	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACATTTAAATGTCACATGCCACGC	841			
Qy	823	AAGTATGGCGAGAAAGTCACTCCATTTACATTTGGCAGCAGGATATAACAGATAAAGAT	882			
Db	842	AAGTATGGCGAGAAAGTCACTCCATTAATTTGGCAGCAGGATATAACAGATAAAGAT	901			
Qy	883	TGTAAGCTGTTTACTGCAACATGAGCTGATGCTCCATGCTAAAGATAAAGTGATCTGGT	942			
Db	902	TGTAAGCTGTTTACTGCAACATGAGCTGATGCTCCATGCTAAAGATAAAGTGATCTGGT	961			
Qy	943	ACCATTAACAATGCTCTTCTTATGGTCAATTAAGAATACTGAATCTTTGGTCAAGCA	1002			
Db	962	ACCATTAACAATGCTCTTCTTATGGTCAATTAAGAATACTGAATCTTTGGTCAAGCA	1021			
Qy	1003	TGGTGCTGTGTAATGCAATGGACTTGTGGCAATTTCACTCTTCTCATGAGGACGCTTC	1062			
Db	1022	TGGTGCTGTGTAATGCAATGGACTTGTGGCAATTTCACTCTTCTCATGAGGACGCTTC	1081			
Qy	1063	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTCAGACCCCAACTGCT	1122			
Db	1082	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTCAGACCCCAACTGCT	1141			
Qy	1123	CAATTGTCACAATAAAGTGTCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGATT	1182			
Db	1142	CAATTGTCACAATAAAGTGTCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGATT	1201			
Qy	1183	AGCATATGAATTTAAAGGCGACTGTTGGTGGAGCTGCAAGAGCTGATGTTACTCG	1242			
Db	1202	AGCATATGAATTTAAAGGCGACTGTTGGTGGAGCTGCAAGAGCTGATGTTACTCG	1261			
Qy	1243	AATCAAAAACATCTCTCTGGAATGCTGAATTTCAAGCATCTCAACACACATGAAAC	1302			
Db	1262	AATCAAAAACATCTCTCTGGAATGCTGAATTTCAAGCATCTCAACACACATGAAAC	1321			
Qy	1303	AGCATTCATTTGCTGCTGCTATCCATATCCCAAAAAGAAAGCAAAATATGTGAATCTGTT	1362			
Db	1322	AGCATTCATTTGCTGCTGCTATCCATATCCCAAAAAGAAAGCAAAATATGTGAATCTGTT	1381			
Qy	1363	GCTAAGAAAAGAGCAAAACATCAATGAAAAGACTAAAGAAATTTCTTGAATCTCTCTGACGT	1422			
Db	1382	GCTAAGAAAAGAGCAAAACATCAATGAAAAGACTAAAGAAATTTCTTGAATCTCTCTGACGT	1441			

Qy	1423	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT	1482			
Db	1442	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT	1501			
Qy	1483	TAATGCTCTGATTAATCTTTGGTCAAGCTTCTCTACAGAGCTGCATATTTGGTGCATCT	1542			
Db	1502	TAATGCTCTGATTAATCTTTGGTCAAGCTTCTCTACAGAGCTGCATATTTGGTGCATCT	1561			
Qy	1543	ACAAACCTGCCGCCCTACTCTCTGAGCTATGGTGTGATCCTAACATTAATATCCCTTCAGGG	1602			
Db	1562	ACAAACCTGCCGCCCTACTCTCTGAGCTATGGTGTGATCCTAACATTAATATCCCTTCAGGG	1621			
Qy	1603	CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCCAAGAGGGTATCTC	1662			
Db	1622	CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCCAAGAGGGTATCTC	1681			
Qy	1663	ATTAGGTAAATTCAGAGCAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGAGATGTGA	1722			
Db	1682	ATTAGGTAAATTCAGAGCAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGAGATGTGA	1741			
Qy	1723	AACGTGTAATAAACTGCTGTAAGTGTCAAGTGTCAACTGACAGACATTTGAAGGGCGTCA	1782			
Db	1742	AACGTGTAATAAACTGCTGTAAGTGTCAAGTGTCAACTGACAGACATTTGAAGGGCGTCA	1801			
Qy	1783	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT	1842			
Db	1802	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT	1861			
Qy	1843	ACAGATGGAGCTGATGTGCATGCTAAAGATAAAGAGGGCTTGTACCTTTGCACAATGC	1902			
Db	1862	ACAGATGGAGCTGATGTGCATGCTAAAGATAAAGAGGGCTTGTACCTTTGCACAATGC	1921			
Qy	1903	ATGTTCTTATGGAATTTGAGGTTGACAGACTTCTTGTGTTAAACATGAGCAGTAGTTAA	1962			
Db	1922	ATGTTCTTATGGAATTTGAGGTTGACAGACTTCTTGTGTTAAACATGAGCAGTAGTTAA	1981			
Qy	1963	TGTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAGAAAGAAATATGA	2022			
Db	1982	TGTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAGAAAGAAATATGA	2041			
Qy	2023	AATTTGCAAACTTCTGCTCCAGCATGTTGCGAGACCTTACCAAAAAAACAAGGATGGAAA	2082			
Db	2042	AATTTGCAAACTTCTGCTCCAGCATGTTGCGAGACCTTACCAAAAAAACAAGGATGGAAA	2101			
Qy	2083	TACTCTCTTGGATCTGTTAAAGATGAGATACAGATATTCAAGATCTGCTTAGGGGAGA	2142			
Db	2102	TACTCTCTTGGATCTGTTAAAGATGAGATACAGATATTCAAGATCTGCTTAGGGGAGA	2161			
Qy	2143	TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAAAGTTGCTTTC	2202			
Db	2162	TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAAAGTTGCTTTC	2221			
Qy	2203	TCCTGATAATGTAATTTGGCCGCGATACCCAAGGCGAGCATTCACACACTTTTACATTTAGC	2262			
Db	2222	TCCTGATAATGTAATTTGGCCGCGATACCCAAGGCGAGCATTCACACACTTTTACATTTAGC	2281			
Qy	2263	AGCTGGTTATAAATTTAGAAAGTTGAGAGTATTTGTTTACCAACCGAGCTGATGTCAA	2322			
Db	2282	AGCTGGTTATAAATTTAGAAAGTTGAGAGTATTTGTTTACCAACCGAGCTGATGTCAA	2341			
Qy	2323	TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCGATGAGA	2382			
Db	2342	TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCGATGAGA	2401			
Qy	2383	TGTAGCAGCTCTACTATAAAGATATAATGATGTGTCAATGCGCATCGGACAAATGGGCTTT	2442			
Db	2402	TGTAGCAGCTCTACTATAAAGATATAATGATGTGTCAATGCGCATCGGACAAATGGGCTTT	2461			
Qy	2443	CACACCTTTGCAACAGCAGCCCAAGGGGACGACAGCTTTGCTTTGTTGCTAGC	2502			
Db	2462	CACACCTTTGCAACAGCAGCCCAAGGGGACGACAGCTTTGCTTTGTTGCTAGC	2521			
Qy	2503	CCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAACACTTTTAGATTTAGTTTC	2562			

Db 2522 CCATGGAGCTGACCCGACTCTTAATAATCAGGAAGGACAAACACCTTTAGATTAGTTTC 2581
Qy 2563 AGCGGATGATGTCAAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTTG 2622
Db 2582 AGCGGATGATGTCAAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTTG 2641
Qy 2623 TTACAGGCTCAAGTGTCTCAATGTGTGTAGAGAGCCAGAGCCACTGCGAGATGCTCTCTC 2682
Db 2642 TTACAAGCCTCAAGTGTCTCAATGTGTGTAGAGAGCCAGAGCCACTGCGAGATGCTCTCTC 2701
Qy 2683 TTCAAGTCCATCTAGCCCATCAAGCCTTTCTGACAGCAGAGTCTTGACAACTTTATCTGG 2742
Db 2702 TTCAGGTCCTATAGCCCATCAAGCCTTTCTGACAGCAGAGTCTTGACAACTTTATCTGG 2761
Qy 2743 GAGTTTTTTCAGAACTGTCTTCCAGTAGTTAGTTCAAGTGGAAACAGAGGGTGTCTCCAGTTT 2802
Db 2762 GAGTTTTTTCAGAACTGTCTTCCAGTAGTTAGTTCAAGTGGAAACAGAGGGTGTCTCCAGTTT 2821
Qy 2803 GGAGAAAAGAGAGGTTCCAGAGTAGATTTTAGCATTAATCTCAATTCGTAGGAATCTTGG 2862
Db 2822 GGAGAAAAGAGAGGTTCCAGAGTAGATTTTAGCATTAATCTCAATTCGTAGGAATCTTGG 2881
Qy 2863 ACTTGAGCACCTAATGGATATATTTTGAGAGAGACAGATCACTTTTGGATGTTAGTTGA 2922
Db 2882 ACTTGAGCACCTAATGGATATATTTTGAGAGAGACAGATCACTTTTGGATGTTAGTTGA 2941
Qy 2923 GATGGGACAAAGAGCTGAAAGAGATTTGGAATCAATGCTTTATGGACATAGCCACAACT 2982
Db 2942 GATGGGACAAAGAGCTGAAAGAGATTTGGAATCAATGCTTTATGGACATAGCCACAACT 3001
Qy 2983 AATTAAAGGAGTCAGAGACTTTATCTCGGACAAAGGCTTTAAACCATATTTAACTTT 3042
Db 3002 AATTAAAGGAGTCAGAGACTTTATCTCGGACAAAGGCTTTAAACCATATTTAACTTT 3061
Qy 3043 GAACACCTCTGGTAGTGGAACTTTCTATAGATCTGTCTCTCATGTATGAAGAGTTTCA 3102
Db 3062 GAACACCTCTGGTAGTGGAACTTTCTATAGATCTGTCTCTCATGTATGAAGAGTTTCA 3121
Qy 3103 GTCTGTGGAGAGAGATGCAAGTACAGTTTCGAGAGACAGAGATGGAGTCAATGAGG 3162
Db 3122 GTCTGTGGAGAGAGATGCAAGTACAGTTTCGAGAGACAGAGATGGAGTCAATGAGG 3181
Qy 3163 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3222
Db 3182 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3241
Qy 3223 GGAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCAATGA 3282
Db 3242 GGAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCAATGA 3301
Qy 3283 ACGAATGCTATTTTCATGGGTCTCTCTTTTGTGAATGCAATTTATCCACAAGGCTTTGATGA 3342
Db 3302 ACGAATGCTATTTTCATGGGTCTCTCTTTTGTGAATGCAATTTATCCACAAGGCTTTGATGA 3361
Qy 3343 AAGGATCGGTACATAGTGTGTATTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCTTC 3402
Db 3362 AAGGATCGGTACATAGTGTGTATTTTGGAGCTGGCAATTTATTTTGTGAAAACCTCTTC 3421
Qy 3403 CAAAGCAATCAATATGTATATGAAATTTGGAGGAGGTACTGGGTGTCAGTTTCAAAAGA 3462
Db 3422 CAAAGCAATCAATATGTATATGAAATTTGGAGGAGGTACTGGGTGTCAGTTTCAAAAGA 3481
Qy 3463 CAGATCTTTGTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTC 3522
Db 3482 CAGATCTTTGTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTC 3541
Qy 3523 TTTCTGAGGTTAGTGCATGAAATGGGACATTTCTCTCCAGGTGTCAGTCACTCAGTCAC 3582
Db 3542 TTTCTGAGGTTAGTGCATGAAATGGGACATTTCTCTCCAGGTGTCAGTCACTCAGTCAC 3601
Qy 3583 TGGTAGGCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTTACAGAGAGAAACA 3642

Db 3602 TGGTAGGCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTTACAGAGAGAAACA 3661
Qy 3643 GGCTTATCTCGAGTATTTTAATTTACTTACAGATTTATGAGGCTCAAGGTATGGTCGATGG 3702
Db 3662 GGCTTATCTCGAGTATTTTAATTTACTTACAGATTTATGAGGCTCAAGGTATGGTCGATGG 3721
Qy 3703 ATAAATAGTTTATTTTAAGAAACTAAATTTCCACTGAACCTAAATCATCAAGCAGCAGTGG 3762
Db 3722 ATAAATAGTTTATTTTAAGAAACTAAATTTCCACTGAACCTAAATCATCAAGCAGCAGTGG 3781
Qy 3763 CCTCTAGCTTTTACTCTCTTTGCTGAAAAAATAA 3797
Db 3782 CCTCTAGCTTTTACTCTCTTTGCTGAAAAAATAA 3816
RESULT 6
ABQ77067
ID ABQ77067 standard; DNA; 3816 BP.
XX
AC ABQ77067;
XX
DT 08-APR-2003 (first entry)
XX
DE Tankyrase H isotype 2 TaHo-2 DNA from clone K23.
XX
KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2;
KW TaHo; cytosolic; immunostimulant; gene therapy; vaccine; cancer; tumour;
KW cell cycle related disorder; poly ADP-ribose polymerase; PARP; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 3..3725
FT /*tag= a
FT /product= "TaHo-2"
FT /partial
FT /note= "no start codon"
XX
FN MO200286170-A1.
XX
PD 31-OCT-2002.
XX
PF 25-APR-2002; 2002WO-US013185.
XX
PR 25-APR-2001; 2001US-00843159.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
XX
DR WPI; 2003-093158/08.
DR P-PSDB; ABG73731.
XX
PT New recombinant nucleic acid encoding a cell cycle protein, useful for
PT diagnosing and treating a cell cycle related disorder, e.g. cancer.
XX
PS Claim 13; Fig 2A-B; 90pp; English.
XX
CC This invention describes a novel recombinant nucleic acid encoding the
CC cell cycle protein TaHo, a tankyrase H isoform. The products of the
CC invention have cytostatic and immunostimulant activity and can be used
CC for gene therapy and in vaccines. The cell cycle protein TaHo and the
CC nucleic acid encoding the protein are useful for diagnosing and treating
CC a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
CC tumour cell. The methods are useful for screening for a bioactive agent
CC capable of binding to a cell cycle protein tankyrase H, or a bioactive
CC agent capable of modulating a cell cycle protein tankyrase H or PARP
CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
CC inducing an immune response against the cell cycle proteins. This
CC sequence encodes the tankyrase H isoform 2, TaHo-2, isolated from clone
CC K23 which is described in the disclosure of the invention
XX
SQ Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;

		Query Match		89.4%; Score 3393.4; DB 8; Length 3816;					
		Best Local Similarity 99.9%; Pred. No. 0;							
		Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;							
Qy	403	AGGTTTTGGCGGGAAGAGCTAGTTGAATATATTTGCTTCAGAAATGTCGAAAGTCCAAAGC	462						
Db	422	AGGTTTTGGCGGGAAGAGCTAGTTGAATATATTTGCTTCAGAAATGTCGAAATGTCGAAAGC	481						
Qy	463	ACGTGATGATGGGGCCCTATTCCTCTCATATGCTCTTTTGGCTCATGCTGAAGT	522						
Db	482	ACGTGATGATGGGGCCCTATTCCTCTCATATGCTCTTTTGGCTCATGCTGAAGT	541						
Qy	523	AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCAGATAATTTGGAATATATAC	582						
Db	542	AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCAGATAATTTGGAATATATAC	601						
Qy	583	TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATGATGTTTGCATGCTGTTACAGCA	642						
Db	602	TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATGATGTTTGCATGCTGTTACAGCA	661						
Qy	643	TGGAGCTGAGCCAAACCATCCGAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC	702						
Db	662	TGGAGCTGAGCCAAACCATCCGAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC	721						
Qy	703	ATCTGCCAAAGCAGTGTCTTACTGTGTGAATATATAGAAAGATGAATCTTTAGAAAGTGCCAG	762						
Db	722	ATCTGCCAAAGCAGTGTCTTACTGTGTGAATATATAGAAAGATGAATCTTTAGAAAGTGCCAG	781						
Qy	763	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCAACCATTTAAATGTCAATGCTCCAGC	822						
Db	782	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCAACCATTTAAATGTCAATGCTCCAGC	841						
Qy	823	AAGTCATGGCAGAAAGTCAATCCATTTACATTTGGCAGCAGATATACAGATGAAGAT	882						
Db	842	AAGTCATGGCAGAAAGTCAATCCATTTACATTTGGCAGCAGATATACAGATGAAGAT	901						
Qy	883	TGTACAGCTGTTTACTGCAACATGGAGCTGATGCTCATGCTTAAAGATAAAGGTGATCTGGT	942						
Db	902	TGTACAGCTGTTTACTGCAACATGGAGCTGATGCTCATGCTTAAAGATAAAGGTGATCTGGT	961						
Qy	943	ACCATTAACAATGCTGTTTATGTTGTCATTTAAGTAAGTAACTGAACTTTTGGTCAAGCA	1002						
Db	962	ACCATTAACAATGCTGTTTATGTTGTCATTTAAGTAAGTAACTGAACTTTTGGTCAAGCA	1021						
Qy	1003	TGGTCCCTGTGTAATGCAATGGACTTGTGGCAATTTCACTCTCTTCATGAGGCGAGCTTC	1062						
Db	1022	TGGTCCCTGTGTAATGCAATGGACTTGTGGCAATTTCACTCTCTTCATGAGGCGAGCTTC	1081						
Qy	1063	TAAGAACAGGGTTGAAGTATGTTCTTCTTTAAGTTATGGTGAGACCCCAACACTGCT	1122						
Db	1082	TAAGAACAGGGTTGAAGTATGTTCTTCTTTAAGTTATGGTGAGACCCCAACACTGCT	1141						
Qy	1123	CAATTTGTCAATAAAGTGCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGATT	1182						
Db	1142	CAATTTGTCAATAAAGTGCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGATT	1201						
Qy	1183	AGCATATGAATTTAAAGGCCACTCGTTGGTGCAGCTGCAAGAGCTGATGTTACTCG	1242						
Db	1202	AGCATATGAATTTAAAGGCCACTCGTTGGTGCAGCTGCAAGAGCTGATGTTACTCG	1261						
Qy	1243	AATCAAAAAACATCTCTCTGGAATGTTGAATTTCAAGCATCTCAAAACACATGAAC	1302						
Db	1262	AATCAAAAAACATCTCTCTGGAATGTTGAATTTCAAGCATCTCAAAACACATGAAC	1321						
Qy	1303	AGCATTGCAATTTGCTGCTGCAATCTCCATATCCCAAAAAAGAAAGCAATATGTGAATGTT	1362						
Db	1322	AGCATTGCAATTTGCTGCTGCAATCTCCATATCCCAAAAAAGAAAGCAATATGTGAATGTT	1381						
Qy	1363	GCTAAGAAAAAGGAGCAACATCAATGAAAAAGCAATGAAATTTCTTGACTCTCTGACGT	1422						
Db	1382	GCTAAGAAAAAGGAGCAACATCAATGAAAAAGCAATGAAATTTCTTGACTCTCTGACGT	1441						

Qy	1423	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAGGT	1482						
Db	1442	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAGGT	1501						
Qy	1483	TAATGCTCTGATTAATCTTGGTTCAGACTTCTCTACACAGAGCTGCATATTTGTCATCT	1542						
Db	1502	TAATGCTCTGATTAATCTTGGTTCAGACTTCTCTACACAGAGCTGCATATTTGTCATCT	1561						
Qy	1543	ACAAACCTGCCGCTTACTCTCTGAGCTATGGGTGTGATCCTAACATTAATCCCTTCAGGG	1602						
Db	1562	ACAAACCTGCCGCTTACTCTCTGAGCTATGGGTGTGATCCTAACATTAATCCCTTCAGGG	1621						
Qy	1603	CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCCAGAGGGTATCTC	1662						
Db	1622	CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCCAGAGGGTATCTC	1681						
Qy	1663	ATTAGGTAATTCAGAGGAGACAGACAAATTCCTGGAAGCTGCAAAAGGCTGAGATGTGA	1722						
Db	1682	ATTAGGTAATTCAGAGGAGACAGACAAATTCCTGGAAGCTGCAAAAGGCTGAGATGTGA	1741						
Qy	1723	AACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGTCA	1782						
Db	1742	AACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGTCA	1801						
Qy	1783	GTCTACACCACTTCAITTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1842						
Db	1802	GTCTACACCACTTCAITTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1861						
Qy	1843	ACAGATGGAGCTGATGTGCATGCTTAAAGTAAAGGAGGCTTGTACCTTTGCACAATGC	1902						
Db	1862	ACAGATGGAGCTGATGTGCATGCTTAAAGTAAAGGAGGCTTGTACCTTTGCACAATGC	1921						
Qy	1903	ATGTTCTTATGGAATATGAAATTTGCAAGACTTCTGTTTAAACATGAGCAGTAGTTAA	1962						
Db	1922	ATGTTCTTATGGAATATGAAATTTGCAAGACTTCTGTTTAAACATGAGCAGTAGTTAA	1981						
Qy	1963	TGTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022						
Db	1982	TGTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2041						
Qy	2023	AATTTGCAAACTTCTGCTCAGCATGCTGAGACCTTACCAAAAAACAGGGATGGAAA	2082						
Db	2042	AATTTGCAAACTTCTGCTCAGCATGCTGAGACCTTACCAAAAAACAGGGATGGAAA	2101						
Qy	2083	TACTCTTTGGATCTGTTTAAAGATGGAGTACAGATATTTCAAGATCTGTTAGGGAGA	2142						
Db	2102	TACTCTTTGGATCTGTTTAAAGATGGAGTACAGATATTTCAAGATCTGTTAGGGAGA	2161						
Qy	2143	TGCAGCTTTGTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTGTCTTTC	2202						
Db	2162	TGCAGCTTTGTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTGTCTTTC	2221						
Qy	2203	TCCTGATAATGTAATTTGCCGCGATACCAAGGAGACATTTCAAACCTTTACATTTAGC	2262						
Db	2222	TCCTGATAATGTAATTTGCCGCGATACCAAGGAGACATTTCAAACCTTTACATTTAGC	2281						
Qy	2263	AGCTGGTTAATAATTTAGAGTTGAGAGTATTTGTTTAAACACGAGCTGATGTCAA	2322						
Db	2282	AGCTGGTTAATAATTTAGAGTTGAGAGTATTTGTTTAAACACGAGCTGATGTCAA	2341						
Qy	2323	TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGTCAGCATCTTACGGGCGATGAGA	2382						
Db	2342	TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGTCAGCATCTTACGGGCGATGAGA	2401						
Qy	2383	TGTAGCAGCTCTACTAATAAAGTATAATGATGTGTCATGTCCTCCACGCAATATGGGCTTT	2442						
Db	2402	TGTAGCAGCTCTACTAATAAAGTATAATGATGTGTCATGTCCTCCACGCAATATGGGCTTT	2461						
Qy	2443	CACACCTTTGACCAAGCAGCCCAAAAGGAGCAACACAGCTTTGTGCTTTGTTGCTAGC	2502						
Db	2462	CACACCTTTGACCAAGCAGCCCAAAAGGAGCAACACAGCTTTGTGCTTTGTTGCTAGC	2521						
Qy	2503	CCATGGAGCTGACCCGACTCTTTAAAAAATCAGGAAGGACAAACACCTTTAGATTGTTTC	2562						

Db 2522 CCATGGAGCTGACCCGACTCTTAAATAATCAGGAAGGACAAACACTTTAGATTAGTTTC 2581
Qy 2563 AGCGGATGATGTCAGCGCTCTTCTGACAGACGCAATGCCCCCATCTGCTCTGCCCTCTTG 2622
Db 2582 AGCGGATGATGTCAGCGCTCTTCTGACAGACGCAATGCCCCCATCTGCTCTGCCCTCTTG 2641
Qy 2623 TTACAAGCCTCAAGTGCTCAATGTGTGTGAGAGAGCCAGGAGCCACTGCGAGATGCTCTTC 2682
Db 2642 TTACAAGCCTCAAGTGCTCAATGTGTGTGAGAGAGCCAGGAGCCACTGCGAGATGCTCTTC 2701
Qy 2683 TTTCAAGTCCATGAGCCCATCAAGCCTTCTGACGCGACGCTCTTGACCACTTATCTGG 2742
Db 2702 TTTCAAGTCCATGAGCCCATCAAGCCTTCTGACGCGACGCTCTTGACCACTTATCTGG 2761
Qy 2743 GAGTTTTTCAGAACTGTCTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTCTCCAGTTT 2802
Db 2762 GAGTTTTTCAGAACTGTCTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTCTCCAGTTT 2821
Qy 2803 GGAGAAAAGAGGTTCCAGAGTAGATTTTGTAGCATAACTCAATTCGTAAGGAATCTTGG 2862
Db 2822 GGAGAAAAGAGGTTCCAGAGTAGATTTTGTAGCATAACTCAATTCGTAAGGAATCTTGG 2881
Qy 2863 ACTTGAGCACCTAATGGATATATTGAGAGAGACAGATCACTTTGGATGTATTAGTTGA 2922
Db 2882 ACTTGAGCACCTAATGGATATATTGAGAGAGACAGATCACTTTGGATGTATTAGTTGA 2941
Qy 2923 GATGGGACCAAGGAGCTGAAGAGAGATGGAATCAATGCTTTATGGACATAGGCACAACT 2982
Db 2942 GATGGGACCAAGGAGCTGAAGAGATGGAATCAATGCTTTATGGACATAGGCACAACT 3001
Qy 2983 AATTAAGGAGTCGAGAGACTTATCTCCGGAACAAGGTTCTTAACCATATTTAACTTT 3042
Db 3002 AATTAAGGAGTCGAGAGACTTATCTCCGGAACAAGGTTCTTAACCATATTTAACTTT 3061
Qy 3043 GAACACCTCTGGTAGTGAACAATTTCTATAGATCTGCTCTGATGATGAAGAGTTTCA 3102
Db 3062 GAACACCTCTGGTAGTGAACAATTTCTATAGATCTGCTCTGATGATGAAGAGTTTCA 3121
Qy 3103 GTCTGTGAGGAAGAGATGCAAGATACAGTTTCGAGAGACAGAGATGGAGTCAATGAGG 3162
Db 3122 GTCTGTGAGGAAGAGATGCAAGATACAGTTTCGAGAGACAGAGATGGAGTCAATGAGG 3181
Qy 3163 TGGAACTTTCAACAGATACAAATATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3222
Db 3182 TGGAACTTTCAACAGATACAAATATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3241
Qy 3223 GGAAAGATACACTCACCGGAGAAAGAGTTTCTGAGAGAAACCAACCAATGCCAATGA 3282
Db 3242 GGAAAGATACACTCACCGGAGAAAGAGTTTCTGAGAGAAACCAACCAATGCCAATGA 3301
Qy 3283 ACGAATGCTATTTTATGGGCTCTCCTTTGTGAATGCAATATCCACAAGGCTTTGATGA 3342
Db 3302 ACGAATGCTATTTTATGGGCTCTCCTTTGTGAATGCAATATCCACAAGGCTTTGATGA 3361
Qy 3343 AAGGATCGGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTC 3402
Db 3362 AAGGATCGGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTC 3421
Qy 3403 CAAAAGCAATCAATATGATATGTAATGGAATGGAGGAGTACTGGGTGTCAGTTCCAAAGA 3462
Db 3422 CAAAAGCAATCAATATGATATGTAATGGAATGGAGGAGTACTGGGTGTCAGTTCCAAAGA 3481
Qy 3463 CAGATCTTTGTACATTTGCCACAGGACGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3522
Db 3482 CAGATCTTTGTACATTTGCCACAGGACGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3541
Qy 3523 TTTCTCGAGTTCAAGTGAATGGAATGGCAATTTCTCTCAGGTCAATCTCAGTCAAC 3582
Db 3542 TTTCTCGAGTTCAAGTGAATGGAATGGCAATTTCTCTCAGGTCAATCTCAGTCAAC 3601
Qy 3583 TGGTAGGCCAGTGTAAATGGCTAGCATAGTGAATATGTTATTTTACAGAGGAGACA 3642

Db 3602 TGGTAGGCCAGTGTAAATGGCCCTAGCATTAGCTGAATATGTTATTTTACAGAGGAGACA 3661
Qy 3643 GGCTTATCTCTGAGTATTTAAATTTACTTACCAGATTTATGAGCCTGAAGGTATGGTCTGATGG 3702
Db 3662 GGCTTATCTCTGAGTATTTAAATTTACTTACCAGATTTATGAGCCTGAAGGTATGGTCTGATGG 3721
Qy 3703 ATAAATAGTTTATTTTAAAGAACTAAATTTCCACTGACCTAAATCATCAAGACGACGATGG 3762
Db 3722 ATAAATAGTTTATTTTAAAGAACTAAATTTCCACTGACCTAAATCATCAAGACGACGATGG 3781
Qy 3763 CCTCTAGCTTTTACTCTCTTTGCTGAAAAA 3797
Db 3782 CCTCTAGCTTTTACTCTCTTTGCTGAAAAA 3816

RESULT 7
ADH69415
ID ADH69415 standard; DNA; 3816 BP.
XX
AC ADH69415;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human tankyrase homologue isotype 2 (TaHo-2) DNA.
XX
KW Tankyrase H cell cycle protein; p21; gene therapy;
KW bioactive agent screening; cancer; cytostatic; gene; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3, .3725
FT a
FT /product= "Human tankyrase homologue isotype 2"
FT /partial
FT /note= "no start codon given"
ET
FN US6617102-B1.
XX
XX 09-SEP-2003.
XX
XX 25-OCT-2000; 2000US-00696668.
XX
XX 25-OCT-1999; 99US-00427154.
PR (RIGE-) RIGEL PHARM INC.
XX
XX Luo Y, Chan E, Xu X, Huang B, Ossoevakaya V;
XX WPI; 2003-895391/82.
DR P-PSDB; ADH69406.
XX
XX Screening for a bioactive agent capable of interfering with the binding
XX of a tankyrase H cell cycle protein and p21 for diagnosing or treating
XX cancer by combining a tankyrase H cell cycle protein, a candidate
XX bioactive agent and p21.
XX
XX Disclosure; SEQ ID NO 2; 39pp; English.
XX
XX The invention relates to a method for screening a bioactive agent capable
XX of interfering with the binding of a tankyrase H cell cycle protein and
XX p21. The invention is useful in gene therapy. The method is useful for
XX screening for a bioactive agent capable of interfering with the binding
XX of a tankyrase H cell cycle protein and p21 for preparing a composition
XX for diagnosing or treating cancer. The present sequence is human
XX tankyrase homologue isotype 2 (TaHo-2) DNA.
XX
SQ Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;
XX
XX Query Match 89.4%; Score 3393.4; DB 10; Length 3816;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 403 AGGTTTTGGGGGAAAGAGCTAGTTGAATATTTGGCTTCAGAAATGGTCAAGTGTCCAAAGC 462
 Db 422 AGGTTTTGGGGGAAAGAGCTAGTTGAATATTTGGCTTCAGAAATGGTCAAGTGTCCAAAGC 481
 QY 463 ACGTGATGATGGGGGCTTTATTCCTCTTCAATAATGCTGCTTTTGGTCAATGCTGAAAGT 522
 Db 482 ACGTGATGATGGGGGCTTTATTCCTCTTCAATAATGCTGCTTTTGGTCAATGCTGAAAGT 541
 QY 523 AGTCAATCTCTTTTGGGACATGGTGACAGCCCAATGCTGAGAAATTTGGAATTTATAC 582
 Db 542 AGTCAATCTCTTTTGGGACATGGTGACAGCCCAATGCTGAGAAATTTGGAATTTATAC 601
 QY 583 TCCTCTCAATGAAGTCAATTTAAAGGAAAGATTTGATTTTGGTCAATGCTGTTTACAGCA 642
 Db 602 TCCTCTCAATGAAGTCAATTTAAAGGAAAGATTTGATTTTGGTCAATGCTGTTTACAGCA 661
 QY 643 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGAATTTAGCAGATCC 702
 Db 662 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGAATTTAGCAGATCC 721
 QY 703 ATCTGCCAAAGCAGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 762
 Db 722 ATCTGCCAAAGCAGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 781
 QY 763 GAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCAGC 822
 Db 782 GAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCAGC 841
 QY 823 AAGTGATGGCAGAAAGTCAATCCATTTATTTGGCAGCAGGATATAACAGAGTAAAGAT 882
 Db 842 AAGTGATGGCAGAAAGTCAATCCATTTATTTGGCAGCAGGATATAACAGAGTAAAGAT 901
 QY 883 TGTACAGCTGTTCTGCAACATGGAGCTGATCTCACTCAAGTAAAGTAAAGTATCTGGT 942
 Db 902 TGTACAGCTGTTCTGCAACATGGAGCTGATCTCACTCAAGTAAAGTAAAGTATCTGGT 961
 QY 943 ACCATTACAATGCTGTTCTTATGTGTCATTATGAAGTAACTGAATCTTTTGGTCAAGCA 1002
 Db 962 ACCATTACAATGCTGTTCTTATGTGTCATTATGAAGTAACTGAATCTTTTGGTCAAGCA 1021
 QY 1003 TGGTGCCTGTGTAATGCAATGGAGCTGTGGCAATTCATCTCTTCAAGAGGAGCTGTC 1062
 Db 1022 TGGTGCCTGTGTAATGCAATGGAGCTGTGGCAATTCATCTCTTCAAGAGGAGCTGTC 1081
 QY 1063 TAAGAACAGGCTTGAAAGTATGTTCTTCTTCTTAAAGTATGGTCAGACCCCAACACTGCT 1122
 Db 1082 TAAGAACAGGCTTGAAAGTATGTTCTTCTTCTTAAAGTATGGTCAGACCCCAACACTGCT 1141
 QY 1123 CAATTTGTCAATAAAGTGTCTATAGACTTGGCTCCACACACAGTTTAAAGAAAGATT 1182
 Db 1142 CAATTTGTCAATAAAGTGTCTATAGACTTGGCTCCACACACAGTTTAAAGAAAGATT 1201
 QY 1183 AGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGCAAGAGCTGATTTACTCG 1242
 Db 1202 AGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGCAAGAGCTGATTTACTCG 1261
 QY 1243 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAACACAGTAAAC 1302
 Db 1262 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAACACAGTAAAC 1321
 QY 1303 AGCATTTGATTTGCTGCTGCTATCTCCATATCCCAAAAAAGCAAAATATGTGAATCTGT 1362
 Db 1322 AGCATTTGATTTGCTGCTGCTATCTCCATATCCCAAAAAAGCAAAATATGTGAATCTGT 1381
 QY 1363 GCTAAGAAAAAGGAGCAACATCAATGAAAGACTTAAAGAAATTTTGAATCTCTGCAAGT 1422
 Db 1382 GCTAAGAAAAAGGAGCAACATCAATGAAAGACTTAAAGAAATTTTGAATCTCTGCAAGT 1441
 QY 1423 GGCATCTGAGAAAGCTCATATATGATGTTTGAAGTAGTGGTGAACATGAGCAAGGT 1482
 Db 1442 GGCATCTGAGAAAGCTCATATATGATGTTTGAAGTAGTGGTGAACATGAGCAAGGT 1501
 QY 1483 TAAATGCTCTGGATTAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTGCATCT 1542

Db 1502 TAAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTGCATCT 1561
 QY 1543 ACAAACCTGGCGGCTACTCTGAGCTATGGTGATGCTTAAACATTTATCCCTTCAGGG 1602
 Db 1562 ACAAACCTGGCGGCTACTCTGAGCTATGGTGATGCTTAAACATTTATCCCTTCAGGG 1621
 QY 1603 CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCACTCTCCAAAGAGGATCTCTC 1662
 Db 1622 CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCACTCTCCAAAGAGGATCTCTC 1681
 QY 1663 ATTAGGTAATTTACAGGACAGACAGCAATTTGCTGGAAGTGCAGAGCTGAGATGTCGA 1722
 Db 1682 ATTAGGTAATTTACAGGACAGACAGCAATTTGCTGGAAGTGCAGAGCTGAGATGTCGA 1741
 QY 1723 AACTGTAAAAAACTGTGTACTGTTTACAGAGTGTCAACTGACAGACATTTGAAGGCGCTCA 1782
 Db 1742 AACTGTAAAAAACTGTGTACTGTTTACAGAGTGTCAACTGACAGACATTTGAAGGCGCTCA 1801
 QY 1783 GTCTACACCACTTCTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1842
 Db 1802 GTCTACACCACTTCTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1861
 QY 1843 ACAGCATGGAGCTGATGTCATGCTTAAAGATAAAAGGAGGCTTGTACTCTTTGCACAATGC 1902
 Db 1862 ACAGCATGGAGCTGATGTCATGCTTAAAGATAAAAGGAGGCTTGTACTCTTTGCACAATGC 1921
 QY 1903 ATGTTCTTATGGACATTTATGAAGTGTGAGAACTTCTTGTTHAAACATGAGAGCAGTAGTTAA 1962
 Db 1922 ATGTTCTTATGGACATTTATGAAGTGTGAGAACTTCTTGTTHAAACATGAGAGCAGTAGTTAA 1981
 QY 1963 TGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
 Db 1982 TGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2041
 QY 2023 AATTTGCAAACTTCTGCTCCAGCA TGGTGCAGACCCCTACCAAAAAAACAAGGAGTGGAAA 2082
 Db 2042 AATTTGCAAACTTCTGCTCCAGCA TGGTGCAGACCCCTACCAAAAAAACAAGGAGTGGAAA 2101
 QY 2083 TACTCTTTTGGATCTTGTTHAAAGTGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2142
 Db 2102 TACTCTTTTGGATCTTGTTHAAAGTGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2161
 QY 2143 TGCAAGCTTTGCTAGATCTGCCAAGAGGGTGTGTAGCCAGAGTGAAGAGTGTCTTTC 2202
 Db 2162 TGCAAGCTTTGCTAGATCTGCCAAGAGGGTGTGTGTAGCCAGAGTGAAGAGTGTCTTTC 2221
 QY 2203 TCCTGATAATGTAATTTGCCGATACCCAGGAGCAGATTTCAACACCTTTTACATTTAGC 2262
 Db 2222 TCCTGATAATGTAATTTGCCGATACCCAGGAGCAGATTTCAACACCTTTTACATTTAGC 2281
 QY 2263 AGCTGGTTTATTAATTTAGAGTGGAGATTTGTTTACAAACAGGAGCTGATGTA 2322
 Db 2282 AGCTGGTTTATTAATTTAGAGTGGAGATTTGTTTACAAACAGGAGCTGATGTA 2341
 QY 2323 TGCCCAAGAGCAAGGAGGAGCTTTTCTTTTACATAATGACAGATCTTACGGGATGTAGA 2382
 Db 2342 TGCCCAAGAGCAAGGAGGAGCTTTTCTTTTACATAATGACAGATCTTACGGGATGTAGA 2401
 QY 2383 TGTAGCAGCTCTACTAATAAAGTATAATGATGTTGTCATGTCGCAACGCAAAATGGGCTTT 2442
 Db 2402 TGTAGCAGCTCTACTAATAAAGTATAATGATGTTGTCATGTCGCAACGCAAAATGGGCTTT 2461
 QY 2443 CACACCTTTTGGACGAGCCCAAAAGGAGCAGACAGCTTTTGTGCTTGTGCTAGC 2502
 Db 2462 CACACCTTTTGGACGAGCCCAAAAGGAGCAGACAGCTTTTGTGCTTGTGCTAGC 2521
 QY 2503 CCATGGAGCTGACCCGACTCTTAAATCAGGAAGGACAAACCTTTTAGATTTAGTTTC 2562
 Db 2522 CCATGGAGCTGACCCGACTCTTAAATCAGGAAGGACAAACCTTTTAGATTTAGTTTC 2581
 QY 2563 AGCGGATGATGTACGCGCTCTTCTGACAGCAGCCATGCCCCATCTGCTGCGCCCTCTTG 2622

Db 2582 AGCGATGATGTACGGCTCTCTCTGACAGCAGCCATGCCCCCATCTGCTGCGCCTCTTG 2641
Qy 2623 TTACAAGCCTCAAGTGCTCAATGTGTGAGAAAGCCAGGAGCCACTGCGAGATGCTCTCTC 2682
Db 2642 TTACAAGCCTCAAGTGCTCAATGTGTGAGAAAGCCAGGAGCCACTGCGAGATGCTCTCTC 2701
Qy 2683 TTCAAGGTCCATCTAGCCCATCAAGCCCTTCTGACGCCAGCAGCTTTGACACACTTATCTGG 2742
Db 2702 TTCAAGGTCCATCTAGCCCATCAAGCCCTTCTGACGCCAGCAGCTTTGACACACTTATCTGG 2761
Qy 2743 GAGTTTTTCAGAACTGTCTTCAGTAGTGTAGTTCAGTGGAAACAGAGGCTGCTCCAGTTT 2802
Db 2762 GAGTTTTTCAGAACTGTCTTCAGTAGTGTAGTTCAGTGGAAACAGAGGCTGCTCCAGTTT 2821
Qy 2803 GGAGAAAAGGAGGTTCAGGAGTAGATTTTTCAGCATAACTCAATTCGTAAGGAATCTTGG 2862
Db 2822 GGAGAAAAGGAGGTTCAGGAGTAGATTTTTCAGCATAACTCAATTCGTAAGGAATCTTGG 2881
Qy 2863 ACTTGAGCACCTAATGATATATTTGAGAGAGACAGATCACTTTGGATGTATTAGTTGA 2922
Db 2882 ACTTGAGCACCTAATGATATATTTGAGAGAGACAGATCACTTTGGATGTATTAGTTGA 2941
Qy 2923 GATGGGCACAAGGAGCTGAAGGAGATTGGAATCAATGCTTTATGACATAGGCACAAACT 2982
Db 2942 GATGGGCACAAGGAGCTGAAGGAGATTGGAATCAATGCTTTATGACATAGGCACAAACT 3001
Qy 2983 AATTAAAGGAGTCCAGAGACTTATCTCCGGACAACAAGGCTTTAAACCATATTTAACTTT 3042
Db 3002 AATTAAAGGAGTCCAGAGACTTATCTCCGGACAACAAGGCTTTAAACCATATTTAACTTT 3061
Qy 3043 GAACACCTCTGTTAGTGGAACTTCTATAGATCTGCTCTCTGATGATGAAGAGTTTCA 3102
Db 3062 GAACACCTCTGTTAGTGGAACTTCTATAGATCTGCTCTCTGATGATGAAGAGTTTCA 3121
Qy 3103 GTCTGTGAGGAAGAGATGCAAGTACAGTTCGAGAGCACAGATGAGAGTCAATGAGG 3162
Db 3122 GTCTGTGAGGAAGAGATGCAAGTACAGTTCGAGAGCACAGATGAGAGTCAATGAGG 3181
Qy 3163 TGGAACTCTTCAACAGATACAAATATCTCAAGATTCAGAAAGTGTGTAACAGAAACTATG 3222
Db 3182 TGGAACTCTTCAACAGATACAAATATCTCAAGATTCAGAAAGTGTGTAACAGAAACTATG 3241
Qy 3223 GGAAGATACACTCACCGGAGAAAAGAGTTCTTGAAGAAACACACACACATGCAATGA 3282
Db 3242 GGAAGATACACTCACCGGAGAAAAGAGTTCTTGAAGAAACACACACACATGCAATGA 3301
Qy 3283 ACGAATGCTATTTCATGCGTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA 3342
Db 3302 ACGAATGCTATTTCATGCGTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA 3361
Qy 3343 AAGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACTCTTC 3402
Db 3362 AAGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACTCTTC 3421
Qy 3403 CAAAAGCAATCAATATGATATGAAATGGAGAGGTACTGGGTGTCAGTTTCAAGA 3462
Db 3422 CAAAAGCAATCAATATGATATGAAATGGAGAGGTACTGGGTGTCAGTTTCAAGA 3481
Qy 3463 CAGATCTTGTACATTTGGCCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3522
Db 3482 CAGATCTTGTACATTTGGCCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3541
Qy 3523 TTTCTCTGAGTTACATGCAATGAAATGGCAATCTCTCTCCAGGTATCACTCAGTCAAC 3582
Db 3542 TTTCTCTGAGTTACATGCAATGAAATGGCAATCTCTCTCCAGGTATCACTCAGTCAAC 3601
Qy 3583 TGGTAGGCCAGTCTAATGCGCTAGCATGATGCAATGCTTATTTTACAGGAGAGACA 3642
Db 3602 TGGTAGGCCAGTCTAATGCGCTAGCATGATGCAATGCTTATTTTACAGGAGAGACA 3661
Qy 3643 GGCTTATCTCTGAGTATTTAATTTACTTACAGATTTATGAGGCTCAAGGTATGGTCGATGG 3702
Db 3662 GGCTTATCTCTGAGTATTTAATTTACTTACAGATTTATGAGGCTCAAGGTATGGTCGATGG 3721

Qy 3703 ATAAATAGTTATTTTAAGAACTAAATTCACCTGAACCTAAATCATCAAGCAGCAGTGG 3762
Db 3722 ATAAATAGTTATTTTAAGAACTAAATTCACCTGAACCTAAATCATCAAGCAGCAGTGG 3781
Qy 3763 CCTCTAGCTTTTACTCTCTTTGCTGAAAAAATAAAA 3797
Db 3782 CCTCTAGCTTTTACTCTCTTTGCTGAAAAAATAAAA 3816

RESULT 8

ADY97760
ID ADY97760 standard; cDNA; 3816 BP.

XX ADY97760;

XX AC

XX ADY97760;

DT 16-JUN-2005 (first entry)

XX Human tankyrase homologue isotype 2 encoding cDNA SEQ ID NO:2.

DE cell cycle; cancer; cytosolic; tankyrase homologue isotype 2; gene; ss.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX CDS

XX 3..3725

XX /*tag= a

XX /product= "tankyrase homologue isotype 2"

XX US2005074825-A1.

XX 07-APR-2005.

XX 08-JUL-2003; 2003US-00616101.

XX 25-OCT-1999; 99US-00427154.

XX 25-OCT-2000; 2000US-00696668.

XX 25-APR-2001; 2001US-00843159.

XX (LUOY/) LUO Y.

XX (CHAN/) CHAN E.

XX (XUX/) XU X.

XX (HUAN/) HUANG B.

XX (OSSO/) OSSOVSKAYA V.

XX Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;

XX WPI; 2005-294737/30.

XX P-PSDB; ADY97762.

XX Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase

XX homolog, useful for screening its modulator.

XX Claim 10; SEQ ID NO 2; 75pp; English.

XX The invention relates to a recombinant polypeptide (I) such as cell cycle

XX protein e.g. tankyrase homologue (TaHo), comprising an amino acid

XX sequence having 85% or more sequence identity to the 1065 amino acid

XX sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also

XX described: (1) diagnosing cancer, which involves determining the activity

XX of (I) from a test sample of an individual and comparing the level with a

XX control with a control; (2) treating (M1) an individual with a cell cycle

XX related disorder, which involves administering to the individual an

XX inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I),

XX comprising a nucleic acid that hybridizes under high stringent conditions

XX to a sequence complementary to the 3797 base pair sequence of ADY97759 or

XX the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or

XX more sequence identity to ADY97759 or ADY97760; (4) an expression vector

XX (III) comprising (II) operably linked to regulatory sequences recognized

XX by a host cell (IV) transformed with the nucleic acid; (5) a host cell

XX comprising (II) or (III); (6) producing (I); (7) a polypeptide that

XX specifically binds to (I); and (8) inhibiting (M2) growth of a tumor

XX cell, involves contacting the tumor with a bioactive agent capable of

CC inhibiting TaHo activity. (I) is useful for screening a bioactive agent
CC capable of modulating (I), or screening for agents capable of interfering
CC with the binding of (I) and P21. (M1) is useful for treating an
CC individual with a cell cycle related disorder. (M2) is useful for
CC inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
CC oligonucleotide. The present sequence encodes the human tankyrase
CC homologue isotype 2.

XX
SQ Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;

Query Match		89.4%;	Score 3393.4;	DB 14;	Length 3816;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 3394;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	403	AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGTCGCAAGTGTCCAAAGC	462		
DB	422	AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGTCGCAAGTGTCCAAAGC	481		
QY	463	AGGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTTCATGCTGAAGT	522		
DB	482	AGGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTTCATGCTGAAGT	541		
QY	523	AGTCAATCTCTTTTGGCAGACATGGTGCAGACCCCAATGCTGCAGATAATTTGAATATATAC	582		
DB	542	AGTCAATCTCTTTTGGCAGACATGGTGCAGACCCCAATGCTGCAGATAATTTGAATATATAC	601		
QY	583	TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCATGTTGCTGTACAGCA	642		
DB	602	TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCATGTTGCTGTACAGCA	661		
QY	643	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC	702		
DB	662	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC	721		
QY	703	ATCTGCCAAAGCAGTCTTACTGTGTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCCAG	762		
DB	722	ATCTGCCAAAGCAGTCTTACTGTGTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCCAG	781		
QY	763	GAGTGGCAATGAAGAAATAAATGATGGCTCTACTCACACATTTAAATGTCACATGCCACGC	822		
DB	782	GAGTGGCAATGAAGAAATAAATGATGGCTCTACTCACACATTTAAATGTCACATGCCACGC	841		
QY	823	AAGTGAATGGCAGAAAGTCAACTTACATTTTGGCAGCAGGATATAACAGAGTAAAGAT	882		
DB	842	AAGTGAATGGCAGAAAGTCAACTTACATTTTGGCAGCAGGATATAACAGAGTAAAGAT	901		
QY	883	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGT	942		
DB	902	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGT	961		
QY	943	ACCATTACCAATGCTGTTCTTATGGTCAATATGAAGTAACTGAACTTTTGGTCAAGCA	1002		
DB	962	ACCATTACCAATGCTGTTCTTATGGTCAATATGAAGTAACTGAACTTTTGGTCAAGCA	1021		
QY	1003	TGGTCCCTGTGTAATGCAATGGACTCTGTGGCAATTTCACTCTCTTCATGAGGAGCTTC	1062		
DB	1022	TGGTCCCTGTGTAATGCAATGGACTCTGTGGCAATTTCACTCTCTTCATGAGGAGCTTC	1081		
QY	1063	TAAAGAACAGGGTGAAGTATGTTCTCTTCTTAAGTTATGGTGAGACCCCAACATCTGCT	1122		
DB	1082	TAAAGAACAGGGTGAAGTATGTTCTCTTCTTCTTAAAGTTATGGTGAGACCCCAACATCTGCT	1141		
QY	1123	CAATTTGTACAAATAAAGTGTATAGACTTGGCTCCCAACACACAGTTAAAGAAAGATT	1182		
DB	1142	CAATTTGTACAAATAAAGTGTATAGACTTGGCTCCCAACACACAGTTAAAGAAAGATT	1201		
QY	1183	AGCATATGAAATTTAAAGGCCACTCGTGTCTGCAAGCTGCAGAGAGCTGATTTACTCG	1242		
DB	1202	AGCATATGAAATTTAAAGGCCACTCGTGTCTGCAAGCTGCAGAGAGCTGATTTACTCG	1261		
QY	1243	AATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTTCAAGCATCTTCAACACATGAAC	1302		
DB	1262	AATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTTCAAGCATCTTCAACACATGAAC	1321		

QY	1303	AGCATTTGCTTGTCTGTCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACCTGT	1362		
DB	1322	AGCATTTGCTTGTCTGTCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACCTGT	1381		
QY	1363	GCTAAGAAAAGGAGCAAAACATCAATGAAGAACATAAAGAAATCTTGTGACCTCTTCACGT	1422		
DB	1382	GCTAAGAAAAGGAGCAAAACATCAATGAAGAACATAAAGAAATCTTGTGACCTCTTCACGT	1441		
QY	1423	GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAGGT	1482		
DB	1442	GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAGGT	1501		
QY	1483	TAAATGCTCTGATTAATCTTGGTCAGACTTCTCTACAGAGCTGCATATTTGTGGTCATCT	1542		
DB	1502	TAAATGCTCTGATTAATCTTGGTCAGACTTCTCTACAGAGCTGCATATTTGTGGTCATCT	1561		
QY	1543	ACAAACCTGCCCGCTACTCTGAGCTATGGGTGATCTTAACATTAATATATCCCTTCAGGG	1602		
DB	1562	ACAAACCTGCCCGCTACTCTGAGCTATGGGTGATCTTAACATTAATATATCCCTTCAGGG	1621		
QY	1603	CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCACTCTCCAAAGAGGGTATCTC	1662		
DB	1622	CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCACTCTCTCCAAAGAGGGTATCTC	1681		
QY	1663	ATTAGGTAAATTCAGAGCAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGTCGA	1722		
DB	1682	ATTAGGTAAATTCAGAGCAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGTCGA	1741		
QY	1723	AACTGTAAAAAACTGTGTACTGTTACAGAGTGTCAACTGACAGACATTTGAAGGCGCTCA	1782		
DB	1742	AACTGTAAAAAACTGTGTACTGTTACAGAGTGTCAACTGACAGACATTTGAAGGCGCTCA	1801		
QY	1783	GTCTACACCCTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT	1842		
DB	1802	GTCTACACCCTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT	1861		
QY	1843	ACAGCATGGAGCTCATGTGCATGCTTAAAGATAAAGGAGGCTCTGTACCTTTGCACAATGC	1902		
DB	1862	ACAGCATGGAGCTCATGTGCATGCTTAAAGATAAAGGAGGCTCTGTACCTTTGCACAATGC	1921		
QY	1903	ATGTTCTTTATGGACATTAAGAAGTTCAGAACTTTCTTTTAAACATGGAGCAGTAGTTAA	1962		
DB	1922	ATGTTCTTTATGGACATTAAGAAGTTCAGAACTTTCTTTTAAACATGGAGCAGTAGTTAA	1981		
QY	1963	TGTAGCTGATTTATGGAAATTTTACACCTTTACATGAAGCAGCAGCAAAAGAAATATGA	2022		
DB	1982	TGTAGCTGATTTATGGAAATTTTACACCTTTACATGAAGCAGCAGCAAAAGAAATATGA	2041		
QY	2023	AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAACACAGGATGGAA	2082		
DB	2042	AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAACACAGGATGGAA	2101		
QY	2083	TACTCTCTTTGATCTTGTAAAGATGGAGATACAGATATTCAAGATCTCTTTAGGGGAGA	2142		
DB	2102	TACTCTCTTTGATCTTGTAAAGATGGAGATACAGATATTCAAGATCTCTTTAGGGGAGA	2161		
QY	2143	TGCAGCTTTGCTAGATGCTGCCAAGAAAGGGTGTGTTAGCCAGAGTGAAGAGTTGCTCTTC	2202		
DB	2162	TGCAGCTTTGCTAGATGCTGCCAAGAAAGGGTGTGTTAGCCAGAGTGAAGAGTTGCTCTTC	2221		
QY	2203	TCCTGATAATGTAATTTGCCCGCATACCCAGGCGAGACATTTCAACCTTTTACATTTAGC	2262		
DB	2222	TCCTGATAATGTAATTTGCCCGCATACCCAGGCGAGACATTTCAACCTTTTACATTTAGC	2281		
QY	2263	AGCTGGTTATAAATTTAGAAAGTTGAGAGTATTTGTTTACAAACACGAGCTGATGTGAA	2322		
DB	2282	AGCTGGTTATAAATTTAGAAAGTTGAGAGTATTTGTTTACAAACACGAGCTGATGTGAA	2341		
QY	2323	TGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATATGACGATCTTACGGGCAATGTAGA	2382		
DB	2342	TGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATATGACGATCTTACGGGCAATGTAGA	2401		

CC	length in a cell	
XX	Sequence 4275 BP; 1247 A; 889 C; 1025 G; 1114 T; 0 U; 0 Other;	
SQ	Query Match 89.2%; Score 3388.8; DB 3; Length 4275; Best Local Similarity 99.9%; Pred. No. 0; Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	403 AGGTTTTCGGGCGGAAGACGTAGTTGAATATTTGCTTCAGAAATGCTGCAAGTGTCCAGGC 462	Db
DB	481 AGGTTTTCGGGCGGAAGACGTAGTTGAATATTTGCTTCAGAAATGCTGCAAGTGTCCAGGC 540	QY
QY	463 ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTCAATGCTGAAGT 522	Db
DB	541 ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTCAATGCTGAAGT 600	QY
QY	523 AGTCAATCTCTTTTGGGACATGCTGAGACGCCCAATGCTGAGAAATTTGGAATTTATAC 582	Db
DB	601 AGTCAATCTCTTTTGGGACATGCTGAGACGCCCAATGCTGAGAAATTTGGAATTTATAC 660	QY
QY	583 TCCTCTCCTCAATGAAGCTGCAATTTAAAGGAAAGATTTGCTGCTGCTTACAGCA 642	Db
DB	661 TCCTCTCCTCAATGAAGCTGCAATTTAAAGGAAAGATTTGCTGCTGCTTACAGCA 720	QY
QY	643 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGACAGCATTTGATTTAGCAGATCC 702	Db
DB	721 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGACAGCATTTGATTTAGCAGATCC 780	QY
QY	703 ATCTGCCAAAGCAGTGTCTTACTGTTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCCAG 762	Db
DB	781 ATCTGCCAAAGCAGTGTCTTACTGTTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCCAG 840	QY
QY	763 GAGTGGCAATGAAGAAATGATGGCTCTACTCACCATTAATGTCRACTGCCAGC 822	Db
DB	841 GAGTGGCAATGAAGAAATGATGGCTCTACTCACCATTAATGTCRACTGCCAGC 900	QY
QY	823 AAGTGATGCGAAGATCAATCCATTAACATTTGGCAGCAGGATATAACAGATAAAGAT 882	Db
DB	901 AAGTGATGCGAAGATCAATCCATTAACATTTGGCAGCAGGATATAACAGATAAAGAT 960	QY
QY	883 TGTACAGCTGTATCTGCAACATGGAAGCTGATGTCATGCTAAAGATAAAGTGATCTGGT 942	Db
DB	961 TGTACAGCTGTATCTGCAACATGGAAGCTGATGTCATGCTAAAGATAAAGTGATCTGGT 1020	QY
QY	943 ACCATTACCAATGCTCTCTTATGCTCAATTAAGTAACTGAATTTGCTCAAGCA 1002	Db
DB	1021 ACCATTACCAATGCTCTCTTATGCTCAATTAAGTAACTGAATTTGCTCAAGCA 1080	QY
QY	1003 TGGTGCTGTGTAATGCAATGGACTGTGGCAATTCATCTCTTCAATGAGGAGCTTC 1062	Db
DB	1081 TGGTGCTGTGTAATGCAATGGACTGTGGCAATTCATCTCTTCAATGAGGAGCTTC 1140	QY
QY	1063 TAAGAACAGGGTTGAAGTATGCTCTTCTTAAAGTATGCTGAGACCCCAACACTGCT 1122	Db
DB	1141 TAAGAACAGGGTTGAAGTATGCTCTTCTTAAAGTATGCTGAGACCCCAACACTGCT 1200	QY
QY	1123 CAATTTGTCATATAAGTGTCTATAGACTGGCTCCCAACACACAGTTAAAGAAAGATT 1182	Db
DB	1201 CAATTTGTCATATAAGTGTCTATAGACTGGCTCCCAACACACAGTTAAAGAAAGATT 1260	QY
QY	1183 AGCATATCAATTTAAAGGCCACTCGTGTGCTGCAAGCTGCAAGAGCTGATTTACTCG 1242	Db
DB	1261 AGCATATCAATTTAAAGGCCACTCGTGTGCTGCAAGCTGCAAGAGCTGATTTACTCG 1320	QY
QY	1243 AATCAAAAAACATCTCTCTCTGAAATGGTGAATTTCAAGCATCTTCAACACATGAAC 1302	Db
DB	1321 AATCAAAAAACATCTCTCTCTGAAATGGTGAATTTCAAGCATCTTCAACACATGAAC 1380	QY
QY	1303 AGCATTTGATTTGCTGCTGCTATCCATATCCCAAAAGAAAGCAATATGTGAATGTT 1362	Db
DB	1381 AGCATTTGATTTGCTGCTGCTATCCATATCCCAAAAGAAAGCAATATGTGAATGTT 1440	QY
QY	1363 GCTAAGAAAAAGGAGCAACATCAATGAAAAAGACTTAAAGAAATTTCTTGACTCTCTGCAAGT 1422	Db
QY	1441 GCTAAGAAAAAGGAGCAACATCAATGAAAAAGACTTAAAGAAATTTCTTGACTCTCTGCAAGT 1500	Db
QY	1423 GGCATCTGAGAAAGCTCATTAATGATGTTGTTGAAGTAGTGGTGAACAATGAGCAAGGT 1482	Db
DB	1501 GGCATCTGAGAAAGCTCATTAATGATGTTGTTGAAGTAGTGGTGAACAATGAGCAAGGT 1560	QY
QY	1483 TAATGCTCTGATATAATCTTGGTCAAGCTTCTCTACACAGAGCTGCATATTTGGTCACT 1542	Db
DB	1561 TAATGCTCTGATATAATCTTGGTCAAGCTTCTCTACACAGAGCTGCATATTTGGTCACT 1620	QY
QY	1543 ACAAACCTGCGGCTACTCTGAGCTATGGGTGATCTCTAAACATTAATATATCCCTTCAGGG 1602	Db
DB	1621 ACAAACCTGCGGCTACTCTGAGCTATGGGTGATCTCTAAACATTAATATATCCCTTCAGGG 1680	QY
QY	1603 CTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCTCCAAAGGGGTATCTC 1662	Db
DB	1681 CTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCTCCAAAGGGGTATCTC 1740	QY
QY	1663 ATTAGGTAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGCGA 1722	Db
DB	1741 ATTAGGTAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGCGA 1800	QY
QY	1723 AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGAGAGACATTTGAAGGGCGTCA 1782	Db
DB	1801 AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGAGAGACATTTGAAGGGCGTCA 1860	QY
QY	1783 GTCTACACCACTTCATTTTGGCAGCTGGGTATAACAGAGTGTCCGTGGGAATATCTGCT 1842	Db
DB	1861 GTCTACACCACTTCATTTTGGCAGCTGGGTATAACAGAGTGTCCGTGGGAATATCTGCT 1920	QY
QY	1843 ACAGCATGGAGCTGATGTCATGCTAAAGATAAGAGGAGGCTCTGTA CTTTGGCAATATGC 1902	Db
DB	1921 ACAGCATGGAGCTGATGTCATGCTAAAGATAAGAGGAGGCTCTGTA CTTTGGCAATATGC 1980	QY
QY	1903 ATGTTCTTATGGACATTTATGAAGTTGCAGAACTCTTTGTTTAAACATGGAGCAGTAGTTAA 1962	Db
DB	1981 ATGTTCTTATGGACATTTATGAAGTTGCAGAACTCTTTGTTTAAACATGGAGCAGTAGTTAA 2040	QY
QY	1963 TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022	Db
DB	2041 TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2100	QY
QY	2023 AATTTGCAAACTCTGCTCCAGCATGCTGAGACCCCTTACCAAAAAAAGAGGATGGA 2082	Db
DB	2101 AATTTGCAAACTCTGCTCCAGCATGCTGAGACCCCTTACCAAAAAAAGAGGATGGA 2160	QY
QY	2083 TACTCTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAAGATCTGCTTGAAGGGAGA 2142	Db
DB	2161 TACTCTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAAGATCTGCTTGAAGGGAGA 2220	QY
QY	2143 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTTGCTTTC 2202	Db
DB	2221 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTTGCTTTC 2280	QY
QY	2203 TCCGTAAATGTAATTTGCGCGCATACCAAGGAGAGATTTCAACACCTTTTACATTTAGC 2262	Db
DB	2281 TCCGTAAATGTAATTTGCGCGCATACCAAGGAGAGATTTCAACACCTTTTACATTTAGC 2340	QY
QY	2263 AGCTGGTTATAAATTTAGAGTTGAGAGTATTTGTTTAAACACCGAGCTGATGTA 2322	Db
DB	2341 AGCTGGTTATAAATTTAGAGTTGAGAGTATTTGTTTAAACACCGAGCTGATGTA 2400	QY
QY	2323 TGCCCAACAGAAAGGAGACTTATTCCTTTTACATAATGTCAGCATCTTACGGGCATGTAGA 2382	Db
DB	2401 TGCCCAACAGAAAGGAGACTTATTCCTTTTACATAATGTCAGCATCTTACGGGCATGTAGA 2460	QY
QY	2383 TGTAGCAGCTCTACTTAATTAAGTATAATGATGTGTCAATGCCCACGCAAAATGGGCTTT 2442	Db
DB	2461 TGTAGCAGCTCTACTTAATTAAGTATAATGATGTGTCAATGCCCACGCAAAATGGGCTTT 2520	QY
QY	2443 CACACCTTTGCGAAGCAGCCCAAAAGGAGCGAACACAGCTTTTGTGCTTTGTTGCTAGC 2502	Db

Db 2521 CACACCTTTGACGAGCAGCCCAAGAGGAGCAACACAGCTTTGTGCTTTGCTAGC 2580
Qy 2503 CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTAGATTAGTTTC 2562
Db 2581 CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTAGATTAGTTTC 2640
Qy 2563 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCGCCCTCTTG 2622
Db 2641 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCGCCCTCTTG 2700
Qy 2623 TTACAAGCCTCAAGTGCTCAATGGTGTGAGAGGCCAGGACCACTGACAGATGCTCTCTC 2682
Db 2701 TTACAAGCCTCAAGTGCTCAATGGTGTGAGAGGCCAGGACCACTGACAGATGCTCTCTC 2760
Qy 2683 TTCAGGTCATCTAGCCCATCAAGCCTTTCTGACAGCCAGAGTCTTGACAACTATTCTGG 2742
Db 2761 TTCAGGTCATCTAGCCCATCAAGCCTTTCTGACAGCCAGAGTCTTGACAACTATTCTGG 2820
Qy 2743 GAGTTTTTTCAGAACCTGCTTCAGTAGTTAGTTCAAGTGGACAGAGGCTTCCAGTTT 2802
Db 2821 GAGTTTTTTCAGAACCTGCTTCAGTAGTTAGTTCAAGTGGACAGAGGCTTCCAGTTT 2880
Qy 2803 GGAGAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGG 2862
Db 2881 GGAGAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGG 2940
Qy 2863 ACTTGAGCACTTAATGGATATATTGAGAGAGAACAGATCACTTTGGATGATTAGTTGA 2922
Db 2941 ACTTGAGCACTTAATGGATATATTGAGAGAGAACAGATCACTTTGGATGATTAGTTGA 3000
Qy 2923 GATGGGCACAAAGAGCTGAAGGAGTTGGAATCAATGCTTATGACATAGGCACAACT 2982
Db 3001 GATGGGCACAAAGAGCTGAAGGAGTTGGAATCAATGCTTATGACATAGGCACAACT 3060
Qy 2983 AATTAAAGGAGTCGAGAGACTTATCTCCGACAAACAGGCTCTAACCCATATTTAACTTT 3042
Db 3061 AATTAAAGGAGTCGAGAGACTTATCTCCGACAAACAGGCTCTAACCCATATTTAACTTT 3120
Qy 3043 GAACACCTCTGGTAGTGGAACAAATCTTTATAGATCTGTCTCTGATGATATAAGAGTTTCA 3102
Db 3121 GAACACCTCTGGTAGTGGAACAAATCTTTATAGATCTGTCTCTGATGATATAAGAGTTTCA 3180
Qy 3103 GTCTGTGGAGNAGAGATGCAAGTCTACAGTTTCGAGACACAGATGGAGTCTATGAGG 3162
Db 3181 GTCTGTGGAGNAGAGATGCAAGTCTACAGTTTCGAGACACAGATGGAGTCTATGAGG 3240
Qy 3163 TGGATCTTCAACAGATACAAATATTCTCAAGATTCAAGAGTTTGTAAACAGAAACTATG 3222
Db 3241 TGGATCTTCAACAGATACAAATATTCTCAAGATTCAAGAGTTTGTAAACAGAAACTATG 3300
Qy 3223 GGAAGATACATCAACCCGAGAAAGAAAGTTTCTGAAGAAAACCAACACCATGCAATGA 3282
Db 3301 GGAAGATACATCAACCCGAGAAAGAAAGTTTCTGAAGAAAACCAACACCATGCAATGA 3360
Qy 3283 ACGAATGCTATTTCATGGGTCCTTTTGTGAATGCAATTTCCACAAAGGCTTTGATGA 3342
Db 3361 ACGAATGCTATTTCATGGGTCCTTTTGTGAATGCAATTTTCACAAAGGCTTTGATGA 3420
Qy 3343 AAGGCATCGGTACATAGTGGTGTATGTTTGGAGCTGGCACTTTATTGTCTGAAAACCTCTTC 3402
Db 3421 AAGGCATCGGTACATAGTGGTGTATGTTTGGAGCTGGCACTTTATTGTCTGAAAACCTCTTC 3480
Qy 3403 CAAAGCAATCAATATGATATGTAATTTGGAAGGAGTACTGGGTTCAGTTTCACAAAGA 3462
Db 3481 CAAAGCAATCAATATGATATGTAATTTGGAAGGAGTACTGGGTTCAGTTTCACAAAGA 3540
Qy 3463 CAGATCTTGTATACATTTCCACAGCAGCTCTTTTGGCGGGTAACTTGGGAAAGTC 3522
Db 3541 CAGATCTTGTATACATTTCCACAGCAGCTCTTTTGGCGGGTAACTTGGGAAAGTC 3600
Qy 3523 TTTCTGCGAGTTTCAGTGAATGAAATGGCACTTCTCTCCAGGTCACTACTCAGTCAC 3582
Db 3601 TTTCTGCGAGTTTCAGTGAATGAAATGGCACTTCTCTCCAGGTCACTACTCAGTCAC 3660

Qy 3583 TGGTAGCCCCAGTGTAAATGGCTTAGCATTAGCTGATATGTTATTTTACAGAGCAGAACA 3642
Db 3661 TGGTAGCCCCAGTGTAAATGGCTTAGCATTAGCTGATATGTTATTTTACAGAGGAGAACA 3720
Qy 3643 GGCTTATCTCTGAGTATTTAAATTTACTTACACAGATTTATGAGGCTTGAAGGTATGGTTCGATGG 3702
Db 3721 GGCTTATCTCTGAGTATTTAAATTTACTTACACAGATTTATGAGGCTTGAAGGTATGGTTCGATGG 3780
Qy 3703 ATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACCTAAATCATCAAGACGACAGTGG 3762
Db 3781 ATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACCTAAATCATCAAGACGACAGTGG 3840
Qy 3763 CCTCTAGCTTTTACTCTCTTGGCTGAAAAAAA 3794
Db 3841 CCTCTAGCTTTTACTCTCTTGGCTGAAAAAAA 3872

RESULT 10
AAC85294
ID AAC85294 standard; cDNA; 6019 BP.
XX
AC AAC85294;
XX
DT 29-MAR-2001 (first entry)
XX
DE Human SPANK cDNA.
XX
KW SPANK; SAM; sterile alpha motif; PARP; insulin resistance;
KW poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK;
KW ankryrin repeat; cyclosoil; insulin-responsive aminopeptidase; IRAP; GLUT4;
KW adipocyte; insulin signalling pathway; hyperlipidaemia;
KW glucose intolerance; atheromatous disease; atherosclerosis; obesity;
KW cardiac insufficiency; coronary insufficiency; stroke;
KW high blood pressure; non-insulin dependent diabetes; hypertension;
KW hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy; ds.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 252..3735
FT /tag= a
FT /product= "Human SPANK"
FT /transl_except= (pos:768..878,aa:173..209)
FT /transl_except= (pos:1230..1337,aa:327..362)
FT /transl_except= (pos:1374..1445,aa:375..398)
FT /transl_except= (pos:1695..1823,aa:482..524)
FT /transl_except= (pos:2172..2282,aa:641..677)
XX
PN WO200077225-A1.
XX
PD 21-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015926.
XX
PR 11-JUN-1999; 99US-0138957P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (GSHO) GEN HOSPITAL CORP.
XX
PI Chi N, Lodish HP;
XX
DR WPI; 2001-091404/10.
DR P-PSDB; AAB47022.
XX
PT New insulin signaling protein SPANK, useful for reducing body mass,
PT glucose intolerance or insulin resistance and for preventing or treating
PT obesity-related and muscle-related diseases.
XX
PS Claim 3; Fig 4; 65pp; English.
XX
CC This sequence represents the human SPANK cDNA. The SPANK protein
comprises 3 domains: (a) a SAM (sterile alpha motif) domain; (b) a PARP

CC (poly adenosine diphosphate-ribose polymerase) catalytic domain; and (c)
CC an ANK domain composed of ankyrin repeats. SPANK is a cytosolic protein
CC which can poly(ADP-ribosyl)ate itself. SPANK binds insulin-responsive
CC aminopeptidase (IRAP) and modulates translocation of GLUT4 in the
CC perinuclear region of adipocytes. It is an effector in the insulin
CC signalling pathway in eukaryotic cells. SPANK is useful for reducing body
CC mass, reducing glucose intolerance or insulin resistance, for preventing
CC or treating obesity-related diseases or disorders, such as obesity,
CC cardiac insufficiency, coronary insufficiency, stroke, hypertension,
CC atherosclerotic disease, atherosclerosis, high blood pressure, non-insulin
CC dependent diabetes, hyperlipidemia, hyperuricemia and Syndrome X and is
CC also useful for preventing or treating muscle-related diseases or
CC disorders, such as muscular dystrophy, muscle atrophy and muscle fatigue.
CC Antibodies immunospecific for SPANK are useful for detecting the presence
CC of SPANK polypeptide in a biological sample
XX

Sequence 6019 BP; 1732 A; 1173 C; 1341 G; 1773 T; 0 U; 0 Other;

Query Match		89.2%;	Score 3388.8;	DB 4;	Length 6019;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 3390;		Conservative	0;	Mismatches	2;
				Indels	0;
				Gaps	0;
Qy	403	AGGTTTGGGCGGAAAGAGCTAGTTGAATATTTGGCTTCAGAAATGGTGCAAGTGTCCAAGC	462		
Db	449	AGGTTTGGGCGGAAAGAGCTAGTTGAATATTTGGCTTCAGAAATGGTGCAAGTGTCCAAGC	508		
Qy	463	ACGTGATGATGGGGCCCTTATTCCTTCATATGATCATGCTCTTTTGGTCATGCTGAAGT	522		
Db	509	ACGTGATGATGGGGCCCTTATTCCTTCATATGATCATGCTCTTTTGGTCATGCTGAAGT	568		
Qy	523	AGTCAATCTCTTTTGGCAGATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATAC	582		
Db	569	AGTCAATCTCTTTTGGCAGATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATAC	628		
Qy	583	TCCTCTCATGAGCTGCAATTAAGGAAAGATTGATGTTTGATGCTGCTGTACAGCA	642		
Db	629	TCCTCTCATGAGCTGCAATTAAGGAAAGATTGATGTTTGATGCTGCTGTACAGCA	688		
Qy	643	TGGAGCTGAGCCCAACATCCGAAATACAGATGGAAGGACAGCATTTAGCAGATCC	702		
Db	689	TGGAGCTGAGCCCAACATCCGAAATACAGATGGAAGGACAGCATTTAGCAGATCC	748		
Qy	703	ATCTGCCAAAGCAGTCTTACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCCAG	762		
Db	749	ATCTGCCAAAGCAGTCTTACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCCAG	808		
Qy	763	GAGTGGCAATGAAGAAATAATGATGGCTCTACTCAACATTAATGATCACTGCCAGC	822		
Db	809	GAGTGGCAATGAAGAAATAATGATGGCTCTACTCAACATTAATGATCACTGCCAGC	868		
Qy	823	AGTGCATGGCAGAAAGTCACTCCATTAACATTTGGCAGCAGATATACAGATGAAGAT	882		
Db	869	AGTGCATGGCAGAAAGTCACTCCATTAACATTTGGCAGCAGATATACAGATGAAGAT	928		
Qy	883	TGTACAGCTGTTTACTGCAACATGGAGCTGATGCTCATGCTAAAGATAAAGGTGATCTGGT	942		
Db	929	TGTACAGCTGTTTACTGCAACATGGAGCTGATGCTCATGCTAAAGATAAAGGTGATCTGGT	988		
Qy	943	ACCATTAACAATAGCTGTTCTTATTTGGTCATTTAAGAACTGAATTTGGTCAAGCA	1002		
Db	989	ACCATTAACAATAGCTGTTCTTATTTGGTCATTTAAGAACTGAATTTGGTCAAGCA	1048		
Qy	1003	TGGTGCCTGTGTAATGCAATGGATGTTGGCAATTCATCTCTTCATGAGGAGCTTC	1062		
Db	1049	TGGTGCCTGTGTAATGCAATGGATGTTGGCAATTCATCTCTTCATGAGGAGCTTC	1108		
Qy	1063	TAAAGAACAGGGTGAAGTATGTTCTCTTCTTTAAGTTATGGTCAGACCCCAACTGCT	1122		
Db	1109	TAAAGAACAGGGTGAAGTATGTTCTCTTCTTTAAGTTATGGTCAGACCCCAACTGCT	1168		
Qy	1123	CAATTGTCAATAAAGTGTATAGACTTGGCTCCCAACACAGTTTAAAGAAAGATT	1182		
Db	1169	CAATTGTCAATAAAGTGTATAGACTTGGCTCCCAACACAGTTTAAAGAAAGATT	1228		

Qy	1183	AGCATATGAATTTAAAGGCCCACTGGTTGCTCAAGCTGCAGAGAAAGCTGATGTTACTCG	1242		
Db	1229	AGCATATGAATTTAAAGGCCCACTGGTTGCTCAAGCTGCAGAGAAAGCTGATGTTACTCG	1288		
Qy	1243	AATCAAAAAACATCTCTCTCTGGAATATGGTGAATTTCAAGCATCTCTCAACACATGAAC	1302		
Db	1289	AATCAAAAAACATCTCTCTCTGGAATATGGTGAATTTCAAGCATCTCTCAACACATGAAC	1348		
Qy	1303	AGCATTCGATTTGCTGCTGCTCATCTCCATATCCCAAAAGAAAGCAATATGTGAATGTT	1362		
Db	1349	AGCATTCGATTTGCTGCTGCTCATCTCCATATCCCAAAAGAAAGCAATATGTGAATGTT	1408		
Qy	1363	GCTAAGAAAAAGGAGCAACATCAATGAAGAAAGCAATTTCTTGACTCTCTCGACGT	1422		
Db	1409	GCTAAGAAAAAGGAGCAACATCAATGAAGAAAGCAATTTCTTGACTCTCTCGACGT	1468		
Qy	1423	GGCATCTGAGAAAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAGGT	1482		
Db	1469	GGCATCTGAGAAAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAGGT	1528		
Qy	1483	TAATGCTCTGATTAATCTTGGTGCAGATCTCTACACAGAGCTGCATATTTGGTCACT	1542		
Db	1529	TAATGCTCTGATTAATCTTGGTGCAGATCTCTACACAGAGCTGCATATTTGGTCACT	1588		
Qy	1543	ACAAACCTGCCCGCTTACTCTGAGCTATGGGTGTGATCCTTAACATTTATATCCCTTCAGGG	1602		
Db	1589	ACAAACCTGCCCGCTTACTCTGAGCTATGGGTGTGATCCTTAACATTTATATCCCTTCAGGG	1648		
Qy	1603	CTTTACTGCTTTACAGATGGGAAATGTAAGCAAACTCTCTCAAGAGGGTATCTC	1662		
Db	1649	CTTTACTGCTTTACAGATGGGAAATGTAAGCAAACTCTCTCAAGAGGGTATCTC	1708		
Qy	1663	ATTAGGTAATTCAGAGCAGACAGCAATTCCTCGAGCTGCAAGGCTGGAGATGTCGA	1722		
Db	1709	ATTAGGTAATTCAGAGCAGACAGCAATTCCTCGAGCTGCAAGGCTGGAGATGTCGA	1768		
Qy	1723	AACTGTAATAAACTGTGTACTGTTGAGAGTGTCAAATGTCAGAGACATTTGAAGGCGTCA	1782		
Db	1769	AACTGTAATAAACTGTGTACTGTTGAGAGTGTCAAATGTCAGAGACATTTGAAGGCGTCA	1828		
Qy	1783	GTCTACACCACTTCAATTTGCGAGTAAAGAGGAGGCGCTTGTACCTTTGCAAAATGTC	1842		
Db	1829	GTCTACACCACTTCAATTTGCGAGTAAAGAGGAGGCGCTTGTACCTTTGCAAAATGTC	1888		
Qy	1843	ACAGATGGAGCTGATGTCATGCTTAAGATAAAGGAGGCGCTTGTACCTTTGCAAAATGTC	1902		
Db	1889	ACAGATGGAGCTGATGTCATGCTTAAGATAAAGGAGGCGCTTGTACCTTTGCAAAATGTC	1948		
Qy	1903	ATGTTCTTTATGACATTAATGAAGTTGCAAGAACTCTTGTAAACATGAGCAGATGTTAA	1962		
Db	1949	ATGTTCTTTATGACATTAATGAAGTTGCAAGAACTCTTGTAAACATGAGCAGATGTTAA	2008		
Qy	1963	TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022		
Db	2009	TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2068		
Qy	2023	AATTTGCAAACTTCTGCTCCAGCATGTCGAGACCTTACCAAAAAAAGGAGGATGAAA	2082		
Db	2069	AATTTGCAAACTTCTGCTCCAGCATGTCGAGACCTTACCAAAAAAAGGAGGATGAAA	2128		
Qy	2083	TACTCTTTTGTGATCTTGTAAAGATGAGATATCAAGATCTGCTTTAGGGGAGA	2142		
Db	2129	TACTCTTTTGTGATCTTGTAAAGATGAGATATCAAGATCTGCTTTAGGGGAGA	2188		
Qy	2143	TGCAAGCTTTGCTAGATGCTGCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTGTCTTC	2202		
Db	2189	TGCAAGCTTTGCTAGATGCTGCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTGTCTTC	2248		
Qy	2203	TCCTGATTAATTAATTCGCCCGGATACCAAGGAGCAGATTTCAACACCTTTTACATTTAGC	2262		
Db	2249	TCCTGATTAATTAATTCGCCCGGATACCAAGGAGCAGATTTCAACACCTTTTACATTTAGC	2308		

CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders

Sequence 4127 BP; 1245 A; 813 C; 934 G; 1135 T; 0 U; 0 Other;

Query Match	89.2%	Score 3387.2	DB 5	Length 4127
Best Local Similarity	99.9%	Pred. No. 0		
Matches 3389	Conservative	0	Mismatches 3	Indels 0
				Gaps 0

Qy	403	AGGTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTCCAAAGC	462
Db <th>208</th> <th>AGGTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCCTCAAGC</th> <th>267</th>	208	AGGTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCCTCAAGC	267

Qy	463	ACGTGATGATGGGGGCCCTATTTCCTCTTTTCATATGCAATGCTCTTTTGGTCATGCTGAAGT	522
D _b	268	ACGTGATGATGGGGGCCCTATTTCCTCTTTTCATATGCAATGCTCTTTTGGTCATGCTGAAGT	327

Qy	523	AGTCAATCTCCTTTTTCGACATGGTGCAGACCCCAATGCTCGAGATAAATTTGGAATTATAC	582
Db	328	AGTCAATCTCCTTTTTCGACATGGTGCAGACCCCAATGCTCGAGATAAATTTGGAATTATAC	387

Qy	583	TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTCACGCA	642
Dh	388	TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTCACGCA	447

QY	643	TGGAGCTGAGCGCAACCATCCGAAATCAGATCGAAGACGACGATTGATTTAGCAGATCC	702
db	448	TGGAGCTGAGCGTACCATCCGAAATCAGATCGAAGACGACGATTGATTTAGCAGATCC	507

[illegible]

763 GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTAATAATGTCACTGCCACGC 822

QY 823 AAGTGATGGCGAAAGTCAACTCCATTACATTTGGCAGCAGGATATACAGAGTAAAGAT 882

QY	883	TGTA CAGCTGTACTCGCAACATGGAGCTGATGCCATGCTAAAGATAAAGGTCATCTGGT	942
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943 ACCATTACACAATGCCGTTCTTATGGTCATATGAAGTAACTGAACCTTTGGTCAAGCA 1002

QY 1003 TGGTGCCGTGTAAATGCAATGGACATTGTGGCAATTCACCTCCTCTTCATGAGGCAGCTTC 1062

Qy 1063 TAAGAACAGGGTTGAAGTATGTCTCTCTCTTAAGTTATGGTCAGACCCCACTGCT 1122

DQ

688 TAAAGACCAAGGTTGAAGAATGCTTCATCATTAATGGTCCAGACCTCACAATGCATGCT
1123 CAATTGTCCACAATAAAGTGCTATAGACTTGGTCCCAACACACAGTTAAAAAGAAAGATT 1182

QY

DB	528	CAATGGTCACCAATATGAGGAGCTATAGACCTGGCTCCACACCAACAGATATAGAGGAGAGAT	567
QY	1183	AGCATATGAATTTAAGGCCCACTGGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG	1242

DB	988	ACGATATGAATTTAAAGGCCACCTCGTTCGTGCAAGCTGCACGAGAAAGCTGATGTTACTCG	104
QY	1243	AATCAAAAAACATCTCTCTCTGAAAAATGGTGAAATTTCAAGCATCTCTCAAAACACATGAAC	1302

DB	1048	AATCAAAAAACATCTCTCTCTGAAAAGTGTAATTTCAAGCATCTCTCAAAACAATGAAC	110
QY	1303	AGCATTCGATTGCTGCTGTCATCTCCATATCCAAAAAGAAACAAATATGTGAACCTTT	1362

DB . 1108 AGCATTGCGTCTGCTGCACTCTCCATATCCCAAAGAAACAAATATGTGAACTGTT 1116

QY	1363	GCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTTAAAGAAATCTTTGACTCCTCTGCAGT	14227
db	1168	GCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTTAAAGAAATCTTTGACTCCTCTGCAGT	1227

Accession	Sequence	Length
Qy	GGCATCTGAGAAAGCTCATATATGATCTTGTGAAGTAGTGGTGAACATATGAACCAAGGT	14823
Db	GGCATCTGAGAAAGCTCATATATGATCTTGTGAAGTAGTGGTGAACATATGAACCAAGGT	12878

Qy	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500	
Qy	TAATGCTCTGGATAA	TCTTGGTCAGACTT	CTTACACAGAGCTT	CTACACAGAGCTT	CTGTCATATTTGGT	CATCT	1542	CTGTCATCT	1543	CTGTCATCT	1544	CTGTCATCT	1545	CTGTCATCT	1546	CTGTCATCT	1547	CTGTCATCT	1548
Db	TAATGCTCTGGATAA	TCTTGGTCAGACTT	CTTACACAGAGCTT	CTACACAGAGCTT	CTGTCATATTTGGT	CATCT	1549	CTGTCATCT	1550	CTGTCATCT	1551	CTGTCATCT	1552	CTGTCATCT	1553	CTGTCATCT	1554	CTGTCATCT	1555

Qy	1543	ACAAACCTGCCGCTACTCCTGAGCTATGGGTGTGATCCTTAACATTATATCCCTTCAGGG	1602
Db	1348	ACAAACCTGCCGCTACTCCTGAGCTATGGGTGTGATCCTTAACATTATATCCCTTCAGGG	1407

Accession	Gene	Accession	Gene
Qy	1603	CTTTACTGCTTTACAGATGGGAAATGAAAATGTAACAGAACTCTCTCCAAAGAGGGTATCTC	1662
Db	1408	CTTTACTGCTTTACAGATGGGAAATGAAAATGTAACAGAACTCTCCAAAGAGGGTATCTC	1467

Qy	1663	ATTAGGTAATTTCAGAGCGACAGACAAATTCGTGGAGCTGC	AAAGCTGGAGATGTCGA	17222
Dp	1468	ATTAGGTAATTTCAGAGCGACAGACAAATTCGTGGAGCTGC	AAAGCTGGAGATGTCGA	15273

QY	1723	AACTGTA	AAAAAA	AACTGT	TACTGT	TTCAGAG	TGTCA	ACTGC	AGACAT	TGAAG	GGCGGT	CA	1782
Dh	1528	AACTGT	AAAA	AAAACT	GTGTCT	TCAGAG	TGTCA	ACTGC	AGACAT	TGAAG	GGCGGT	CA	1587

Qy	1783	GTCTACACCACTTCATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGTGGGAATATCTGCT	1842
ph	1590	CGCTGTACACCGCTTCCTCATTTTGGCTGCTGAGCTATTAACAGAGTGTCCGTGTGGGAATATCTGCT	1647

QY	1843	ACAGCATTGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTTGTACTTTTGCAACAATGC	1902
b-	1548	TTCCTTCCCTCGCTGCTGGCTGCTTAAGCATTAAGCGCGCCCTGTCATCTTTTGTGCAATGC	1702

[illegible][illegible]

QY 2023 AATTTGCAAACTTCTGCTCCAGCATGGTGAGACCCCTACCAAAAAAAACAGGGATGAAA 2082

QY 2083 TACTCCTTTGGATCTGTTAAGATGCGAGATACAGATATTACAGATCTCTTAGGGGAGA 2142

QY 2143 TGCAGCTTTGCTAGATGCTGCCAAGAAGGTTGTTTACCCAGAGTGAAGAAGTTGTCTTC 2202

2203 TCCTGATTAATGTCCTGGATACCAAGCAGACATTCAACACCTTTACATTATGC 22622

[illegible]

QY 2323 TGCCCAAGACAAAGGAGCATTTATTCCTTACATAATGCAGCATCTTACGGGCATGTAGA 2382

2168 TGGCAGACACACAGGAGAGCATTATTCCTTACACATAATGCAGACATCATACCGGACATGACG 220
2383 TGTAGCAGCTCTACTAATAAGTATAATGCATGTGTCAATGCCACGGACAAATATGGGCGTTT 2442

DD
2188 TGTAGCAGCTCTACTTAATATAGTATATAAGCATGTGTGTCAATGCTCCAGGGACAAAATGGGCTTTT 2294

Qy 2443 CACACCTTTGCGAAGCAGCCCAAAAGGCGAACAACAGCTTTGTGCTTTGCTAGC 2502
Db |||||
Qy 2248 CACACCTTTGCGAAGCAGCCCAAAAGGCGAACAACAGCTTTGTGCTTTGCTAGC 2307
Db |||||
Qy 2503 CCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGCAACAACCTTTAGATTTAGTTTC 2562
Db |||||
Qy 2308 CCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGCAACAACCTTTAGATTTAGTTTC 2367
Db |||||
Qy 2563 AGCGATGATGTACGCGCTCTTTGACAGCAGCCATGCCCCCTCTGCTCTGCGCCCTTTG 2622
Db |||||
Qy 2368 AGCAGATGATGTACGCGCTCTTTGACAGCAGCCATGCCCCCTCTGCTCTGCGCCCTTTG 2427
Db |||||
Qy 2623 TTACAAGCCTCAAGTGTCTCAATGTGTGAGAGGCCAGGCCAATGCTGCTCTCTC 2682
Db |||||
Qy 2428 TTACAAGCCTCAAGTGTCTCAATGTGTGAGAGGCCAGGCCAATGCTGCTCTCTC 2487
Db |||||
Qy 2683 TTCAAGGTCATCTAGCCCATCAAGCCCTTTCTGACAGCAGCTCTTGACACTTTATCTGG 2742
Db |||||
Qy 2488 TTCAAGGTCATCTAGCCCATCAAGCCCTTTCTGACAGCAGCTCTTGACACTTTATCTGG 2547
Db |||||
Qy 2743 GAGTTTTTTCAGAACTGTCTTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTGCTCCAGTTT 2802
Db |||||
Qy 2548 GAGTTTTTTCAGAACTGTCTTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTGCTCCAGTTT 2607
Db |||||
Qy 2803 GGAGAAAAGAGAGGTTCCAGAGTAGATTTTAGCATTAATCTCAATTCGTAGGAATCTTGG 2862
Db |||||
Qy 2608 GGAGAAAAGAGAGGTTCCAGAGTAGATTTTAGCATTAATCTCAATTCGTAGGAATCTTGG 2667
Db |||||
Qy 2863 ACTTGAGCACCCTAATGATATATTTTGAGAGAGACAGATCACTTTGGATGATTTAGTTGA 2922
Db |||||
Qy 2668 ACTTGAGCACCCTAATGATATATTTTGAGAGAGACAGATCACTTTGGATGATTTAGTTGA 2727
Db |||||
Qy 2923 GATGGGGCAACAGGAGCTGAAGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 2982
Db |||||
Qy 2728 GATGGGGCAACAGGAGCTGAAGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 2787
Db |||||
Qy 2983 AATTAAAGGAGTCAGAGACTTATCTCGGACAAACAGGCTTTAAACCATATTTAACTTT 3042
Db |||||
Qy 2788 AATTAAAGGAGTCAGAGACTTATCTCGGACAAACAGGCTTTAAACCATATTTAACTTT 2847
Db |||||
Qy 3043 GAACACCTCTGGTAGTGGACAACTTTATAGATCTGTCTCTGATGATAAGAGTTTCA 3102
Db |||||
Qy 2848 GAACACCTCTGGTAGTGGACAACTTTATAGATCTGTCTCTGATGATAAGAGTTTCA 2907
Db |||||
Qy 3103 GTCTGTGGAGAGAGATGCAAGATACAGTTTCGAGAGCAGAGATGGAGTCAATGCAGG 3162
Db |||||
Qy 2908 GTCTGTGGAGAGAGATGCAAGATACAGTTTCGAGAGCAGAGATGGAGTCAATGCAGG 2967
Db |||||
Qy 3163 TGGAACTCTTCAACAGATACAAATATTTCTCAAGATTCAGAGGTTTGTAAACAAGAACTATG 3222
Db |||||
Qy 2968 TGGAACTCTTCAACAGATACAAATATTTCTCAAGATTCAGAGGTTTGTAAACAAGAACTATG 3027
Db |||||
Qy 3223 GGAAGATACACTCACCGGAGAAAGAGTTTCTGAAAGAAACCAACCAATGCATGA 3282
Db |||||
Qy 3028 GGAAGATACACTCACCGGAGAAAGAGTTTCTGAAAGAAACCAACCAATGCATGA 3087
Db |||||
Qy 3283 ACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 3342
Db |||||
Qy 3088 ACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 3147
Db |||||
Qy 3343 AAGCATCGGTACATAGTGTGTATTTTGGAGCTGGCAATTTATTTTGGTGAAGAACTCTTC 3402
Db |||||
Qy 3148 AAGCATCGGTACATAGTGTGTATTTTGGAGCTGGCAATTTATTTTGGTGAAGAACTCTTC 3207
Db |||||
Qy 3403 CAAAAGCAATCAATATGATATGAAATTTGAGAGGAGTACTGGGTGTCAGTTTCAACAAGA 3462
Db |||||
Qy 3208 CAAAAGCAATCAATATGATATGAAATTTGAGAGGAGTACTGGGTGTCAGTTTCAACAAGA 3267
Db |||||
Qy 3463 CAGATCTTTGTTACATTTGCCACAGGAGCTCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3522
Db |||||
Qy 3268 CAGATCTTTGTTACATTTGCCACAGGAGCTCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3327
Db |||||
Qy 3523 TTTCCTGCAGTTTCAGTGCATGAAATGGCACATTTCTCTCCAGGTCTACTCAGTCAAC 3582

Db |||||
Qy 3328 TTTCCTGCAGTTTCAGTGCATGAAATGGCACATTTCTCTCCAGGTCTACTCAGTCAAC 3387
Db |||||
Qy 3583 TGGTAGGCCAGGTGTAATGGCCCTAGCATTTAGCTGAAATATGTTATTTACAGAGGAGAAC 3642
Db |||||
Qy 3388 TGGTAGGCCAGGTGTAATGGCCCTAGCATTTAGCTGAAATATGTTATTTACAGAGGAGAAC 3447
Db |||||
Qy 3643 GGCTTATCTGAGTATTTTAAATTTACTTTACAGATTTATGAGGCTGAAAGTATGGTTCGATGG 3702
Db |||||
Qy 3448 GGCTTATCTGAGTATTTTAAATTTACTTTACAGATTTATGAGGCTGAAAGTATGGTTCGATGG 3507
Db |||||
Qy 3703 ATAAATAGTTTATTTTAAAGAACTAAATTTCCACTGAACCTTAAATCATCAAGCAGCAGTGG 3762
Db |||||
Qy 3508 ATAAATAGTTTATTTTAAAGAACTAAATTTCCACTGAACCTTAAATCATCAAGCAGCAGTGG 3567
Db |||||
Qy 3763 CCTCTAGCTTTTACTCTCTCTTCTGCTGAAAAAAA 3794
Db |||||
Qy 3568 CCTCTAGCTTTTACTCTCTCTTCTGCTGAAAAAAA 3599
Db |||||
RESULT 12
AAF63930
ID AAF63930 standard; DNA; 4406 BP.
XX
AC AAF63930;
XX
XX 05-APR-2001 (first entry)
DT
DE Human tankyrase2 clone consensus oligonucleotide SEQ ID NO: 106.
XX
XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
KW inflammatory disorder; ds.
XX
XX Homo sapiens.
OS
PN W0200100849-A1.
XX
PD 04-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US017827.
XX
PR 29-JUN-1999; 99US-0141582P.
XX
XX (ICOS-) ICOS CORP.
PA
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
PI WPI; 2001-102896/11.
DR P-PSDB; AAB66290.
XX
PT New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX
PS Example 2; Page 168-173; 242pp; English.
XX
CC The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
XX
SQ Sequence 4406 BP; 1268 A; 910 C; 1054 G; 1174 T; 0 U; 0 Other;
Query Match 89.2%; Score 3387.2; DB 5; Length 4406;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTGGCGGGAAGACCGTAGTTGAATTTGCTTCAGAAATGGTCAAGTGTCCAGC 462
|||

Qy 2623 TTCAAGCCTCAAGTGTCTCAATGTTGTGAGNAGCCGAGAGCCACTGCAGATGCTCTCTC 2682
Db |||||
Qy 2707 TTCAAGCCTCAAGTGTCTCAATGTTGTGAGNAGCCGAGAGCCACTGCAGATGCTCTCTC 2766
Db |||||
Qy 2683 TTCAAGTCCATCTAGCCCATCAAGCCTTTCTGACGACGAGCTCTGACAACTTATCTGG 2742
Db |||||
Qy 2767 TTCAAGTCCATCTAGCCCATCAAGCCTTTCTGACGACGAGCTCTGACAACTTATCTGG 2826
Db |||||
Qy 2743 GAGTTTTTCAGAACTGCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGCTCTCCAGTTT 2802
Db |||||
Qy 2827 GAGTTTTTCAGAACTGCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGCTCTCCAGTTT 2886
Db |||||
Qy 2803 GGAGAAAAGAGGTTCCAGAGTAGATTTTAGCATAACTCAATTCGTAAAGGATCTTGG 2862
Db |||||
Qy 2887 GGAGAAAAGAGGTTCCAGAGTAGATTTTAGCATAACTCAATTCGTAAAGGATCTTGG 2946
Db |||||
Qy 2863 ACTTGAGCACCCTAATGATATATTTTGAGAGAGACAGATCACTTTGGATGTATTAGTTGA 2922
Db |||||
Qy 2947 ACTTGAGCACCCTAATGATATATTTTGAGAGAGACAGATCACTTTGGATGTATTAGTTGA 3006
Db |||||
Qy 2923 GATGGGCAACAGAGCTGAAGGAGATTTGGAACTCAATGCTTATGGACATAGGCACAACT 2982
Db |||||
Qy 3007 GATGGGCAACAGAGCTGAAGGAGATTTGGAACTCAATGCTTATGGACATAGGCACAACT 3066
Db |||||
Qy 2983 AATTAAAGGATCGAGAGCTTATCTCGGACCAAGAGGCTTTAAACCATATTTAACTTT 3042
Db |||||
Qy 3067 AATTAAAGGATCGAGAGCTTATCTCGGACCAAGAGGCTTTAAACCATATTTAACTTT 3126
Db |||||
Qy 3043 GAACACCTCTGGTAGTGGAACTTCTATAGATCTGTCTCTGATGATAAGAGTTTCA 3102
Db |||||
Qy 3127 GAACACCTCTGGTAGTGGAACTTCTATAGATCTGTCTCTGATGATAAGAGTTTCA 3186
Db |||||
Qy 3103 GTCTGTGGAGAAAGATGCAAGTACAGTTTCGAGACACAGATGGAGTCAATGAGG 3162
Db |||||
Qy 3187 GTCTGTGGAGAAAGATGCAAGTACAGTTTCGAGACACAGATGGAGTCAATGAGG 3246
Db |||||
Qy 3163 TGGAACTCTCAACAGATACATATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3222
Db |||||
Qy 3247 TGGAACTCTCAACAGATACATATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3306
Db |||||
Qy 3223 GGAAGATACACTCAACGGAGAAAAGTTCTGAAAGAAACCAACCAATGCAATGA 3282
Db |||||
Qy 3307 GGAAGATACACTCAACGGAGAAAAGTTCTGAAAGAAACCAACCAATGCAATGA 3366
Db |||||
Qy 3283 ACGAATGCTATTTCAATGGTCTCTTTTGTGAATGCAATATCAAAAGCTTTGATGA 3342
Db |||||
Qy 3367 ACGAATGCTATTTCAATGGTCTCTTTTGTGAATGCAATATCAAAAGCTTTGATGA 3426
Db |||||
Qy 3343 AAGGCATGCGTACATAGTGTGATGTTTGGAGCTGGCATTTATTTGCTGAAAACCTCTTC 3402
Db |||||
Qy 3427 AAGGCATGCGTACATAGTGTGATGTTTGGAGCTGGCATTTATTTTGTGAAAACCTCTTC 3486
Db |||||
Qy 3403 CAAAAGCAATCAATATGTATATGAAATTTGAGAGAGGTACTGGGTGTCAGTTTCAAAAGA 3462
Db |||||
Qy 3487 CAAAAGCAATCAATATGTATATGAAATTTGAGAGAGGTACTGGGTGTCAGTTTCAAAAGA 3546
Db |||||
Qy 3463 CAGATCTGTGTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAAACCTTTGGGAAAGTC 3522
Db |||||
Qy 3547 CAGATCTGTGTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAAACCTTTGGGAAAGTC 3606
Db |||||
Qy 3523 TTTCTCGAGTTTCAATGCAATGAAATGGGACATTTCTCTCCAGGTCACTCACTCAGTCAC 3582
Db |||||
Qy 3607 TTTCTCGAGTTTCAATGCAATGAAATGGGACATTTCTCTCCAGGTCACTCACTCAGTCAC 3666
Db |||||
Qy 3583 TGGTAGGCCAGTGTAAATGGCCCTAGCATTAGCTGAAATATGTTATTTACAGAGAGAAACA 3642
Db |||||
Qy 3667 TGGTAGGCCAGTGTAAATGGCCCTAGCATTAGCTGAAATATGTTATTTACAGAGAGAAACA 3726
Db |||||
Qy 3643 GGCTTATCTCGAGTATTTAATTAATTACAGATATGAGGCTGAAAGTATGTCGATGG 3702
Db |||||
Qy 3727 GGCTTATCTCGAGTATTTAATTAATTACAGATATGAGGCTGAAAGTATGTCGATGG 3786
Db |||||
Qy 3703 ATAAATAGTTATTTTAAGAACTAATTTCCACTGAACCTTAAATCATCAAGACGACGATGG 3762

Db 3787 ATAAATAGTTATTTTAAGAACTAATTTCCACTGACCTAAATCTCAAGACGACGATGG 3846
Qy 3763 CCTCTAGTTTACTCCTTTGCTGAAAAAAA 3794
Db 3847 CCTCTAGTTTACTCCTTTGCTGAAAAAAA 3878
RESULT 13
AAF63953
ID AAF63953 standard; DNA; 4992 BP.
XX AAF63953;
AC AAF63953;
XX 05-APR-2001 (first entry)
XX Human tankyrase2 TANK2-SHORT coding sequence SEQ ID NO: 134.
XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
XX inflammatory disorder; ds.
XX Homo sapiens.
XX WO200100849-A1.
XX 04-JAN-2001.
XX 28-JUN-2000; 2000WO-US017827.
XX 29-JUN-1999; 99US-0141582P.
XX (ICOS-) ICOS CORP.
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
XX WPI: 2001-102896/11.
XX P-PSDB; AAB66295.
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
XX poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
XX inflammatory and autoimmune disorders.
XX Claim 6; Page 195-200; 242pp; English.
XX The present invention provides the protein and coding sequence for the
XX human tankyrase2 protein. This is found in two different versions,
XX designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
XX ribosylation activity and is involved in the modification of TRF1, which
XX is a telomere-specific binding protein. The regulation of telomere
XX length, in which TRF1 has a role, is linked to ageing and cancer. The
XX sequences are useful in the treatment of cancers and inflammatory
XX disorders
SQ Sequence 4992 BP; 1454 A; 1064 C; 1191 G; 1283 T; 0 U; 0 Other;
Query Match 89.28; Score 3387.2; DB 5; Length 4992;
Best Local Similarity 99.94; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTGGCGGAAAGACGCTAGTTGAAATATTTGCTTCAGAAATGGTCCAAAGC 462
Db 1073 AGGTTTTGGCGGAAAGACGCTAGTTGAAATATTTGCTTCAGAAATGGTCCAAAGC 1132
Qy 463 ACGTGATGATGGGGGCTTATTCCTCTTCATAATGCAATGCTCTTTGGTCATGCTGAAGT 522
Db 1133 ACGTGATGATGGGGGCTTATTCCTCTTCATAATGCAATGCTCTTTGGTCATGCTGAAGT 1192
Qy 523 AGTCNAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATTCGAATTATAC 582
Db 1193 AGTCNAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATTCGAATTATAC 1252
Qy 583 TCCTCTCCATGAAGCTGCAATTAAGGAAAGATGATGTTTGCATTTGCTGTTTACAGCA 642

Db 1253 TCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGCTATGCTTTACAGCA 1312
 Qy 643 TGGAGCTGAGCCAAACCAATCCGAATACAGATGGAAGGACAGATTTAGCAGATCC 702
 Db 1313 TGGAGCTGAGCCAAACCAATCCGAATACAGATGGAAGGACAGATTTAGCAGATCC 1372
 Qy 703 ATCTGCCAAAGCAGTGTCTTACTGTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 762
 Db 1373 ATCTGCCAAAGCAGTGTCTTACTGTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 1432
 Qy 763 GAGTGGCAATGAAGAAATAATGATGGCTCTACTCAACCAATTAAGTGAATGCAATGCGCAGC 822
 Db 1433 GAGTGGCAATGAAGAAATAATGATGGCTCTACTCAACCAATTAAGTGAATGCAATGCGCAGC 1492
 Qy 823 AAGTCATGCGCAGAAAGTCAACTCCATTAATTTGCGACGAGATATAACAGATTAAGAT 882
 Db 1493 AAGTCATGCGCAGAAAGTCAACTCCATTAATTTGCGACGAGATATAACAGATTAAGAT 1552
 Qy 883 TGTCAGCTGTTTACTGCAACATGAGCTGATGTCATGCTAAAGATAAAGGTGATCTGGT 942
 Db 1553 TGTCAGCTGTTTACTGCAACATGAGCTGATGTCATGCTAAAGATAAAGGTGATCTGGT 1612
 Qy 943 ACCATTACAAATGCTGTTTATTGTCATTAATGAAGTAATGAATGCTGTTTGGTCAAGCA 1002
 Db 1613 ACCATTACAAATGCTGTTTATTGTCATTAATGAAGTAATGAATGCTGTTTGGTCAAGCA 1672
 Qy 1003 TGGTCCCTGTGAATGCAATGGACTGTGGCAATTTCACTCTTTCATGAGGCGAGCTTC 1062
 Db 1673 TGGTCCCTGTGAATGCAATGGACTGTGGCAATTTCACTCTTTCATGAGGCGAGCTTC 1732
 Qy 1063 TAAGAAACAGGGTGTGAAGTATGTTCTCTCTTTAAGTTATGGTCAGACCCCAACACTGCT 1122
 Db 1733 TAAGAAACAGGGTGTGAAGTATGTTCTCTCTTTAAGTTATGGTCAGACCCCAACACTGCT 1792
 Qy 1123 CAATTTGTCAAAATAAAGTGTATAGACTGTGCTCCCAACACACAGTTTAAAGAAAGATT 1182
 Db 1793 CAATTTGTCAAAATAAAGTGTATAGACTGTGCTCCCAACACACAGTTTAAAGAAAGATT 1852
 Qy 1183 AGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG 1242
 Db 1853 AGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG 1912
 Qy 1243 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAAAACACATGAAC 1302
 Db 1913 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAAAACACATGAAC 1972
 Qy 1303 AGCATGCTGCTGCTGCTGCTATCCATATCCCAAAAGAAAGCAATATGGAATCTGT 1362
 Db 1973 AGCATGCTGCTGCTGCTGCTATCCATATCCCAAAAGAAAGCAATATGGAATCTGT 2032
 Qy 1363 GCTAAGAAAGGAGCAACATCAATGAAGAAAGTAAAGAACTTCTTGACTCTCTGCACT 1422
 Db 2033 GCTAAGAAAGGAGCAACATCAATGAAGAAAGTAAAGAACTTCTTGACTCTCTGCACT 2092
 Qy 1423 GGCATCTGAGAAAGTCAATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT 1482
 Db 2093 GGCATCTGAGAAAGTCAATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT 2152
 Qy 1483 TAAATGCTCTGGATAATCTTTGGTCAGACTCTCTACACAGAGCTGATATTTGGTCACT 1542
 Db 2153 TAAATGCTCTGGATAATCTTTGGTCAGACTCTCTACACAGAGCTGATATTTGGTCACT 2212
 Qy 1543 ACAACCTGCGCCCTACTCTGAGCTATGGGTGATGCTTAACATTAATATCCCTTCAGGG 1602
 Db 2213 ACAACCTGCGCCCTACTCTGAGCTATGGGTGATGCTTAACATTAATATCCCTTCAGGG 2272
 Qy 1603 CTTTACTCTTTACAGATGGGAAATGAATAATGATCAAGCACTCTCCAGAGGGTATCTC 1662
 Db 2273 CTTTACTCTTTACAGATGGGAAATGAATAATGATCAAGCACTCTCCAGAGGGTATCTC 2332
 Qy 1663 ATTAGGTAAATCAGAGGAGCAGACAAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTCGA 1722
 Db 2333 ATTAGGTAAATCAGAGGAGCAGACAAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTCGA 2392

Qy 1723 AACTGTAAAAAACTGTGTACTGTTTCAAGTGTCAACTGCAGAGACATTTGAAGGCGGTCA 1782
 Db 2393 AACTGTAAAAAACTGTGTACTGTTTCAAGTGTCAACTGCAGAGACATTTGAAGGCGGTCA 2452
 Qy 1783 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1842
 Db 2453 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 2512
 Qy 1843 ACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCCCTTTGACCTTTGCACAATGC 1902
 Db 2513 ACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCCCTTTGACCTTTGCACAATGC 2572
 Qy 1903 ATGTTCTTATGCAATTAATGAAGTTGCAAGACTTCTGTTTAAACATGAGCAGTAGTTAA 1962
 Db 2573 ATGTTCTTATGCAATTAATGAAGTTGCAAGACTTCTGTTTAAACATGAGCAGTAGTTAA 2632
 Qy 1963 TGTAAGTGAATTTATGGAATTTTACACCTTTATCAATGAAGCAGCAGCAAAAGGAAATATGA 2022
 Db 2633 TGTAAGTGAATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2692
 Qy 2023 AATTTGCAAACTTCTGCTCCAGCATGTGTCAGACCTTACCAAAAAAACAAGGATGGAA 2082
 Db 2693 AATTTGCAAACTTCTGCTCCAGCATGTGTCAGACCTTACCAAAAAAACAAGGATGGAA 2752
 Qy 2083 TACTCCTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGTTAGGGGAGA 2142
 Db 2753 TACTCCTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2812
 Qy 2143 TGCAAGCTTTGCTAGATGCTGCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTTGTCTTC 2202
 Db 2813 TGCAAGCTTTGCTAGATGCTGCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTTGTCTTC 2872
 Qy 2203 TCCTGTAATTAATTAATTTAGAAAGTTGCAAGATTTGTTTACAACACGAGCTGATGCA 2322
 Db 2873 TCCTGTAATTAATTAATTTAGAAAGTTGCAAGATTTGTTTACAACACGAGCTGATGCA 2392
 Qy 2323 TGCCCAAGCAAAAGGAGGACTTATTTCTTTTACAATAATGCAAGCATCTTACGGGCAATGAGA 2382
 Db 2993 TGCCCAAGCAAAAGGAGGACTTATTTCTTTTACAATAATGCAAGCATCTTACGGGCAATGAGA 3052
 Qy 2383 TGTAGCAGCTCTACTAATAAAGTATAATGCAATGCTGTCATGTCGCAAGCAATGCGGCTTT 2442
 Db 3053 TGTAGCAGCTCTACTAATAAAGTATAATGCAATGCTGTCATGTCGCAAGCAATGCGGCTTT 3112
 Qy 2443 CACACCTTTGCAAGCAGCCCAAAAGGAGCAACACAGCTTTGCTGCTTTGTTGCTAGC 2502
 Db 3113 CACACCTTTGCAAGCAGCCCAAAAGGAGCAACACAGCTTTGCTGCTTTGTTGCTAGC 3172
 Qy 2503 CCATGGAGCTGACCCGACTCTTTAAAAATCAGAAAGGAGCAACACCTTTAGATTTAGTTTC 2562
 Db 3173 CCATGGAGCTGACCCGACTCTTTAAAAATCAGAAAGGAGCAACACCTTTAGATTTAGTTTC 3232
 Qy 2563 AGCGGATGATGTCAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTGCCCCCTTC 2622
 Db 3233 AGCGGATGATGTCAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTGCCCCCTTC 3292
 Qy 2623 TTACAAGCCTCAAGTGTCTAATGTTGAGAAAGCCAGGAGCCACTGCAGATGCTCTC 2682
 Db 3293 TTACAAGCCTCAAGTGTCTAATGTTGAGAAAGCCAGGAGCCACTGCAGATGCTCTC 3352
 Qy 2683 TTCAAGCTCCATCTAGCCCATCAAGCTTTCTGACAGCAGAGTCTTGAACCTTATCTGG 2742
 Db 3353 TTCAAGCTCCATCTAGCCCATCAAGCTTTCTGACAGCAGAGTCTTGAACCTTATCTGG 3412
 Qy 2743 GAGTTTTTACAGACTGCTCTTCAAGTGTAGTTTCAAGTGAAGCAGAGGCTGCTTCCAGTTT 2802
 Db 3413 GAGTTTTTACAGACTGCTCTTCAAGTGTAGTTTCAAGTGAAGCAGAGGCTGCTTCCAGTTT 3472

QY 2803 GGAGAAAAAGGAGGTTCCAGAGTAGATTTTAGCATAACTCAATTCGTAAAGGAATCTTGG 2862
DB 3473 GGAGAAAAAGGAGGTTCCAGAGTAGATTTTAGCATAACTCAATTCGTAAAGGAATCTTGG 3532
QY 2863 ACTTGAGCACCTAATGGATATATTTTGAGAGAGAACAGATCACTTTTGGATGTATTAGTTGA 2922
DB 3533 ACTTGAGCACCTAATGGATATATTTTGAGAGAGAACAGATCACTTTTGGATGTATTAGTTGA 3592
QY 2923 GATGGGCACAAGAGAGCTGAAGAGATTTGGAATCAATGCTTTATCGACATAGGCACAACT 2982
DB 3593 GATGGGCACAAGAGAGCTGAAGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 3652
QY 2983 AATTAAAGGAGTCAGAGACTTATCTCCGGACAAAGGCTTTAACCCATATTTAACTTT 3042
DB 3653 AATTAAAGGAGTCAGAGACTTATCTCCGGACAAAGGCTTTAACCCATATTTAACTTT 3712
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DB 3713 GAACACCTCTGCTAGTGAACAAATCTTTATAGATCTGTCTCTGATGATGAAGAGTTTCA 3772
QY 3103 GTCTGTGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCATGCAGG 3162
DB 3773 GTCTGTGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCATGCAGG 3832
QY 3163 TGGAAATCTTCAACAGATCAATATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3222
DB 3833 TGGAAATCTTCAACAGATCAATATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3892
QY 3223 GGAAAGATACACTCAACCGGAGAAAGAGTTTCTGAAGAAACCAACACCATGCCAATGA 3282
DB 3893 GGAAAGATACACTCAACCGGAGAAAGAGTTTCTGAAGAAACCAACACCATGCCAATGA 3952
QY 3283 ACGAATGCTATTTTCATGGGTCCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 3342
DB 3953 ACGAATGCTATTTTCATGGGTCCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 4012
QY 3343 AAGCATCGGTACATAGTGGTGTATTTTGGAGCTGGCATTTATTTTGGTGAAGAACTCTTC 3402
DB 4013 AAGCATCGGTACATAGTGGTGTATTTTGGAGCTGGCATTTATTTTGGTGAAGAACTCTTC 4072
QY 3403 CAAGAAGCAATCAATATGTATATGAAATTTGGAGGAGTACTGGGTGCCAGTTCCAAAGA 3462
DB 4073 CAAGAAGCAATCAATATGTATATGAAATTTGGAGGAGTACTGGGTGCCAGTTCCAAAGA 4132
QY 3463 CAGATCTTTGTACATTTGCCACAGCAGCTGCTCTTTTGGCGGTAACCTTTGGGAAAGTC 3522
DB 4133 CAGATCTTTGTACATTTGCCACAGCAGCTGCTCTTTTGGCGGTAACCTTTGGGAAAGTC 4192
QY 3523 TTTCTGTCAGTTTCAATGCAATGCAATGCGACATCTCTCTCAGGTGCATCTACTCAGTCAC 3582
DB 4193 TTTCTGTCAGTTTCAATGCAATGCAATGCGACATCTCTCTCAGGTGCATCTACTCAGTCAC 4252
QY 3583 TGGTAGGCCAGTGAATGSCCTAGCATTTAGTGAATATGTTATTTACAGAGGAGAAACA 3642
DB 4253 TGGTAGGCCAGTGAATGSCCTAGCATTTAGTGAATATGTTATTTACAGAGGAGAAACA 4312
QY 3643 GGCCTTATCTGAGTATTTAAATTTACTTACCAGATTTAGAGGCTGAAGGTATGGTCGATGG 3702
DB 4313 GGCCTTATCTGAGTATTTAAATTTACTTACCAGATTTAGAGGCTGAAGGTATGGTCGATGG 4372
QY 3703 ATAAATAGTATTTTAAAGAACTAAATTCACCTGAACCTTAAATCATCAAGCAGCAGTGG 3762
DB 4373 ATAAATAGTATTTTAAAGAACTAAATTCACCTGAACCTTAAATCATCAAGCAGCAGTGG 4432
QY 3763 CCTCTACGTTTTTACTCCTTTGCTGAAAAAAA 3794
DB 4433 CCTCTACGTTTTTACTCCTTTGCTGAAAAAAA 4464

RESULT 14
ID AAF63952
XX AAF63952 standard; DNA; 5002 BP.

AAFP63952;
05-APR-2001 (first entry)
Human tankyrase2 TANK2-LONG coding sequence SEQ ID NO: 132.
Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
inflammatory disorder; ds.
Homo sapiens.
WO200100849-A1.
04-JAN-2001.
28-JUN-2000; 2000WO-US017827.
29-JUN-1999; 99US-0141582P.
(ICOS-) ICOS CORP.
Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
WPI; 2001-102896/11.
P-PSDB; AAB66294.
New tankyrase2 polypeptides, useful for treating conditions mediated by
poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
inflammatory and autoimmune disorders.
Claim 5; Page 185-190; 242pp; English.
The present invention provides the protein and coding sequence for the
human tankyrase2 protein. This is found in two different versions,
designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
ribosylation activity and is involved in the modification of TRF1, which
is a telomere-specific binding protein. The regulation of telomere
length, in which TRF1 has a role, is linked to ageing and cancer. The
sequences are useful in the treatment of cancers and inflammatory
disorders
SQ Sequence 5002 BP; 1456 A; 1065 C; 1196 G; 1285 T; 0 U; 0 Other;
Query Match 89.2%; Score 3387.2; DB 5; Length 5002;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 403 AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGCCAAAGC 462
DB 1083 AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGCCAAAGC 1142
QY 463 ACGTGATGATGGGGCCCTTATCTCTTCATTAATGCAATGCTCTTTTGGTCATGTGAAAGT 522
DB 1143 ACGTGATGATGGGGCCCTTATCTCTTCATTAATGCAATGCTCTTTTGGTCATGTGAAAGT 1202
QY 523 AGTCAATCTCTTTTGGGACATGTGTGACAGCCCAATGCTCGAGATTAATTCGAATTTATAC 582
DB 1203 AGTCAATCTCTTTTGGGACATGTGTGACAGCCCAATGCTCGAGATTAATTCGAATTTATAC 1262
QY 583 TCCTCTCATGAAGCTCAATTTAAAGGAAGATTTGATGTTTGGCTGTTGTACAGCA 642
DB 1263 TCCTCTCATGAAGCTCAATTTAAAGGAAGATTTGATGTTTGGCTGTTGTACAGCA 1322
QY 643 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 702
DB 1323 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 1382
QY 703 ATCTGCCAAGCAGTGTCTTACTGTGATATTAAGAAAGATCACTTTAGAAAGTCCAG 762
DB 1383 ATCTGCCAAGCAGTGTCTTACTGTGATATTAAGAAAGATCACTTTAGAAAGTCCAG 1442
QY 763 GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCATTAATGTCAACTGCCACGC 822

Db 1443 GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACCACTTAAATGTCAATGCCACGC 1502
 Qy 823 AAGTCATGCGAAGAGTCAACTCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGAT 882
 Db 1503 AAGTATGCGAAGAGTCAACTCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGAT 1562
 Qy 883 TGTACAGCTGTTTACGCAACATGAGAGTGAATGTCATGCTAAAGATAAAGGTGATCTGGT 942
 Db 1563 TGTACAGCTGTTTACGCAACATGAGAGTGAATGTCATGCTAAAGATAAAGGTGATCTGGT 1622
 Qy 943 ACCATTACCAATGCTGTTCTTATGCTGATTAATGAGTAACTGAACTTTTGGTCAAGCA 1002
 Db 1623 ACCATTACCAATGCTGTTCTTATGCTGATTAATGAGTAACTGAACTTTTGGTCAAGCA 1682
 Qy 1003 TGGTCCCTGTTGTAATGCAATGCAATGCTGCTGCAATTTCACTCTCTTCAATGAGGAGCTTC 1062
 Db 1683 TGGTCCCTGTTGTAATGCAATGCAATGCTGCTGCAATTTCACTCTCTTCAATGAGGAGCTTC 1742
 Qy 1063 TAAGAACAGGGTTGAAGTATGTTCTTCTTCTTAAAGTTATGGTCAGACCCCAACACTGCT 1122
 Db 1743 TAAGAACAGGGTTGAAGTATGTTCTTCTTCTTAAAGTTATGGTCAGACCCCAACACTGCT 1802
 Qy 1123 CAATTGTCACAAATAAAGTCTATAGACTTGGCTCCCAACCAAGTTAAAGAAAGATT 1182
 Db 1803 CAATTGTCACAAATAAAGTCTATAGACTTGGCTCCCAACCAAGTTAAAGAAAGATT 1862
 Qy 1183 AGCATATGAATTTAAAGGCCACTCGTCTGCTGCAAGCTGCAGAGAGCTGATGTTACTCG 1242
 Db 1863 AGCATATGAATTTAAAGGCCACTCGTCTGCTGCAAGCTGCAGAGAGCTGATGTTACTCG 1922
 Qy 1243 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAAAACACATGAAAC 1302
 Db 1923 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAAAACACATGAAAC 1982
 Qy 1303 AGCATGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1362
 Db 1983 AGCATGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2042
 Qy 1363 GCTAAGAAAGGAGCAACATCAATGAAGAAAGTAAAGAAATTTCTGACCTCTGCAAGT 1422
 Db 2043 GCTAAGAAAGGAGCAACATCAATGAAGAAAGTAAAGAAATTTCTGACCTCTGCAAGT 2102
 Qy 1423 GGCACTCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAGCAAAAGGT 1482
 Db 2103 GGCACTCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAGCAAAAGGT 2162
 Qy 1483 TAATGCTCTGGAATATTTGTTGTCAGATCTCTCTACACAGAGCTGATATGTTGTCATCT 1542
 Db 2163 TAATGCTCTGGAATATTTGTTGTCAGATCTCTCTACACAGAGCTGATATGTTGTCATCT 2222
 Qy 1543 ACMAACCTGCCCTTACTCTGAGCTATGGGTGATGCTTAACTATATCCCTTCAGGG 1602
 Db 2223 ACMAACCTGCCCTTACTCTGAGCTATGGGTGATGCTTAACTATATCCCTTCAGGG 2282
 Qy 1603 CTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCAAGAGGGTATCTC 1662
 Db 2283 CTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCAAGAGGGTATCTC 2342
 Qy 1663 ATTAGGTAATTCAGAGGAGCAGACAGCAATTTGCTGGAAGCTGCAAGGCTGAGATGTCGA 1722
 Db 2343 ATTAGGTAATTCAGAGGAGCAGACAGCAATTTGCTGGAAGCTGCAAGGCTGAGATGTCGA 2402
 Qy 1723 AACTGTAAATAAATCTGTACTGTTTCAAGTGTCACTGAGAGCAATTTGAAGGGCGTCA 1782
 Db 2403 AACTGTAAATAAATCTGTACTGTTTCAAGTGTCACTGAGAGCAATTTGAAGGGCGTCA 2462
 Qy 1783 GTCTACACCACTTCAATTTTGGAGCTGGGTATTAACAGAGTGTCCGTGGGAATATCTGCT 1842
 Db 2463 GTCTACACCACTTCAATTTTGGAGCTGGGTATTAACAGAGTGTCCGTGGGAATATCTGCT 2522
 Qy 1843 ACAGCATGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1902
 Db 2523 ACAGCATGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2582

Qy 1903 ATGTTCTTATGGACATTTATGAAGTTGACAGAACTTCTTGTTTAAACATGGAGCAGTAGTTAA 1962
 Db 2583 ATGTTCTTATGGACATTTATGAAGTTGACAGAACTTCTTGTTTAAACATGGAGCAGTAGTTAA 2642
 Qy 1963 TGTAGCTGATTTATGGAAATTTTACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
 Db 2643 TGTAGCTGATTTATGGAAATTTTACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2702
 Qy 2023 AATTGGCAAACTTCTGCTCCAGCATGCTGAGAGCCCTTACCAAAAAACACAGGATGGAAA 2082
 Db 2703 AATTGGCAAACTTCTGCTCCAGCATGCTGAGAGCCCTTACCAAAAAACACAGGATGGAAA 2762
 Qy 2083 TACTCTTGTGATCTTGTTTAAAGATGAGAGTACAGATATTCAGATCTGCTTTAGGGGAGA 2142
 Db 2763 TACTCTTGTGATCTTGTTTAAAGATGAGAGTACAGATATTCAGATCTGCTTTAGGGGAGA 2822
 Qy 2143 TGCAGCTTGTGATGCTGCCAAAGAGGGTTTGTAGCCAGAGTGAAGAAAGTTGCTTTC 2202
 Db 2823 TGCAGCTTGTGATGCTGCCAAAGAGGGTTTGTAGCCAGAGTGAAGAAAGTTGCTTTC 2882
 Qy 2203 TCCTGATAATGTAATTTGCCCGGATACCCAGGCGAGACATTTCAACACCTTTACATTTAGC 2262
 Db 2883 TCCTGATAATGTAATTTGCCCGGATACCCAGGCGAGACATTTCAACACCTTTACATTTAGC 2942
 Qy 2263 AGCTGGTTTATTAATTTAGAAAGTTGCAAGATATTTGTTTACAAACCGAGCTGATGTGAA 2322
 Db 2943 AGCTGGTTTATTAATTTAGAAAGTTGCAAGATATTTGTTTACAAACCGAGCTGATGTGAA 3002
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 Db 3003 TGCCCAAGACAAAGAGGAGCTTATTTCTTTTACATAATGTCAGCATCTTACGGGCGATGTAGA 3062
 Qy 2383 TGTAGCAGCTCTACTAATTAAGTATATGCAATGCTCAATGCTCAATGCTCAATGCTCAATGCTCAAT 2442
 Db 3063 TGTAGCAGCTCTACTAATTAAGTATATGCAATGCTCAATGCTCAATGCTCAATGCTCAATGCTCAAT 3122
 Qy 2443 CACACCTTTGCAAGAGCAGCCCAAGAGGAGCAAGCAACAGCTTTGCTTTGCTTTGCTTAC 2502
 Db 3123 CACACCTTTGCAAGAGCAGCCCAAGAGGAGCAAGCAACAGCTTTGCTTTGCTTTGCTTAC 3182
 Qy 2503 CCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAACACCTTTTGTAGATTTTTC 2562
 Db 3183 CCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAACACCTTTTGTAGATTTTTC 3242
 Qy 2563 AGCGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTTG 2622
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 Qy 2623 TTACAAGCTTCAAGTGTCTCAATGCTGTGAGAAAGCCAGGAGCCACTGCGAGATGCTCTCTC 2682
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 Qy 2683 TTCAAGTCCATCTAGCCCATCAAGCCTTTTGTAGCCAGCAGCTTTGACAACTTATCTGG 2742
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 Db 3423 GAGTTTTTCAAGACTGCTTCTCAGTAGTGTAGTTTCAAGTGGAAACAGAGGCTGCTTCCAGTTT 3482
 Qy 2803 GGAGAAAAAGAGGAGTCTCAGGAGTAGATTTTGTAGCATAACTCAATTCGTAAGGATCTTGG 2862
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QY 2983 AATTAAAGGAGTCGAGAGACTTATCTCCGACACACAGGCTCTTAACCCATATTTAACTTT 3042
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QY 3043 GAACACCTCTGGTAGTGGAACAACTTCTTATAGATCTGTCTCTGATGATAAGAGTTTCA 3102
Db 3723 GAACACCTCTGGTAGTGGAACAACTTCTTATAGATCTGTCTCTGATGATAAGAGTTTCA 3782
QY 3103 GTCTGTGGAGGAAGATGCAAGGTACAGTTTCGAGAGCACAGAGATGAGGTCATGCGAG 3162
Db 3783 GTCTGTGGAGGAAGATGCAAGGTACAGTTTCGAGAGCACAGAGATGAGGTCATGCGAG 3842
QY 3163 TGGATCTTCAACAGATACATATTTCTCAAGATTCAGAGGTTTGTAAACAAGAACTATG 3222
Db 3843 TGGATCTTCAACAGATACATATTTCTCAAGATTCAGAGGTTTGTAAACAAGAACTATG 3902
QY 3223 GGAAGATACACTCACCGGAGAAAAGTCTTCTGAAGAAAACCAACCAACCATGCAATGA 3282
Db 3903 GGAAGATACACTCACCGGAGAAAAGTCTTCTGAAGAAAACCAACCAACCATGCAATGA 3962
QY 3283 ACGAATGCTATTTCAATGGGCTCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 3342
Db 3963 ACGAATGCTATTTCAATGGGCTCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 4022
QY 3343 AAGGATCGGTACATAGTGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCTTC 3402
Db 4023 AAGGATCGGTACATAGTGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCTTC 4082
QY 3403 CAAAGCAATCAATATGATATGTAATGGAGGAGGTACTGGGTCTCAGTTCACAAAGA 3462
Db 4083 CAAAGCAATCAATATGATATGTAATGGAGGAGGTACTGGGTCTCAGTTCACAAAGA 4142
QY 3463 CAGATCTTTGTACATTTCCACAGCAGCTCTCTTTTGGCGGGTAACCTTTGGGAAAGTC 3522
Db 4143 CAGATCTTTGTACATTTCCACAGCAGCTCTCTTTTGGCGGGTAACCTTTGGGAAAGTC 4202
QY 3523 TTTCTGCACTTCAGTGAATGAAATGGCAATTCCTCTCAGGTCATCACTCAGTCAC 3582
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QY 3583 TGGTAGGCCAGTGTAAATGGCTAGCAATAGCTGAATATGTTATTTACAGAGAGACA 3642
Db 4263 TGGTAGGCCAGTGTAAATGGCTAGCAATAGCTGAATATGTTATTTACAGAGAGACA 4322
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Db 4323 GCCTATCTCAGATTTAAATTAATCTTACCAGATATGAGGCTGAAGGTATGTCGATGG 4382
QY 3703 ATAAATAGTTATTTTAAAGAACTAATTCACCTGAACCTAAATCATCAAGCAGCAGTGG 3762
Db 4383 ATAAATAGTTATTTTAAAGAACTAATTCACCTGAACCTAAATCATCAAGCAGCAGTGG 4442
QY 3763 CCTCTACGTTTACTCTCTTCTGTAAGAAAAA 3794
Db 4443 CCTCTACGTTTACTCTCTTCTGTAAGAAAAA 4474

RESULT 15

ABZ11674

ID ABZ11674 standard; cDNA; 5075 BP.

XX AC ABZ11674;

XX DT 20-JAN-2003 (first entry)

XX DE Human polynucleotide SEQ ID NO 556.

XX KW Human; genome mapping; gene therapy; food supplement; virus; fungus;

KW cell-proliferative disorder; neurodegenerative disease; bacterial;

KW Parkinson's disease; Alzheimer's disease; autoimmune disease;

KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;

KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;

KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;

KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic; gene; ss.

OS Homo sapiens.

PN WO200270539-A2.

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US005095.

XX 05-MAR-2001; 2001US-00799451.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;

XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

XX Wehrman T, Wang J, Wang D, Drmanac RT;

XX WPI; 2002-759812/82.

XX P-PSDB; ABP69457.

XX New polynucleotides comprising sequences assembled from expressed
XX sequence tags (ESTs), useful for treating cell-proliferative,
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
XX or coagulation disorders.

XX Claim 1; SEQ ID NO 556; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ11119-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 5075 BP; 1487 A; 1055 C; 1166 G; 1367 T; 0 U; 0 Other;

Query Match 89.28; Score 3387.2; DB 6; Length 5075;

Best Local Similarity 99.98; Pred. No. 0;

Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 403 AGGTTTTGGGCGGAAAGACGCTAGTTGAATATTTGCTTCAGAAATGGTCCAAAGC 462

Db 450 AGGTTTTGGGCGGAAAGACGCTAGTTGAATATTTGCTTCAGAAATGGTCCAAAGC 509

QY 463 ACGTGATGATGGGGCCCTTATCTCTTCATATGCAATGCTCTTTGGTCAATGCTGAGT 522

Db 510 ACGTGATGATGGGGCCCTTATCTCTTCATATGCAATGCTCTTTGGTCAATGCTGAGT 569

QY 523 AGTCAATCTCTTTTGGGACATGGTGACAGCCCAATGCTGAGATATTTGGAATTATAC 582

Db 570 AGTCAATCTCTTTTGGGACATGGTGACAGCCCAATGCTGAGATATTTGGAATTATAC 629

QY 583 TCCTCTCCATGAGCTGCAATTTAAAGGAAAGATTGATGTTTGGCATTTGCTGTTACAGCA 642

Db 630 TCCTCTCCATGAGCTGCAATTTAAAGGAAAGATTGATGTTTGGCATTTGCTGTTACAGCA 689

QY 643 TGGAGCTGAGCAACCATCCGAAATACAGATGGAAGACAGCATTTGATTTAGCAGATCC 702

Db 690 TGGAGCTGAGCAACCATCCGAAATACAGATGGAAGACAGCATTTGATTTAGCAGATCC 749

QY 703 ATCTGCCAAAGCAGTGTCTTACTGGTGAATATAGAAAGATGAACTCTTAGAAAGTGCCAG 762

Db 750 ATCTGCCAAGCAGTGTCTTACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCCAG 809
Qy 763 GAGTGGCAATGAAGAAAATGATGGCTCTACTACACCAATTAATGTCAACTGCCAGC 822
Db 810 GAGTGGCAATGAAGAAAATGATGGCTCTACTACACCAATTAATGTCAACTGCCAGC 869
Qy 823 AAGTGATGCGAGAAAGTCAACTCCAAATACATTTGGCAGCAGGATATAACAGAGTAAAGAT 882
Db 870 AAGTGATGCGAGAAAGTCAACTCCAAATACATTTGGCAGCAGGATATAACAGAGTAAAGAT 929
Qy 883 TGTAAGCTGTTTACGCAACATGGAAGTGAATGCTTCTTAAAGTAAAGGTGATCTGGT 942
Db 930 TGTAAGCTGTTTACGCAACATGGAAGTGAATGCTTCTTAAAGTAAAGGTGATCTGGT 989
Qy 943 ACCATTTACCAATGCTGTTCTTATGCTCATTTAGCTTAAGTAACTGAATTTGGTCAAGCA 1002
Db 990 ACCATTTACCAATGCTGTTCTTATGCTCATTTAGCTTAAGTAACTGAATTTGGTCAAGCA 1049
Qy 1003 TGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTTCACTCTCTTCATGAGGAGCTTC 1062
Db 1050 TGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTTCACTCTCTTCATGAGGAGCTTC 1109
Qy 1063 TAAGAACAGGGTGAAGTATGTTCTTCTTAAAGTATGCTGAGACCCCAACTGCT 1122
Db 1110 TAAGAACAGGGTGAAGTATGTTCTTCTTAAAGTATGCTGAGACCCCAACTGCT 1169
Qy 1123 CAATTTGTCACAATAAAGTGTATAGACTTGGCTCCACACCAAGTTAAAGAAAGATT 1182
Db 1170 CAATTTGTCACAATAAAGTGTATAGACTTGGCTCCACACCAAGTTAAAGAAAGATT 1229
Qy 1183 AGCATATGAATTTAAAGCCACTGTTGCTGCAAGCTGCAGAGAGCTGATTTACTCG 1242
Db 1230 AGCATATGAATTTAAAGCCACTGTTGCTGCAAGCTGCAGAGAGCTGATTTACTCG 1289
Qy 1243 AATCAAAAAACATCTCTCTGGAATGTTGAATTTCAAGCATCTCTCAAAACATGAAC 1302
Db 1290 AATCAAAAAACATCTCTCTGGAATGTTGAATTTCAAGCATCTCTCAAAACATGAAC 1349
Qy 1303 AGCATATGATGTTGCTGCTGATCTCCATATCCAAAAGAAAGAAATATGTGAATGTT 1362
Db 1350 AGCATATGATGTTGCTGCTGATCTCCATATCCAAAAGAAAGAAATATGTGAATGTT 1409
Qy 1363 GCTAAGAAAAGGAGCAACATCAATGAAGAAAGTAAAGAAATTTCTTGACTCTCTGCAAGT 1422
Db 1410 GCTAAGAAAAGGAGCAACATCAATGAAGAAAGTAAAGAAATTTCTTGACTCTCTGCAAGT 1469
Qy 1423 GGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTGTGTTGAACATGAAGCAAGGT 1482
Db 1470 GGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTGTGTTGAACATGAAGCAAGGT 1529
Qy 1483 TAATGCTCTGGAATATCTTGGTCAAGCTCTCTACACAGAGTGCATATTTGTTGTCATCT 1542
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Qy 1543 ACAAACTGCGCCCTACTCTGAGCTATGGGTGATCTTAACATTAATCCCTTCAGGG 1602
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Qy 1603 CTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCCAAAGGGGTATCTC 1662
Db 1650 CTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCCAAAGGGGTATCTC 1709
Qy 1663 ATTAGGTAAATTCAGAGGCAAGACAGCAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTGA 1722
Db 1710 ATTAGGTAAATTCAGAGGCAAGACAGCAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTGA 1769
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Qy 1843 ACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCTTGTACCTTTGCAAAATGC 1902
Db 1890 ACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCTTGTACCTTTGCAAAATGC 1949
Qy 1903 ATGTTCTTATGGACATTTATGAAGTTTGCAGAACTTCTTGTAAACATGAGCAGTAGTTAA 1962
Db 1950 ATGTTCTTATGGACATTTATGAAGTTTGCAGAACTTCTTGTAAACATGAGCAGTAGTTAA 2009
Qy 1963 TGTAGCTGATTTATGGAATTTTACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
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Db 2070 AATTTGCAAACTTCTGCTCCAGCATGTTGTCAGACCTTACCAAAAAACAGGATGGAAA 2129
Qy 2083 TACTCCTTTGGATCTTGTAAAGATGGAGATPACAGATATTCAGATCTGCTTAGGGGAGA 2142
Db 2130 TACTCCTTTGGATCTTGTAAAGATGGAGATPACAGATATTCAGATCTGCTTAGGGGAGA 2189
Qy 2143 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTAGCCAGAGTGAAGAGTGTCTTC 2202
Db 2190 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTAGCCAGAGTGAAGAGTGTCTTC 2249
Qy 2203 TCCTGATTAATGTAATTTAGAGTTTGCAGAGTATTTGTTTACAAACCGGAGCTGATGTGAA 2262
Db 2250 TCCTGATTAATGTAATTTAGAGTTTGCAGAGTATTTGTTTACAAACCGGAGCTGATGTGAA 2309
Qy 2263 AGCTGGTTTATAATTTAGAGTTTGCAGAGTATTTGTTTACAAACCGGAGCTGATGTGAA 2322
Db 2310 AGCTGGTTTATAATTTAGAGTTTGCAGAGTATTTGTTTACAAACCGGAGCTGATGTGAA 2369
Qy 2323 TGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGTCAGCATCTTACGGGCGATGTAGA 2382
Db 2370 TGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGTCAGCATCTTACGGGCGATGTAGA 2429
Qy 2383 TGTAGCAGCTCTACTAATAAAGTATATGTCATGTCATGTCACCGGACCAATGGGCTTT 2442
Db 2430 TGTAGCAGCTCTACTAATAAAGTATATGTCATGTCATGTCACCGGACCAATGGGCTTT 2489
Qy 2443 CACACCTTTGCAAGAGCAGCCCAAGAGGAGCAACACAGCTTTTGTGCTTTGCTGCTAGC 2502
Db 2490 CACACCTTTGCAAGAGCAGCCCAAGAGGAGCAACACAGCTTTTGTGCTTTGCTGCTAGC 2549
Qy 2503 CCATGGAGCTGACCCGACTCTTAAATAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2562
Db 2550 CCATGGAGCTGACCCGACTCTTAAATAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2609
Qy 2563 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTGCGCCCTTTG 2622
Db 2610 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTGCGCCCTTTG 2669
Qy 2623 TTACAAGCCTCAAGTGTCTCAATGTTGTCAGGAAGCCAGGAGCCACTGTCAGATGCTCTCTC 2682
Db 2670 TTACAAGCCTCAAGTGTCTCAATGTTGTCAGGAAGCCAGGAGCCACTGTCAGATGCTCTCTC 2729
Qy 2683 TTCAGGTCATCTAGCCCATCAAGCCTTTTTCAGCCAGCAGCTTTCAGCAACTATCTG 2742
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Qy 2743 GAGTTTTTCAGAACTGTCTTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTTCCAGTTT 2802
Db 2790 GAGTTTTTCAGAACTGTCTTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTTCCAGTTT 2849
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Db 2850 GGAGAAAAGAGAGGTTCCAGGAGTAGATTTTTCAGTAATCTCAATTCGTAAGGAAATCTTGG 2909
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Qy	2983	AATTAAGGAGTCCAGAGACTTATCTCCGGACAACAGGCTCTTAACCCATATTTAACTTT	3042
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Qy	3043	GAACACCTCTGGTATGGAACAATTTCTTTATAGATCTGTCTCCTGATGATAAAGAGTTTCA	3102
Db	3090	GAACACCTCTGGTATGGAACAATTTCTTTATAGATCTGTCTCCTGATGATAAAGAGTTTCA	3149
Qy	3103	GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCTATGCAGG	3162
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Qy	3163	TGGAATCTTCAACAGATACAATATTTCTCAAGATTCAAGAGTTTGTAAACAAGAAACTATG	3222
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Qy	3223	GGAAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCCAATGA	3282
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Qy	3283	ACGAATGCTATTTCAATGGGTCTCTTTTGTGAATGCAATTAATCCACAAGGCTTTGATGA	3342
Db	3330	ACGAATGCTATTTCAATGGGTCTCTTTTGTGAATGCAATTAATCCACAAGGCTTTGATGA	3389
Qy	3343	AAGGCATGCTACATAGGTGTGTGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCTTC	3402
Db	3390	AAGGCATGCTACATAGGTGTGTGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCTTC	3449
Qy	3403	CAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCCAGTTCAACAAGA	3462
Db	3450	CAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCCAGTTCAACAAGA	3509
Qy	3463	CAGATCTTTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAACCTTGGGAAAAGTC	3522
Db	3510	CAGATCTTTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAACCTTGGGAAAAGTC	3569
Qy	3523	TTTCTGCGAGTTCAAGTCAATGAAATGGCACATTTCTCTCCAGGTCACTCAGTCAAC	3582
Db	3570	TTTCTGCGAGTTCAAGTCAATGAAATGGCACATTTCTCTCCAGGTCACTCAGTCAAC	3629
Qy	3583	TGGTAGGCCCAAGTGTAAATGGCCTAGCATTAAGCTCAATATGTTATTTACAGAGAGAACA	3642
Db	3630	TGGTAGGCCCAAGTGTAAATGGCCTAGCATTAAGCTCAATATGTTATTTACAGAGAGAACA	3689
Qy	3643	GGCTTATCCTGAGTATTTAATTTACTTACCAGATTAATGAGGCTGAAGGTATGGTTCGATGG	3702
Db	3690	GGCTTATCCTGAGTATTTAATTTACTTACCAGATTAATGAGGCTGAAGGTATGGTTCGATGG	3749
Qy	3703	ATAAATAGTTATTTTAAGAACTAATTCACCTGAACCTTAAATCATCAAGCAGCAGTGG	3762
Db	3750	ATAAATAGTTATTTTAAGAACTAATTTCCACTGAACCTTAAATCATCAAGCAGCAGTGG	3809
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Db	3810	CCTCTACGTTTTTACTCTCTTTGCTGAAAAAAA	3841

Search completed: December 18, 2006, 13:14:52
Job time : 2059.86 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 13:00:27 ; Search time 16793.5 Seconds
(without alignments)
12643.339 Million cell updates/sec

Title: US-10-616-101-1

Perfect score: 3797

Sequence: 1 ctttgaagacactgatttc.....cctttgctgaaaaaaaaa 3797

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_ges1:*
12: gb_ges2:*
13: gb_ges3:*
14: gb_ges4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1609.8	42.4	3417	6	AK048860 Mus muscu
2	1481.8	39.0	2226	6	AK149368 Mus muscu
3	1369.8	36.1	1967	6	AK047094 Mus muscu
4	1360.4	35.8	3194	6	AK080913 Mus muscu
5	1221.6	32.2	3612	14	DQ034114 Homo sapi
6	892.2	23.5	3107	14	DQ034115 Pan trogl
7	884.4	23.3	888	8	CR983155 CR983155
8	859.6	22.6	926	8	CR987822 CR987822
9	784.2	20.7	838	1	AU140145 AU140145
10	770.6	20.3	898	10	DR808067 LB0173.CR
11	766.8	20.2	834	5	CR847047 969630 MA
12	709	18.7	848	9	DN536421 1372517 M
13	692.8	18.2	819	9	DAY33094 DAY33094
14	687.8	18.1	955	4	CB183123 AGENCOURT
15	672.4	17.7	675	4	CB128566 K-EST0178
16	672.2	17.7	1128	2	BM457025 AGENCOURT
17	665.2	17.5	754	4	CB170279 CEY603161
18	661.4	17.4	663	9	DA326495 DA326495
19	652	17.2	661	8	CR767085 DKF2p469A

C	20	652	17.2	923	5	CF407574	CH3R049_C
	21	649.2	17.1	659	10	R64714	R64714 EST54a09 WA
	22	648.2	17.1	781	8	CN525726	UI-M-HNO-
	23	644.2	17.0	753	8	CV558255	UI-M-HZO-
	24	643.8	17.0	691	2	BG391376	602417447
C	25	643	16.9	750	9	DN537809	1374053 M
	26	642.8	16.9	759	1	AL601027	DKF2p313G
	27	637	16.8	709	4	BX925031	BK925031
	28	636.6	16.8	756	8	CN459472	UI-M-HNO-
	29	635.4	16.7	759	5	CK635046	UI-M-HNO-
	30	634.4	16.7	950	3	BQ885764	AGENCOURT
	31	632.6	16.7	743	5	CF539235	UI-M-GHO-
	32	629.2	16.6	642	8	CR550014	DKF2p459D
	33	628.8	16.6	730	9	DN268735	LI830320
	34	623	16.4	729	8	CN527536	UI-M-HQO-
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	38	617.6	16.3	740	8	CO433927	UI-M-HXO-
	39	617.2	16.3	776	8	CO434293	UI-M-HXO-
	40	616.4	16.2	724	5	CF533694	UI-M-FYO-
	41	615.4	16.2	732	8	CO429777	UI-M-HXO-
	42	614.2	16.2	747	5	CF727485	UI-M-HBO-
	43	612	16.1	733	8	CN534125	UI-M-HO-
	44	610.6	16.1	746	8	CN455195	UI-M-HNO-
	45	605	15.9	648	2	BG875327	RC1-BT062

ALIGNMENTS

RESULT 1	AK048860	3417 bp	mRNA	linear	HTC 02-SEP-2005
LOCUS	AK048860	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length			
DEFINITION	AK048860	enriched library, clone: C230076L23 product: tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase, full insert sequence.			
ACCESSION	AK048860				
VERSION	AK048860.1	GI:26339607			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	10349636				
REFERENCE	1				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Maetumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				

TITLE
JOURNAL
REFERENCE
AUTHORS

Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5

TITLE
JOURNAL
REFERENCE
AUTHORS

The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6

TITLE
JOURNAL
REFERENCE
AUTHORS

RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
 Antisense Transcription in the Mammalian Transcriptome
 Science 309, 1564-1566 (2005)
 7

TITLE
JOURNAL
REFERENCE
AUTHORS

The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
 The Transcriptional Landscape of the Mammalian Genome
 Science 309, 1559-1563 (2005)
 8 (bases 1 to 3417)

TITLE
JOURNAL
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
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 /codon_start=1
 /protein_id="BAC33475.1"
 /db_xref="GI:26339608"
 /translation="MALLTPLNVNCHADGKSTPLHLAAGYNVRIVQLLOHGDV HAKDGLVPLHNACSGYEVTELLKHGCVNMDLWQPTPLHEASKNRVEVCSL LLSHGADPLVNHGSAVNAWPTPELRLERTYEFKGHSLSLQAAAREDLAKVKTAL E1INFKPQSHETALCAVSLHPKQVAELLRKGNVNEKNKDMFTPLHVAERA HNDYEVHLKHGKNAALSLQGTALHRAALHLOTCRLLSYGSDPSIISLQGFTA AQMGNEAVQOITLSSTPMRTSDVDYRLLEASKAGDLETVKOLCSPQWNCRDLEGRHS TPLHFAAGYNVRVSVVEILLHHGADVHAKDGLVPLHNACSGYHYVEALLVRHGSV

TITLE
JOURNAL
REFERENCE
AUTHORS

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TITLE
JOURNAL
REFERENCE
AUTHORS

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 Best Local Similarity 72.4%; Pred. No. 0;
 Matches 2126; Conservative 0; Mismatches 782; Indels 27; Gaps 2;

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 Qy 821 GCAAGTGCATGGCGAAAGTCAACTCCATTATTTGGCAGCAGGATATAACAGAGTAAAG 880
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 Qy 459 GCAAGTGCATGGCGAAAGTCTACTCCGTTACACCTGGCAGCAGGCTACAAACAGAGTTCGG 518
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 Qy 519 ATAGTTACAGCTGTCTTACAGCATGGTGGTGTGTCCACCGGAAAGACAAAGGTGGACTT 578
 Db |||||
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 Qy 1061 TCTAAGAACAGGTTGAAGTATGTTCTCTCTTAAAGTTATGGTGCAGACCCCAACTG 1120
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 Qy 699 TCAAGAACCGGGTAGAAGTCTGTCTCTTACTTACTTACCGTGGCGATCCAACTCTG 758
 Db |||||
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 Db |||||
 Qy 759 GTCATTTGCCATGGCAAAAGTGTGTGCAATGGCTCCAATCTCTGAGCTCCGCGAAGA 818
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 Qy 939 ACTGCAATGCACTGTGTGTGGCTCTCTTGCATCCCAACGAAAGCAGGTGGCAGAGCTG 998
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 Db |||||
 Qy 1541 CTACAAACCTGCCGCTTACTCTTGAGCTATGGGTGATGCTCTTAACTATATATCCCTTCAG 1600
 Db |||||
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AK149368 1 GI:74143548
 HRC; CAP trapper.
 Mus musculus (house mouse)
 ORGANSIM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS

1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, M., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, K., Izawa, M., Nishikawa, K., Kiyosawa, H., Kondo, S., Aizawa, K., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaudo, I., Pesole, G., Quackenbush, J., Schrim, L.M., Staab, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaeerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S. and Hayashizaki, Y. RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 11217851

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Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertes, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Iehii, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. FANTOM Consortium Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12466851

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Db	1321	CTGAAGAAAACCAACCATGCAACGAAGGATGTTATTTTCATGGGTCTCCTTTTGTGA	1380
Qy	3315	ATGCAATTATCCACAAAGGCTTTGATGAAGGCAATGCGTACATAGTGGTATGTTTGGAG	3374
Db	1381	ATGCGATTATCCATAAGGCTTTGATGAAGGCAATGCGTACATAGTGGTATGTTTGGAG	1440
Qy	3375	CTGCGATTATTTTGGCTGGAACACTCTTCCAAAGCAATCAATATGATGGAATTTGGAG	3434
Db	1441	CTGGAATTTATTTTGGCTGGAACACTCTTCCAAAGCAATCAATATGATGGAATTTGGAG	1500
Qy	3435	GAGTACTGGGTGCCAGTTTACAAAGACAGACTTGTTCATATTTGCCACAGGCGAGCTGC	3494
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Qy	3495	TCTTTTCCCGGGTAACCTTGGGAAGTCTTTCCTGCGAGTTTCAGTGCAATGAAATGCGCAC	3554
Db	1561	TGTTTTCGAGTAACCTTGGGAAGTCTTTCCTGCGAGTTTCAGTGCAATGAAATGCGCAC	1620
Qy	3555	ATTCTCTCCAGGTCATCACTACATGCTAGTGTAGGCCAGGTAAATGGCTAGCATTAG	3614
Db	1621	ATTCTCTCCCGGCATCACTCGGTCACTGCGCCGCCAGGTAAATGGCTAGCATTAG	1680
Qy	3615	CTGAATATGTTATTACAGAGGAGCAAGCGCTTATCTGAGTATTCTAATTAATTAATACAGA	3674
Db	1681	CTGAATATGTTATTACAGAGGAGCAAGCGCTTATCTGAGTATTCTAATTAATTAATACAGA	1740
Qy	3675	TTATGAGCGCTTGAAGGTATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT	3707
Db	1741	TTGTAAGCGCTTGAAGGTATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT	1773
RESULT 3			
AK047094			
LOCUS	AK047094	1967 bp mRNA linear HTC 02-SEP-2005	
DEFINITION	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930018021 product:TANKYRASE-RELATED PROTEIN (FRAGMENT) homolog [Homo sapiens], full insert sequence.		
ACCESSION	AK047094		
VERSION	AK047094.1	GI:26338577	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Teshikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	11076861		
REFERENCE			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		

JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE			
AUTHORS	5 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
PUBMED	12020000		
REFERENCE			
AUTHORS	6 RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.		
TITLE	Antisense Transcription in the Mammalian Transcriptome		
JOURNAL	Science 309, 1564-1566 (2005)		
PUBMED	15841111		
REFERENCE			
AUTHORS	7 The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).		
TITLE	The Transcriptional Landscape of the Mammalian Genome		
JOURNAL	Science 309, 1559-1563 (2005)		
PUBMED	15841111		
REFERENCE			
AUTHORS	8 (bases 1 to 1967)		
TITLE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT			
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.		
	Please visit our web site for further details.		
	URL: http://genome.gsc.riken.jp/		
	URL: http://fantom.gsc.riken.jp/		
FEATURES			
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	/db_xref="GI:74217481"		
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CDS			

LLLSYCDPNIISLQFTALOMNENVOQLQEGASLHSEADROLLEAKAGDVETV
KKLCTVQVNCNRDIEGROSTPLHFAAGYNRSVVEYLLQHGDAVHAKDGGGLVPLHNA
CSYGHVEVAELLVKHGAVVNVADLWKFPPLHEAA"

ORIGIN

Qy	403	AGGTTTGGCGGAAGAGCTAGTTGAATATTGCTTCAGATGTCGCAAGTGTCCAAGC	462
Db	363	AGGTTTGGACGGAAGAGTGTAGTTGAATATTCTTCAGAACGGTGCATGTCGAAGC	422
Qy	463	AGCTGATGATGGGGGCTTATTCTCTTCATATGATGCTCTTTTGGTGCATGCTGAAGT	522
Db	423	GGTGTGATGGGGGCTTATTCTCTTCATATGATGCTCTTTTGGTGCATGCTGAAGT	482
Qy	523	AGTCAATCTCTTTTGGGAGATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTTATAC	582
Db	483	AGTCAATCTCTTTTACAAACCGTGCACACCCAAATGCTGGGATAATTGGAATTTATAC	542
Qy	583	TCCTCTCATGAGCTGCAATTTAAAGGAAGATTGATGTTTGCATGCTGCTTACAGCA	642
Db	543	TCCTCTCATGAGCTGCAATTTAAAGGAAGATTGATGTTTGCATGCTGCTTACAGCA	602
Qy	643	TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGAGCAGATCC	702
Db	603	TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGAGCAGATCC	662
Qy	703	ATCTGCCAAAGCAGTCTTACTTGGTGAATATGAAGAAAGATGAATCTTTAGAAAGTGCAG	762
Db	663	ATCTGCCAAAGCAGTCTTACTTGGTGAATATGAAGAAAGATGAATCTTTAGAAAGTGCAG	722
Qy	763	GAGTGGCAATGAAGAAAATGATGGCTCTACTCACAATTAATGTCATGCTGCAAGC	822
Db	723	GAGTGGCAATGAAGAAAATGATGGCTCTACTCACAATTAATGTCATGCTGCAAGC	782
Qy	823	AAGTCATGSCAGAAAGTCAACTCCATTAATTTGGCAGCAGGATATACAGATGAAGAT	882
Db	783	AAGTCATGSCAGAAAGTCAACTCCATTAATTTGGCAGCAGGATATACAGATGAAGAT	842
Qy	883	TGTACAGCTGTTTACTGCAACATGAGCTGATGCTCCTTCAAGATAAAGGTGATCTGGT	942
Db	843	TGTACAGCTGTTTACTGCAACATGAGCTGATGCTCCTTCAAGATAAAGGTGATCTGGT	902
Qy	943	ACCATTACAAATGCTGTTCTTATGCTGCTATGATGAATGAATGAACTTTTGGTCAAGCA	1002
Db	903	ACCATTACAAATGCTGTTCTTATGCTGCTATGATGAATGAATGAACTTTTGGTCAAGCA	962
Qy	1003	TGGTGCCTGTGTAATGCAATGCACTGTGGCAATTTCACTCTCTTCATGAGGCAAGCTTC	1062
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Qy	1063	TAAAGAACAGGGTGAAGTATGTTCTCTTCTTAAAGTATGTCGAGACCCCAACTGCT	1122
Db	1023	TAAAGAACAGGGTGAAGTATGTTCTCTCTTCTTAAAGTATGTCGAGACCCCAACTGCT	1082
Qy	1123	CAATTGTCAATAAAGTGTATGATGCTGCTCCACACACAGTGTAAAGAAAGATT	1182
Db	1083	GAACGTGTCAATAAAGTGTATGATGCTGCTCCACACACAGTGTAAAGAAAGATT	1142
Qy	1183	AGCATATGAAATTAAGGCCACTGCTGTCGAGCTGCAGAGAGCTGATGTTACTCG	1242
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Qy	1243	AATCAAAAAACATCTCTCTGGAATGTTGAATTTCAAGCATCTCAAAACATGAAGC	1302
Db	1203	AATCAAAAAACATCTCTCTGGAATGTTGAATTTCAAAACATCTCAAGACATGAAGC	1262
Qy	1303	AGCATGTGATGCTGCTGCTGCTATGCTGCTATCCCAATATCCCAAAAAAGAAATATGTAAGT	1362
Db	1263	AGCATGTGATGCTGCTGCTGCTATGCTGCTATCCCAATATCCCAAAAAAGAAATATGTAAGT	1322

Qy	1363	GCTAAGAAAAGGAGCAAAACATCAATGAAAAAGCTAAAGAAATTTCTGACTCTCTGACGT	1422
Db	1323	GCTCAGAAAAGGAGCAAAACATCAATGAAAAAGCTAAAGAAATTTCTGACTCTCTGACGT	1382
Qy	1423	GGCATCTGAGAAAAGCTCATATGATGTTGTTGAAGTAGTGTGTAAGCAATGAAGCAAGGT	1482
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Qy	1483	TAATGCTCTGATTAATCTTTGGTTCAGACTTCTCTACAGAGAGCTGCATATTTGGTTCATCT	1542
Db	1443	TAATGCTCTGATTAATCTTTGGTTCAGACTTCTCTACAGAGAGCTGCATATTTGGTTCATCT	1502
Qy	1543	ACAAACCTGCCGCTTACTCTCTGAGCTATGGGTGTCATCTTAACATATATATCCCTTCAGGG	1602
Db	1503	GCAGACCTGCCGCTTACTCTCTGAGCTATGGGTGTCATCTTAACATATATATCCCTTCAGGG	1562
Qy	1603	CTTTACTGCTTTACAGATGGGAAATGAAATGTTACAGCAACTCTCTCCAAAGGGGTATCTC	1662
Db	1563	TTTCACCGCTTGCAAATGGGAAATGAAATGTTACAGCAACTCTCTCCAAAGGGGTATCTC	1622
Qy	1663	ATTAGTAAATTCAGAGCGAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGTGCA	1722
Db	1623	ACTAGTCACTCAGAGCGGAGACAGCACTGCTGGAAGCTGCAAGGCTGGAGATGTGCA	1682
Qy	1723	AACTGTAATAAACTGTGTACTGTTTCAAGTGTCAACTGTCAGAGACATTTGAAGGCGCTCA	1782
Db	1683	AACTGTAATAAACTGTGTACTGTTTCAAGTGTCAACTGTCAGAGACATTTGAAGGCGCTCA	1742
Qy	1783	GCTACACCACTTCAATTTGAGCTGGGTAATAAGAGTGTCCGCTGGTGGAAATATCTGCT	1842
Db	1743	GTCACCCCACTTCAATTTGAGCTGGGTAATAAGAGTGTCCGCTGGTGGAAATATCTGCT	1802
Qy	1843	ACAGATGAGCTGATGTCATGCTTAAGATAAAGGAGGCTTGTACCTTTGCACAATGC	1902
Db	1803	GCAACATGAGCTGATGTCATGCTTAAGATAAAGGAGGCTTGTACCTTTGCACAATGC	1862
Qy	1903	ATGTTCTTATGCAATTAATGAAGTTGCAAGAACTTCTTGTAAACATGAGCAGTAGTTAA	1962
Db	1863	ATGTTCTTATGCAATTAATGAAGTTGCAAGAACTTCTTGTAAACATGAGCAGTAGTTAA	1922
Qy	1963	TGTAGCTGAATTTAGAAATTTACACCTTTTACATGAAGCAGCAGC	2007
Db	1923	TGTAGCTGAATTTAGAAATTTACACCTTTTACATGAAGCAGCAGC	1967

RESULT 4

AK080913

LOCUS

DEFINITION

AK080913

VERSION

AK080913.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AK080913 3194 bp mRNA linear HTC 02-SEP-2005

Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length

enriched library, clone:B430206N15 product:TRF1-INTERACTING

ANKYRIN-RELATED ADP-RIBOSE POLYMERASE homolog [Homo sapiens], full

insert sequence.

AK080913

AK080913.1 GI:26099551

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

11042159

3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
TITLE Antisense Transcription in the Mammalian Transcriptome
JOURNAL Science 309, 1564-1566 (2005)
REFERENCE 7
AUTHORS The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE The Transcriptional Landscape of the Mammalian Genome
JOURNAL Science 309, 1559-1563 (2005)
REFERENCE 8
AUTHORS (bases 1 to 3194)
Adachi, J., Aizawa, K., Akimura, T., Azakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saiboh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
FEATURES source location/Qualifiers
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Best Local Similarity 72.0%; Pred. No. 0;
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ACCESSION	DQ034114
VERSION	DQ034114.1 GI:66885323
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 3612) Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL	(er) PLOS Biol. 3 (6), E170 (2005)
PUBMED	15869325
REFERENCE	2 (bases 1 to 3612)
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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mRNA sequence.
CR983155 CR983155.1 GI:68221489
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 888)
Heil.O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
and Korn,B.
Human T-Lymphocytes library
Unpublished (2005)
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPDp9017K2313.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB NO. 9017
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact:
Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9017K2313
contact RZPD (product- support@rzpd.de) for further information.
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NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned.pic.shtml
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human T-Lymphocytes with a NotI - oligo(dT) primer [5'
GACTAGTCTTAGATCGGCGCGCCCTTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to SalI adaptors,
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ORIGIN
Query Match 23.3%; Score 884.4; DB 8; Length 888;
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Qy	1628	GA	AAATG	TACAG	CAACTC	CTCC	AAAGGGGTATCTCATTAGGTAAATTCAGAGGCAGACAGA	1687		
Db	1	GA	AAATG	TACAG	CAACTC	CTCC	AAAGGGGTATCTCATTAGGTAAATTCAGAGGCAGACAGA	60		
Qy	1688	CA	ATTGCTG	GAAGCTG	CAAAAGGCTG	GAGAGTGT	CGAAACTGTAA	AAAAAACTGTGTACTGTT	1747	
Db	61	CA	ATTGCTG	GAAGCTG	CAAAAGGCTG	GAGAGTGT	CGAAACTGT	AAAAAACTGTGTACTGTT	119	
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Db	120	CAG	AGTGTCA	ACTG	CGAGAGACAT	TGAAGGGCGTCAGTCT	ACACACTTCAT	TTTGTGAGCT	179	
Qy	1808	GG	GTATAAC	CAGAGTGTCC	GTGTGG	GAATATCTGCTA	CAGACATG	CGAGCTGATG	GCATGCT	1867
Db	180	GG	GTATAAC	CAGAGTGTCC	GTGTGG	GAATATCTGCTA	CAGACATG	CGAGCTGATG	GCATGCT	239
Qy	1868	AA	AGATAAA	AGGAGGCC	TTGTAC	CTTTGC	CAAAATG	CGATGTTCTTATG	GCATAATATGAAGTT	1927
Db	240	AA	AGATAAA	AGGAGGCC	TTGTAC	CTTTGC	CAAAATG	CGATGTTCTTATG	GCATAATATGAAGTT	299
Qy	1928	GC	AGACTTCT	TGTTAA	ACATG	CAGACG	ATGAGTTAA	TGTAGCTGATTTA	TGGAAATTTACA	1987
Db	300	GC	AGACTTCT	TGTTAA	ACATG	CAGACG	ATGAGTTAA	TGTAGCTGATTTA	TGGAAATTTACA	359
Qy	1988	CC	TTTACATGA	ACGACAG	CACAAAGG	AAATATG	AAATTTG	CAAACTTCCTG	CTCCAGCAT	2047
Db	360	CC	TTTACATGA	ACGACAG	CACAAAGG	AAATATG	AAATTTG	CAAACTTCCTG	CTCCAGCAT	419
Qy	2048	GGT	CGACAGC	CTTAC	CAAAAAA	ACAGGGATG	GAAATACTCCTCTT	TGGATCTGTTTAA	AGAT	2107
Db	420	GGT	CGACAGC	CTTAC	CAAAAAA	ACAGGGATG	GAAATACTCCTCTT	TGGATCTGTTTAA	AGAT	479
Qy	2108	GG	AGATACAG	ATATTC	AAAGATCTG	TTAGGGG	AGATGCAGCTTTG	CTAGATG	CTGCCAAG	2167
Db	480	GG	AGATACAG	ATATTC	AAAGATCTG	TTAGGGG	AGATGCAGCTTTG	CTAGATG	CTGCCAAG	539
Qy	2168	A	AGGGTGT	TTTAC	CCAGAGTGA	AGAGTGTCTTCT	CTCATATG	ATGAAATTC	CCCGCAT	2227
Db	540	A	AGGGTGT	TTTAC	CCAGAGTGA	AGAGTGTCTTCT	CTCATATG	ATGAAATTC	CCCGCAT	599
Qy	2228	AC	CAAGGC	CAGACATTC	CAACAC	CTTTTAC	ATTAGCAGCTGGT	TATATA	TATAGAGTT	2287

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QY 2715 CAGCCAGCAGTCTTGACAACTTATCTGGAGTGTCTTCAGAACTGTCTTCAGTAGTGTAGTT 2774
Db 1 CAGCCAGCAGTCTTGACAACTTATCTGGAGTGTCTTCAGAACTGTCTTCAGTAGTGTAGTT 60
QY 2775 CAAGTGGAAACAGAGGTGCTTCAGTTTGGAGAAAGAGGTTCCAGAGTAGATTTTA 2834
Db 61 CAAGTGGAAACAGAGGTGCTTCAGTTTGGAGAAAGAGGTTCCAGAGTAGATTTTA 120
QY 2835 GCATTAACCTCAATTCGTAAGGAATCTTGGACTTGGACCTGAGCACCCTAATGATATATTGGAGAG 2894
Db 121 GCATTAACCTCAATTCGTAAGGAATCTTGGACTTGGACACCCTAATGATATATTGGAGAG 180
QY 2895 AACAGATCACTTTGGATGTATTAGTTGAGATGGGCACAAGGAGCTGGAAGGAGATTGGA 2954
Db 181 AACAGATCACTTTGGATGTATTAGTTGAGATGGGCACAAGGAGCTGGAAGGAGATTGGA 240
QY 2955 TCAATGCTTATGACATAGGCAAACTAATTAAGGAGTCCAGAGACTTATCTCCGGAC 3014
Db 241 TCAATGCTTATGACATAGGCAAACTAATTAAGGAGTCCAGAGACTTATCTCCGGAC 300
QY 3015 AACAGGTCCTTAACCCATATTAACTTTGAAACCTCTGTTAGTGGAACTTCTTATAG 3074
Db 301 AACAGGTCCTTAACCCATATTAACTTTGAAACCTCTGTTAGTGGAACTTCTTATAG 360
QY 3075 ATCTGTCTCTGATGATAAGAGTTTTCAGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTT 3134
Db 361 ATCTGTCTCTGATGATAAGAGTTTTCAGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTT 420
QY 3135 GAGAGCACAGAGATGAGGTCTATGAGGTGGAATCTTCAACAGATACAAATTTCTCAAGA 3194
Db 421 GAGAGCACAGAGATGAGGTCTATGAGGTGGAATCTTCAACAGATACAAATTTCTCAAGA 480
QY 3195 TTCAGAGGTTTGTACAGAACTATGGAAGATACACTCACCGGAGAAAAGTTT 3254
Db 481 TTCAGAGGTTTGTACAGAACTATGGAAGATACACTCACCGGAGAAAAGTTT 540
QY 3255 CTGAAGAAAACCAACCACTGCAATGAACGAATGCTATTTTCATGGGTCTCCTTTTGTGA 3314
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Db 601 ATGCAATATTCCAAAGGCTTTGATGAAAGCATGCGTACATAGTGGTGTATGTTGGAG 660
QY 3375 CTGGCAATTTATTTGCTGAAACTCTTCCAAAGCAATCAATATGATATGAAATGGAG 3434
Db 661 CTGGCAATTTATTTGCTGAAACTCTTCCAAAGCAATCAATATGATATGAAATGGAG 719
QY 3435 GAGGTACTGGGTGTCCAGTTTCAAAAGACAGATCTTTGTTTACATTTTGGCCACAGCAGTGC 3494
Db 720 GAGGTACTGGGTGTCCAGTTTCAAAAGACAGATCTTTGTTTACATTTTGGCCACAGCAGTGC 778
QY 3495 TCTTTTGG--CCGGGTAACTTGGGAAAGTCTTTTCTTCGAGTTTCAAGTGAATGCAATGCG 3552
Db 779 TCTTTTGGCGGGTAACCTTGGGAAAGTCTTTTCTTCGAGTTTCAAGTGAATGCAATGCG 838

RESULT 10
D808067
LOCUS
DEFINITION LB0173.CR.I04.GC.BGC-17 Bos taurus cDNA clone IMAGE:8121774 5',
            mRNA linear EST 12-OCT-2005
ACCESSION D808067
VERSION D808067.1 GI:75739943
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 898)
AUTHORS Moore,S., Alexander,L., Brownstein,M., Guan,L., Lobo,S., Meng,Y.,
```

Tanaguchi,M., Wang,Z., Yu,J., Prange,C., Schreiber K., Shenmen,C.,
Wagner L., Bala,M., Barbazuk,S., Barber S., Babakaiff,R.,
Beland,J., Chun,E., Del Rio,L., Gibson,S., Hanson,R.,
Kirkpatrick,R., Liu,J., Matsuo,C., Mayo,M., Santos,R.R., Stott,J.,
Tsai,M., Wong,D., Siddiqui,A., Holt,R., Jones,S.J. and Marra,M.A.
Bovine Genome Sequencing Program: Full-length cDNA sequencing
Unpublished (2005)

TITLE
JOURNAL
COMMENT

Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
Canada, V5Z 4S6
Tel: 1-604-707-5900 x5406
Fax: 1-604-876-3561
Email: robertk@bcgsc.ca
Plate: LB0173 row: 1 column: 4
High quality sequence stop: 898.

FEATURES
source

1..898
Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/strain="L1 Hereford"
/db_xref="taxon:9913"
/clone="IMAGE:8121774"
/sex="male"
/tissue_type="Ascending colon"
/dev_stage="6 months old fetus"
/lab_host="E. coli DH10B T1 Phage Resistant"
/clone_lib="GC.BGC-17"
/note="Organ: Ascending colon; Vector: pExpress 1; Site_1:
Blunt (5' end of cDNA); Site_2: NotI (3' end of cDNA)"

ORIGIN

Query Match 20.3%; Score 770.6; DB 10; Length 898;
Best Local Similarity 92.1%; Pred. No. 5.8e-194;
Matches 824; Conservative 0; Mismatches 69; Indels 2; Gaps 1;
QY 2901 TCACCTTTCGATGTATTAGTTGAGATGGGCGCACAGGAGCTGAAGGAGATTGGAATCAATG 2960
Db 1 TCACGTTTCGATGTATTAGTTGAGATGGGCGCACAGGAGTTGAAGAGATCGGAATCAATG 60
QY 2961 CTTATGGACATAGGCACAACTTAATTAAGGAGTCCGAGAGACTTATCTCCGACACAAAG 3020
Db 61 CTTACGGACATAGACACAACTTAATTAAGGAGTTGAGAGACTTATCTCTGACACAAAG 120
QY 3021 GTCCTAACCCATATTTAACCTTGAACACTCTCTGGTAGTGGAACTTCTTATAGATCTGT 3080
Db 121 GTCCTAACCCATATTTAACCTCTGAACACTCTCTGGAAGTGGAACTTCTCAATTGATCTGT 180
QY 3081 CTCCTGTATGATAAGAGTTTCAGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTCGAGAGC 3140
Db 181 CTGCTGAAGATAAAGAGTTTCAGTCTGTGGAGGAAGAGATGCAAGATGACAGTCCGAGAGC 240
QY 3141 ACAGAGATGGAGGTTCATGAGGTGGAATCTTTCAACAGATACAAATTTCTCAAGATTGAGA 3200
Db 241 ACAGAGATGGAGGTTCACCGAGTGGGATCTTCAACAGATACAAATTTCTCAAGATTGAGA 300
QY 3201 AGCTTTGTAAACAGAACTATGGGAAAGATACACTCACCAGGAGAAAGAGTTTCTGAAG 3260
Db 301 AAGTTGTAAACAGAACTATGGGAAAGATACACTCATAAGGAGAAAGAGTTTCTGAAG 360
QY 3261 AAAACCAACCACTCCCAATGAACGAATGCTATTTTCATGGGTCTCCTTTTGGGAATGCAA 3320
Db 361 AAAACCAACCACTCCCAATGAAGAGATGCTATTTTCATGGGTCTCCTTTTGGGAATGCAA 420
QY 3321 TTATCCACAAAGGCTTTGATGAAAGGATGCGGTACATAGGTGGTATGTTTGGAGCTGGCA 3380
Db 421 TTATCCATAAAGGCTTTGATGAAAGGATGCGGTACATAGGTGGATGTTTGGAGCTGGCA 480
QY 3381 TTTATTTGCTGAAACTCTTCCAAAAGCAATCAATATGATATGGAATTTGAGAGGTTA 3440
Db 481 TCTATTTGCTGAAACTCTTCCAAAAGCAATCAGTATGATATGGAATTTGAGAGGTTA 540

Qy 3441 CTGGGTGTCAGTTTCAAAAGACAGATCTTGTTCATTTGGCCACAGCAGTGTCTCTTT 3500
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 Db 541 CTGGATGTCAGTACATAAAGACAGATCTTGTTCATCTGTCACAGCAGTGTCTCTCT 600
 |||||
 Qy 3501 GCCGGTAACTCTGGGAAAGTCTTCTGCGAGTTTCAGTGCATGAAATGCGCATTTCTC 3560
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 Db 721 ATGTTATTACAGAGGAGAACAGCCTTATCTCTAGTATTTAATTACTTACAGATTATGA 780
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 Qy 3681 GGCTCGAAGGTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3740
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 Db 781 GGCTCGAAGGTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
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 Qy 3741 AAAATCATCAAGCAGCAG--TGCCCTCTACGTTTCTCTCTCTCTCTCTCTCTCTCTCT 3793
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 Db 841 AAAATCATCAAGCAGCAGTGGTGGCTCGTAAGTTTCTCTCTCTCTCTCTCTCTCTCTCT 895
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RESULT 11

CK847047/c 834 bp mRNA linear EST 05-MAR-2004
 LOCUS 969630 MARC 4BOV Bos taurus cDNA 3', mRNA sequence.

DEFINITION CK847047.1 GI:45208162
 ACCESSION CK847047.1
 VERSION EST.
 KEYWORDS Bos taurus (cattle)
 SOURCE Bos taurus

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 834)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
 Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
 Chitko-McKown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F.,
 Quackenbush, J., and Keane, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)

TITLE 11282978
 JOURNAL Contact: Smith TPL
 PUBMED USDA, ARS, US Meat Animal Research Center
 COMMENT PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: 98 row: I column: 7
 Seq primer: GTAATACGACTCACTATAGG.
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from day 20 and day 40
 embryos."

ORIGIN

Query Match 20.2%; Score 766.8; DB 5; Length 834;
 . Best Local Similarity 95.0%; Pred. No. 5.8e-193;

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 Qy 1228 AGCTGATGTTTACGAAATCAAAAAACATCTCTCTCTGGAATGGTGAATTTCAAGCATCC 1287
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 Qy 1288 TCAACACATGAAACAGCATTGTCATGCTGCTGCTGCTCCATATCCAAAAAGAAAGCA 1347
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 Db 774 TCAACACATGAAACAGCATTGTCATGCTGCTGCTGCTCCATATCCAAAAAGAAAGCA 715
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 Qy 1348 AATATGTGAATCTTGTCTAAGAAAAGGAGCAAAACATCAATGAAAGAAAGCTTAAAGAAATCTT 1407
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 Db 714 AATATGTGAATCTTGTCTAAGAAAAGGAGCAAAACATCAATGAAAGAAAGCTTAAAGAAATCTT 655
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 Qy 1408 GACTCTCTGCACTGCGCATCTGAGAAAAGCTCATATAATGATGTTTCTTGAAGTAGTGGTGA 1467
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 Db 654 GACTCTCTGCACTGCGCTTCTGAGAAAAGCTCATATAATGATGTTTCTTGAAGTAGTGGTGA 595
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 Qy 1468 ACATGAAGCAAGGTTAATGCTCTGGAATAATCTTGGTCAGACTTCTCTACACAGAGCTGC 1527
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 Db 594 ACATGAAGCAAGGTTAATGCTCTGGAATAATCTTGGTCAGACTTCTTTCACAGAGCTGC 535
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 Qy 1528 ATATTGTGCTCATCTACAAACCTGCGCCTACTCTCTGAGCTATCGGTGTGATCTCTAAACAT 1587
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 Db 534 ACATTGTGCTCATCTGCAAACTGCGCTTACTCTCTGAGCTATGATGATGATCTAATCAT 475
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 Db 414 TCAAGAGGTTATCCCATTTAGGTAAATTCAGAGGCGACAGACAGTTGCTGGAAGCTGCAAA 355
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 Qy 1708 GGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAGAGA 1767
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 Qy 1768 CATTTGAAGGCGTCAGTCTACACCATTTCAATTTTGCAGCTGGGTATTAACAGAGTGTCCGT 1827
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 Qy 1828 GGTGGAATATCTGTCAGCATGGAGCTGTGTCATGCTTAAAGCTAAAGAGAGCGCTTGT 1887
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 Qy 1948 TGGAGCAGTAGTTAATGCTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCGAGCAG 2007
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 Db 114 TGGAGCAGTAGTTAATGCTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCTGAGC 55
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 Qy 2008 AAAGGAAATATCAAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTAC 2061
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 Db 54 CAAAGGAAATATGAAATTTGCAAACTTCTGCTTTCAGCATGGTGCAGACCCCTAC 1

RESULT 12

DN536421 848 bp mRNA linear EST 11-MAR-2005
 LOCUS 1372517 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.

DEFINITION DN536421
 ACCESSION DN536421
 VERSION DN536421.1 GI:60988240
 KEYWORDS EST.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 848)
 Smith, T.P.L., Roberts, A.J., Ehternkamp, S.E., Chitko-McKown, C.G.,

TITLE Wray, J.E. and Keele, J.W.
JOURNAL A second set of bovine ESTs from pooled-tissue normalized libraries
COMMENT Unpublished (2003)

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Contact: Smith TPL
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLK8064 row: G column: 17
Seq primer: GTAATACGACTCACTATAGGG.

FEATURES

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Location/Qualifiers
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Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN

Query Match 18.7%; Score 709; DB 9; Length 848;
Best Local Similarity 91.5%; Pred. No. 1.7e-177;
Matches 762; Conservative 0; Mismatches 70; Indels 1; Gaps 1;
QY 1589 ATATCCCTCAGGCTTACTGCTTTACAGATGGGAATGAATGTACAGCAACTCTCTC 1648
DB 15 AGATCCCTCAGGCTTACTGCTTTACAGATGGGAATGAATGTACAGCAACTCTCT 74
QY 1649 CAAGAGGGTATCTCAATAGTAAATTCAGAGGAGAGAGCAATGCTGGAAGCTGCAAG 1708
DB 75 CAAGAGGGTATCCCATAGTAAATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 134
QY 1709 GCTGAGAGTGTCCGAACCTGTAATAAATCTGTCTACTGTTTCAGAGTGTCAACTGCGAGAGAC 1768
DB 135 GCTGAGAGTGTAGAAACCGTAAATAAATCTGTCTACTGTTTCAGAGTGTCAACTGCGAGAGAC 194
QY 1769 ATTGAAGGGCTCAGTCTACACACTTCAATTTGCGAGCTGGGTATATACAGAGTGTCCGCTG 1828
DB 195 ATTGAAGGAGCTCAGTCTACACCGCTCCCAATTTGCGAGCTGGGTATATATCGGGTGTCTGTG 254
QY 1829 GTGGGAATATCTGCTACAGCATGGAGCTGATGTGCTGCTAAAGATAAAGAGGAGGCTTGTGA 1888
DB 255 GTGGGAATATCTGCTGCAACAGGAGCTGACGTGCTATGCGAAGAGACAAAGAGGAGGCTTGTGA 314
QY 1889 CTTTGTGCAATGCATGTTCTTATGGACATTAATGAAGTTGCGAGAACTTCTTGTAAACAT 1948
DB 315 CTTTGTGCAATGCATGTTCTTATGGACATTAATGAAGTTGCGAGAACTTCTTGTAAACAT 374
QY 1949 GGAGCAGTAGTAAATGCTAGTCAATTTATGGAATTTACACCTTTACATGAAGCAGCAGCA 2008
DB 375 GGAGCAGTAGTAAATGCTAGTCAATTTATGGAATTTACACCTTTACATGAAGCAGCAGC 434
QY 2009 AAAGGAAAATATGAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAA 2068
DB 435 AAAGGAAAATATGAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAA 494
QY 2069 AACAGGGATGGAATATCTCTTTGGATCTTGTAAAGATGGAGATACAGATATCAAGAT 2128
DB 495 AACAGAGATGGAATAACACCCCTTTGGATCTGTTGGAAGAGGAGATACAGATATCAAGAT 554
QY 2129 CTGCTTAGGGAGATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTG 2188
DB 555 CTGCTTAGGGAGATGCAGCTTTATTTGGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTA 614
QY 2189 AAGAAGTTGCTCTCTCTGATTAATGTAATTTGCGCGATACCCAGGCGAGACATTCACCA 2248

Db 615 AAGAAGTGTCTTCCACAGATAATGTAATAAGTCCGTGATACCAAGCGCGCATTCACCA 674
QY 2249 CCTTTACATTTAGCAGCTGGTTATTAATAATTTAGAGTTGCGAGATATTTGTACACAC 2308
Db 675 CCTTTACATTTAGCAGCTGGTTATTAATAATTTAGAGTTGCGAGATATTCCTACAGCAT 734
QY 2309 GGAGCTGATGTGAATGCCCAAGACAAAGAGGAGCTATTTCCTTTACATAAATGAGCATCT 2368
Db 735 GGAGCTGATGTGAATGCTCAGGACAAAGAGGAGCTATTTCCTTTACACAAATGAGCATCT 794
QY 2369 TACGGCATGTAGATGTAGCAGCTCTACTATAAAGTATAATGCAATGTGTCAA 2421
Db 795 TACGGCATGTAGATGTAGCAGCTTTGCTAATAAA-TATAATGCGTGTGTCAA 846

RESULT 13

DAY733094 819 bp mRNA linear EST 09-NOV-2005
LOCUS DAY733094 NT2RP2 Homo sapiens cDNA clone NT2RP2002155 5', mRNA
DEFINITION sequence.
ACCESSION DAY733094
VERSION DAY733094.1 GI:81281747
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 819)

REFERENCE

AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Teuritani, K., Wakaquri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)

TITLE

16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com

JOURNAL

PUBMED
COMMENT HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
HRI.
Location/Qualifiers
1..819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2002155"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RP2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

FEATURES

source
1..819
Location/Qualifiers
18.2%; Score 692.8; DB 9; Length 819;
Best Local Similarity 93.0%; Pred. No. 3.5e-173;
Matches 763; Conservative 0; Mismatches 52; Indels 5; Gaps 4;
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DB 1 TGCATATTTGGTCTATCTACAAACCTGGCGCTACTCTCTGAGCTATGGTGTGATCTTAA 60

ORIGIN

Query Match 18.2%; Score 692.8; DB 9; Length 819;
Best Local Similarity 93.0%; Pred. No. 3.5e-173;
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DEFINITION AGENCOURT 11385409 NIH MGC 164 Mus musculus cDNA clone
IMAGE:30244272 5', mRNA sequence.
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VERSION CB183123.1 GI:28181571
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 955)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
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CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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directionally, priming method: Oligo-dT. cDNA enrichment:
>1k bp. Average insert size 1.8k bp. Priming sequence:
5'GACTAGTCTAGATCGGAGCGCGCC(T) 3'. Tissue contributed
by David Rowe. Library constructed by ResGen, Invitrogen
Corp."
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Best Local Similarity 88.5%; Pred. No. 8.1e-172;
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CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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Location/Qualifiers

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Non-normalized full-length enriched library from pooled

mouse embryonic limb, maxilla and mandible, day 10.5 and

11.5 (size selected for the 0.5-1 kb fragments) Cloned

directionally, priming method: Oligo-dT. cDNA enrichment:

>1k bp. Average insert size 1.8k bp. Priming sequence:

5'GACTAGTCTAGATCGGAGCGCGCC(T) 3'. Tissue contributed

by David Rowe. Library constructed by ResGen, Invitrogen

Corp."

ORIGIN

Query Match 18.1%; Score 687.8; DB 4; Length 955;

Best Local Similarity 88.5%; Pred. No. 8.1e-172;

Matches 768; Conservative 0; Mismatches 98; Indels 2; Gaps 2;

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 VERSION CB128566.1 GI:28091690
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 675)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel.: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
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 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transfection of
 competent cells E. coli Top10F by electroporation method.

FEATURES

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 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transfection of
 competent cells E. coli Top10F by electroporation method.

Search completed: December 19, 2006, 01:59:33
 Job time : 16800.5 secs

The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN
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 Best Local Similarity .99.7%; Pred. No. 9.4e-168;
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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(without alignments)
10890.483 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3393.4	89.4	3816	3	US-09-696-668-2 Sequence 2, Appli
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5	3388.8	89.2	4275	3	US-09-972-115A-5 Sequence 5, Appli
6	3387.2	89.2	5075	3	US-09-799-451-556 Sequence 556, App
7	3387.2	89.2	6018	3	US-09-849-602-11 Sequence 11, Appli
8	3386	89.2	3394	3	US-09-427-154-1 Sequence 1, Appli
9	3382.8	89.1	4512	3	US-09-350-982C-3 Sequence 3, Appli
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15	1813.4	47.8	4134	3	US-09-972-115A-7 Sequence 7, Appli
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20	994	26.2	2409	3	US-09-964-899-40 Sequence 40, Appli
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ALIGNMENTS

RESULT 1

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; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS C
; FILE REFERENCE: A-68292-1/RMS/DIR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-696-668-1

Query Match	100.0%	Score 3797;	DB 3;	Length 3797;
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RESULT 3

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US-09-696-668-2
; Sequence 2, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossoskaya, Valeria
; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS (
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-696-668-2
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Query Match 89.4%; Score 3393.4; DB 3; Length 3816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db	1922	ATGT	TCTTATGGACATTA	TGAAGTTG	CAGAACTTCTCTTTTAAACAT	TGGAGCAGTAGTTAA	1981

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Db	2042	AA	TTTGCAAACTTTCTGCTCCAGCATGGTCAGACCCCTACCAAAAAAAGGATGGAA	2101
Qy	2083	TACT	CTCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAAGGGAGA	2142
Db	2102	TACT	CTCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAAGGGAGA	2161
Qy	2143	TGCAG	CTTCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTCAAGAGTTGTCTTC	2202
Db	2162	TGCAG	CTTCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTCAAGAGTTGTCTTC	2221
Qy	2203	TCCT	GTATAATGTTAAATTTGCCCGCATACCCAAAGGCAGACATTTCAACACCTTTACATTTAGC	2262
Db	2222	TCCT	GTATAATGTTAAATTTGCCCGCATACCCAAAGGCAGACATTTCAACACCTTTACATTTAGC	2281
Qy	2263	AGCT	TGTTATAATAATTTAGAGTTTCGAGAGTATTTGTTACAACACGGAGCTGATGTGA	2322
Db	2282	AGCT	TGTTATAATAATTTAGAGTTTCGAGAGTATTTGTTACAACACGGAGCTGATGTGA	2341
Qy	2323	TGCC	CAAGACAAAGGAGGACTTATTCCTTTACATAATAGCAGCATCTTTACGGGCATGTAGA	2382
Db	2342	TGCC	CAAGACAAAGGAGGACTTATTCCTTTACATAATAGCAGCATCTTTACGGGCATGTAGA	2401
Qy	2383	TGTAG	CAGCTCTACTAATAAAGTATAATGCAATGTGTCAATGCCACGGACAAATATGGGCTTT	2442
Db	2402	TGTAG	CAGCTCTACTAATAAAGTATAATGCAATGTGTCAATGCCACGGACAAATATGGGCTTT	2461
Qy	2443	CACAC	TTTTGCAGAGACGCCCAAAAGGGACAAACACAGCTTTTGTGCTGTAGC	2502
Db	2462	CACAC	TTTTGCAGAGACGCCCAAAAGGGACAAACACAGCTTTTGTGCTGTAGC	2521
Qy	2503	CCAT	TGGAGCTGACCCCGACTTTTAAAAATCAGGAAGGACAAACCTTTAGATTTAGTTTC	2562
Db	2522	CCAT	TGGAGCTGACCCCGACTTTTAAAAATCAGGAAGGACAAACCTTTAGATTTAGTTTC	2581
Qy	2563	AGCG	ATGATGTTCAGCGCTCTTGTGACAGCAGCATGCCCCCACTGTCTGCTGCCCTCTTG	2622
Db	2582	AGCG	ATGATGTTCAGCGCTCTTGTGACAGCAGCATGCCCCCACTGTCTGCTGCCCTCTTG	2641
Qy	2623	TTACA	GCCTCAAGTGTCTCAATGGTGTGAAGGCCAGGACCACTGCAGATGCTCTCTC	2682
Db	2642	TTACA	GCCTCAAGTGTCTCAATGGTGTGAAGGCCAGGACCACTGCAGATGCTCTCTC	2701
Qy	2683	TTCA	GFTCCATCTAGCCCATCAAGCCTTTCTGCAGCCAGCAGTCTTGAACATTTATCTGG	2742
Db	2702	TTCA	GFTCCATCTAGCCCATCAAGCCTTTCTGCAGCCAGCAGTCTTGAACATTTATCTGG	2761
Qy	2743	GAGT	TTTTTCAGAACTGTCTTCAGTGTAGTTAGTTCAAGTGGAAACAGAGGGTCTTCCAGTTT	2802
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Qy	2803	GGAG	AAAAAGGAGGTTCCAGAGGTAGATTTTACATAACTCAATTCGTAAAGGAATCTTGG	2862
Db	2822	GGAG	AAAAAGGAGGTTCCAGAGGTAGATTTTACATAACTCAATTCGTAAAGGAATCTTGG	2881
Qy	2863	ACTT	GAGCCTTAATGGATATATTTGAGAGAGAACAGATCACITTTGGATGCTATTAGTTGA	2922
Db	2882	ACTT	GAGCCTTAATGGATATATTTGAGAGAGAACAGATCACITTTGGATGCTATTAGTTGA	2941
Qy	2923	GATG	GGGCGCAAGGAGCTGAAGGAGATTTGGAATCAATGCTTTATGGACATAGGCACAAACT	2982
Db	2942	GATG	GGGCGCAAGGAGCTGAAGGAGATTTGGAATCAATGCTTTATGGACATAGGCACAAACT	3001
Qy	2983	AA	TTAAAGGATCGAGAGACTTATCTCCGGAACAAAGGTCCTTAAACCATATTTACTTTT	3042
Db	3002	AA	TTAAAGGATCGAGAGACTTATCTCCGGAACAAAGGTCCTTAAACCATATTTACTTTT	3061
Qy	3043	GAAC	CACCTCTGGTAGTGGAAATTTCTTATAGATCTGTCTCTCTGATGATAAAGAGTTTCA	3102

Db 3062 GAACACCTCTGCTAGTGGAACTTCTTATAGATCTGCTCTGATGATAAAGATTCA 3121
Qy 3103 GTCTGTGGAGGAAGAGATCCAAAGTACAGTTCCAGAGCAACAGATGAGGTCATGCGAGG 3162
Db 3122 GTCTGTGGAGGAAGAGATCCAAAGTACAGTTCCAGAGCAACAGATGAGGTCATGCGAGG 3181
Qy 3163 TGGAAATCTTCAACAGATACAAATATCTCAAGATTCAGAGGTTTGTAAACAAGAACTATG 3222
Db 3182 TGGAAATCTTCAACAGATACAAATATCTCAAGATTCAGAGGTTTGTAAACAAGAACTATG 3241
Qy 3223 GGAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCCAATGA 3282
Db 3242 GGAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCCAATGA 3301
Qy 3283 ACGAATGCTATTTCATGGGTCTCTTCTGTGAATGCCAATATCCCAAGGCTTTGATGA 3342
Db 3302 ACGAATGCTATTTCATGGGTCTCTTCTGTGAATGCCAATATCCCAAGGCTTTGATGA 3361
Qy 3343 AAGGATGCTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAACTCTTC 3402
Db 3362 AAGGATGCTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAACTCTTC 3421
Qy 3403 CAAAAGCAATCAATATGATATGTAATGGAAATGGAGAGGTACTGGGTGTCCAGTTTCAAAAAGA 3462
Db 3422 CAAAAGCAATCAATATGATATGTAATGGAAATGGAGAGGTACTGGGTGTCCAGTTTCAAAAAGA 3481
Qy 3463 CAGATCTTGTTCATTTGCGACAGGAGCTGCTCTTTTGGCGGGTAAACCTTGGGAAAGTC 3522
Db 3482 CAGATCTTGTTCATTTGCGACAGGAGCTGCTCTTTTGGCGGGTAAACCTTGGGAAAGTC 3541
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Db 3662 GCCTATCTCTGATGATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3721
Qy 3703 ATAAATAGTTATTTTAAAGAACTAAATTCACCTGAACCTTAAATATCAATCAATCAAT 3762
Db 3722 ATAAATAGTTATTTTAAAGAACTAAATTCACCTGAACCTTAAATATCAATCAATCAAT 3781
Qy 3763 CCTCTACGTTTCT 3797
Db 3782 CCTCTACGTTTCT 3816

RESULT 4
US-09-843-159B-2
; Sequence 2, Application US/09843159B
; Patent No. 6857675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; PRIORITY FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3816

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-843-159B-2
Query Match 89.4%; Score 3393.4; DB 3; Length 3816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 422 AGTTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGATGCTGCAAGTGTCCAAGC 481
Qy 463 ACGTGATGATGGGGCCCTTATTTCTCTTATAATGATGCTCTTTTGGTTCATGCTGAAGT 522
Db 482 ACGTGATGATGGGGCCCTTATTTCTCTTATAATGATGCTCTTTTGGTTCATGCTGAAGT 541
Qy 523 AGTCAATCTCTTTTGGACATGCTGAGAGCCCAATGCTGAGATTAATTTGAATTTATAC 582
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Qy 583 TCCTCTCCATGAAGTGCATTTAAAGGAAAGATTGATGTTTGCATTTGCTGCTTACAGCA 642
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Qy 643 TGGAGCTGAGCCAAACATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 702
Db 662 TGGAGCTGAGCCAAACATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 721
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Db 722 ATCTGCCAAAGCAGTGTCTTATGTTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCAG 781
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Db 782 GAGTGGCAATCAAGAAATGATGGCTCTACTCACCATTTAAATGTCACTGCCAGC 841
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Db 842 AAGTATGCGCAGAAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGAT 901
Qy 883 TGTACAGCTGTTTACGCAACATGAGAGCTGATGCTCATGCTAAAGATAAAGGTGATCTGTT 942
Db 902 TGTACAGCTGTTTACGCAACATGAGAGCTGATGCTCATGCTAAAGATAAAGGTGATCTGTT 961
Qy 943 ACCATTACCAATGCTGCTTCTTATGCTCATTTAAGATTAAGTAACTTTTGGTCAAGCA 1002
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Db 1022 TGGTGCCTGTGTAATGCAATGGAGCTTGTGCAATTTCACTCTCTTCATGAGGAGCTTC 1081
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Qy 1123 CAATTTGTCACATTAAGTGTCTATAGACTTGGCTCCCAACACAGTAAAGAAAGATT 1182
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Db 1262 AATCAAAAAACATCTCTCTCTGGAATGTTTCAAGCATCTTCAAGCATGAAAC 1321
Qy 1303 AGCATTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1362
Db 1322 AGCATTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381
Qy 1363 GCTAAGAAAAAGGAGCAAAACATCAATGAAAAAGACTAAAGAAATTTCTTGAATCTCTGCACT 1422

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Db 1382 GCTAAGAAAGGAGCAACATCAATGAAAGACATAAGAAATCTTGACTCTCTGCAAGT 1441
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Qy 1603 CTTTACTGCTTTACAGATGGGAATGAAAATGTACAGCAACTCTCCAAAGAGGCTATCTC 1662
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Qy 1843 ACAGCATGGAGCTGATGTGCATGTCTAAAGATPAAAGGAGCCCTGTACCTTTGCAACAATGC 1902
Db 1862 ACAGCATGGAGCTGATGTGCATGTCTAAAGATPAAAGGAGCCCTGTACCTTTGCAACAATGC 1921
Qy 1903 ATGTTCTTATGGACATATGAAGTTGACAGACTCTTGTGTTAAACATCGAGCAGTAGTTAA 1962
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Qy 1963 TGTAGCTGATTTATGGAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
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Qy 2083 TACTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2142
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Db 2702 TTCAAGTCTCAATCTAGCCCTTCAAGCCTTTCTGACAGCAGCAGTCTTGACAACCTTATCTGG 2761
Qy 2743 GAGTTTTTCAAGACTGTCTTCAAGTGTAGTTCAAGTGGACAGAGGCTCTTCCAGTTT 2802
Db 2762 GAGTTTTTCAAGACTGTCTTCAAGTGTAGTTCAAGTGGACAGAGGCTCTTCCAGTTT 2821
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Db 3002 AATTAAAGGAGTCCAGAGACTTATCTCCGACAAACAGGCTTTAAACCATATTTAACTTT 3061
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Db 3542 TTTCTCAGTTCAGTGCATTAATGAAAATGGCACATTTCTCTCCAGGTCACTCAGTCAAC 3601
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QY 1843 ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCTTGTACCTTTGCCAATGC 1902
DB 1921 ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCTTGTACCTTTGCCAATGC 1980
QY 1903 ATGTTCTTATGGACATATGAAGTTTGCAGAACTTCTTGTAAACATGAGAGCAGTAGTTAA 1962
DB 1981 ATGTTCTTATGGACATATGAAGTTTGCAGAACTTCTTGTAAACATGAGAGCAGTAGTTAA 2040
QY 1963 TGTAGCTGATTTATGGAAATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
DB 2041 TGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2100
QY 2023 AATTGGCAACTCTCTGCTCAGCATGTGTGCAGACCTTACCAAAAAAACAGGGATGGAAA 2082
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DB 2161 TACTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTGCTTACGGGAGA 2220
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DB 2401 TGCCCAAGCAAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTACGGGCGATGAGA 2460
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DB 2461 TGTAGCAGCTCTAATAAAGTATAATGCAATGCTGCAATGCCACGCAAAATGGGCTTT 2520
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QY 2503 CCATGGAGCTGACCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2562
DB 2581 CCATGGAGCTGACCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2640
QY 2563 AGCGGATGATGTACGCGCTCTTTCGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTTG 2622
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DB 2881 GGAGAAAAGGAGGTTCCAGAGTAGATTTTAGCACTACTCAATTCGTAAGCAATCTTGG 2940
QY 2863 ACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGATTAGTTGA 2922
DB 2941 ACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGATTAGTTGA 3000

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DB 3061 AATTAAAGAGTCCGAGAGACTTATCTCCGACAAACAGGCTCTTAACCCATATTTAACTTT 3120
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DB 3481 CAAAAGCAATCAATATGATATGGAATTTGGAAGGAGTACTGGGTGTCAGTTTCAAAAGA 3540
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QY 3583 TGGTAGCCCGAGTGTAAATGGCCTAGCATTTAGCTGAATATGTTATTTTACAGAGAGAAC 3642
DB 3661 TGGTAGCCCGAGTGTAAATGGCCTAGCATTTAGCTGAATATGTTATTTTACAGAGAGAAC 3720
QY 3643 GGCTTATCTGAGTATTTAATTTACTTACCAGATTTATGAGGCTCGAAGTATGGTTCGATGG 3702
DB 3721 GGCTTATCTGAGTATTTAATTTACTTACCAGATTTATGAGGCTCGAAGTATGGTTCGATGG 3780
QY 3703 ATAAATAGTTATTTTAAAGAACTAAATTTCCACTGAACCTAAATCATCAAAGCAGCAGTGG 3762
DB 3781 ATAAATAGTTATTTTAAAGAACTAAATTTCCACTGAACCTAAATCATCAAAGCAGCAGTGG 3840
QY 3763 CCTCTAGCTTTTACTCTCTCTTGGTGAAGAAAAA 3794
DB 3841 CCTCTAGCTTTTACTCTCTCTTGGTGAAGAAAAA 3872

RESULT 6

US-09-799-451-556

; Sequence 556, Application US/09799451

; Patent No. 6783969

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

; APPLICANT: Zhang, Jie

; APPLICANT: Xue, Aidong J.

```
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yuning
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghoeh, Reena
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 556
; LENGTH: 5075
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3750)
US-09-799-451-556

Query Match      89.2%; Score 3387.2; DB 3; Length 5075;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 403 AGCTTTTGGCGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAGC 462
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QY 463 AGCTGATGATGGGGCCCTTATTCCTTCATATGATGATGCTCTTTGGTGCATGCTGAAGT 522
DB 510 AGCTGATGATGGGGCCCTTATTCCTTCATATGATGATGCTCTTTGGTGCATGCTGAAGT 569
QY 523 AGTCAATCTCTTTTGGCAGATGGTGCAGACCCCAATGCTCCAGATATTTGAATATATAC 582
DB 570 AGTCAATCTCTTTTGGCAGATGGTGCAGACCCCAATGCTCCAGATATTTGAATATATAC 629
QY 583 TCCTCTCCATGAAGTGCATTAATAAGGAAGATGATGTTTGCATTTGCTGTACAGCA 642
DB 630 TCCTCTCCATGAAGTGCATTAATAAGGAAGATGATGTTTGCATTTGCTGTACAGCA 689
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DB 690 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 749
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DB 750 ATCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCAG 809
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QY 823 AAGTGTGTCAGAAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGAT 882
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QY 883 TGTACAGCTGTTACTGCAACATGGAGCTGATGCTCATGCTAAAGATAAGAGTGTCTGT 942
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QY 943 ACCATTACCAATGCTGTTCTTATGCTCATATGAAGTAACTGAATCTTTGGTCAAGCA 1002
DB 990 ACCATTACCAATGCTGTTCTTATGCTCATATGAAGTAACTGAATCTTTGGTCAAGCA 1049
QY 1003 TGGTGCCTGTGTAAATGCAATGGACTTTGTGGCAATTCACCTCTTTCATGAGGACAGCTTC 1062
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QY 1123 CAATTTGTCACAATAAAGTGTCTATAGACTTTGGCTCCCAACACACAGTTTAAAAAGAAAT 1182
DB 1170 CAATTTGTCACAATAAAGTGTCTATAGACTTTGGCTCCCAACACACAGTTTAAAAAGAAAT 1229
QY 1183 AGCATATGAATTTAAAGGCCACTCTTGTGTGCAAGCTGCAAGAGCTGATGTTACTCG 1242
DB 1230 AGCATATGAATTTAAAGGCCACTCTTGTGTGCAAGCTGCAAGAGCTGATGTTACTCG 1289
QY 1243 AATCAAAAAACATCTCTCTCTGGAATGTTCAAGTATCTCAACACATGAAAC 1302
DB 1290 AATCAAAAAACATCTCTCTCTGGAATGTTCAAGTATCTCAACACATGAAAC 1349
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DB 1350 AGCATTTGCAATTTGCTGCTGCTATCTCCATATCCCAAAAAAGCAATATGTTGAATGTT 1409
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DB 1590 ACAAACTGCGCCCTTACTCTCTGAGCTATGGGTGATCTTAACATATATATCCCTTCAGGG 1649
QY 1603 CTTTACTGCTTTTACAGATGGGAAATGAAATGTACAGAACTCTCCCAAGAGGATATCTC 1662
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QY 1783 GTCTACACCACTTCATTTTTCAGCTGGGTATAACAGAGTGTCCGTTGGTGAATATCTGCT 1842
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QY 1843 ACAGCATGGAGCTGATGTGCTGCTTAAAGATAAGAGGAGGCTTTGTACCTTTGCAAAATGC 1902
DB 1890 ACAGCATGGAGCTGATGTGCTGCTTAAAGATAAGAGGAGGCTTTGTACCTTTGCAAAATGC 1949
QY 1903 ATGTTCTTATGGACATTAATGAAGTTGCAAGACTTCTTGTAAACATGAGCAGTATGTTAA 1962
DB 1950 ATGTTCTTATGGACATTAATGAAGTTGCAAGACTTCTTGTAAACATGAGCAGTATGTTAA 2009
QY 1963 TGTAGCTGATTTATGGAAATTTTACCTTTTACATGAAGCAGCAGCAAGGAAATATGA 2022
DB 2010 TGTAGCTGATTTATGGAAATTTTACCTTTTACATGAAGCAGCAGCAAGGAAATATGA 2069
QY 2023 AATTGTCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAAGAGGATGGAAA 2082
DB 2070 AATTGTCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAAGAGGATGGAAA 2129
QY 2083 TACTCTTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAGA 2142
DB 2130 TACTCTTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAGA 2189
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QY	523	AGTCAATCTCCTTTTCCGACATGGTGCAGACCCCAATGCTCGAGATAAATTGGAATTATAC	582
DB	538	AGTCAATCTCCTTTTCCGACATGGTGCAGACCCCAATGCTCGAGATAAATTGGAATTATAC	597
QY	583	TCCTCTCCATGAAGCTGCAATTAAAGGAAGATTGATTTGCTGCTGTTACAGCA	642
DB	598	TCCTCTCCATGAAGCTGCAATTAAAGGAAGATTGATTTGCTGCTGTTACAGCA	657
QY	643	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGACAGCATTTGATTTAGCAGATCC	702
DB	658	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGACAGCATTTGATTTAGCAGATCC	717
QY	703	ATCTGCGAAAGCAGTCTTACTGGTGAATATAGAAAGATGAATCTTAAAGAAAGTGCCAG	762
DB	718	ATCTGCGAAAGCAGTCTTACTGGTGAATATAGAAAGATGAATCTTAAAGAAAGTGCCAG	777
QY	763	GAGTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATGTCAAATGCGACGCG	822
DB	778	GAGTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATGTCAAATGCGACGCG	837
QY	823	AAATGATGCGAGAAAGTCAATCCATTAATTTGGCAGCAGGATATACAGAGTAAAGAT	882
DB	838	AAATGATGCGAGAAAGTCAATCCATTAATTTGGCAGCAGGATATACAGAGTAAAGAT	897
QY	883	TGTACAGCTGTTACTGCAACATGGAGCTGATGCTCAATGCTAAAGATAAAGGTGATCTGGT	942
DB	898	TGTACAGCTGTTACTGCAACATGGAGCTGATGCTCAATGCTAAAGATAAAGGTGATCTGGT	957
QY	943	ACCAATTACAAATGCTGTTCTTATGCTCAATTAAGTAACTGAATTTGGTCAAGCA	1002
DB	958	ACCAATTACAAATGCTGTTCTTATGCTCAATTAAGTAACTGAATTTGGTCAAGCA	1017
QY	1003	TGGTGCCTGTGTAAATGCAATGCACTGTGGCAATTTCACTCTCTTCATGAGGCGACTTC	1062
DB	1018	TGGTGCCTGTGTAAATGCAATGCACTGTGGCAATTTCACTCTCTTCATGAGGCGACTTC	1077
QY	1063	TAAAGAACAGGGTTGAAGTATGTTCTTCTTAAAGTATGCTGAGACCCCAACTGCT	1122
DB	1078	TAAAGAACAGGGTTGAAGTATGTTCTTCTTAAAGTATGCTGAGACCCCAACTGCT	1137
QY	1123	CAATTGTCAATAAAGTGTATAGACTTGGCTCCACACACAGTTAAAGAAAGATT	1182
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DB	1198	AGCATATGAAATTAAGGCGCACTGTTGCTGCAAGCTGCAAGAGCTGATTTACTCG	1257
QY	1243	AATCAAAAACATCTCTCTGGAATGCTGAAATTTCAAGCATCTCAAAACATGAAAC	1302
DB	1258	AATCAAAAACATCTCTCTGGAATGCTGAAATTTCAAGCATCTCAAAACATGAAAC	1317
QY	1303	AGCATTTGCTGCTGCTGCTATCCATATCCAAAAGAAAGCAAAATATGGAATGTT	1362
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QY	1363	GCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTAAAGAAATTTCTGACTCTGCAAGT	1422
DB	1378	GCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTAAAGAAATTTCTGACTCTGCAAGT	1437
QY	1423	GGCATCTGAGAAAGCTCAATAATGATGTTCTGTAAGTGTGGTGAACATGAAGCAAGGT	1482
DB	1438	GGCATCTGAGAAAGCTCAATAATGATGTTGTAAGTGTGGTGAACATGAAGCAAGGT	1497
QY	1483	TAAATGCTCTGGATAATCTTTGGTCAAGCTTCTTACACAGAGCTGATATTTGGTCACT	1542
DB	1498	TAAATGCTCTGGATAATCTTTGGTCAAGCTTCTTACACAGAGCTGATATTTGGTCACT	1557
QY	1543	ACAAACCTGCGCGCTACTCTGAGCTATGGGTGTGATCCCTAATATATATCCCTTCAGGG	1602
DB	1558	ACAAACCTGCGCGCTACTCTGAGCTATGGGTGTGATCCCTAATATATATATATCCCTTCAGGG	1617

QY	1603	CTTTACTGCTTTTACAGATGGGAAATGAAATGTAAGCAAACTCTCCCAAGAGGGTATCTC	1662
DB	1618	CTTTACTGCTTTTACAGATGGGAAATGAAATGTAAGCAAACTCTCCCAAGAGGGTATCTC	1677
QY	1663	ATTAGGTAAATTCAGAGGCGAGACAGCAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTCGA	1722
DB	1678	ATTAGGTAAATTCAGAGGCGAGACAGCAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTCGA	1737
QY	1723	AACTGTAAAAAACTGTGTACTGTTTACAGATGCTCAACTGACAGACATTTAAAGGGCGTCA	1782
DB	1738	AACTGTAAAAAACTGTGTACTGTTTACAGATGCTCAACTGACAGACATTTAAAGGGCGTCA	1797
QY	1783	GTCTACACCACTTCAATTTTGGCAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGCT	1842
DB	1798	GTCTACACCACTTCAATTTTGGCAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGCT	1857
QY	1843	ACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGAGGCGCTTGTACCTTGCACAAATGC	1902
DB	1858	ACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGAGGCGCTTGTACCTTGCACAAATGC	1917
QY	1903	ATGTTCTTTATGACATTAATGAAGTTGACAACTCTTGTGTTAAACATGGAGCAGTACTTAA	1962
DB	1918	ATGTTCTTTATGACATTAATGAAGTTGACAACTCTTGTGTTAAACATGGAGCAGTACTTAA	1977
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DB	2098	TACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTCTTAGGGGAGA	2157
QY	2143	TGCAGCTTTGCTAGATGCTGCGCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTTTC	2202
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DB	2218	TCCTGATTAATGTAATTTGCGCGATACCCAGGCGAGACATTCAAACACTTTACATTTAGC	2277
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DB	2278	AGCTGGTTATTAATTTAGAGTTGACAGATTTGTTTACAAACAGGAGCTGATGGA	2337
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DB	2338	TGCCCAAGCAAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCATGTAGA	2397
QY	2383	TGTAGCAGCTCTAATAATAAGTATAATGCTGCTCAATGTCACGGACAATAATGGGCTTT	2442
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DB	2458	CACACCTTTGACGAAGCAGCCCAAAAGGAGGAGACACAGCTTTTGTGCTTGTGCTAGC	2517
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QY	2563	AGCGATGATGTACGGCTCTTCTGACAGAGCCATGCCCCCATCTGCTGCCCCCTCTTG	2622
DB	2578	AGCGATGATGTACGGCTCTTCTGACAGAGCCATGCCCCCATCTGCTGCCCCCTCTTG	2637
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Db 2818 GGAGAAAAGAGGTTCCAGGAGTAGATTTTTCAGTAACTCAATTCGTAAGGAATCTTGG 2877
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Qy 2983 AATTAAAGGAGTCCAGAGACTTATCTCCGGACAAAGGCTTTAAACCATATTTAACTTT 3042
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Db 3718 ATAAATAGTTATTTTAAGAACTAATTCCACTGAACCTTAAATCATCAAAGCAGCAGTGG 3777
Qy 3763 CCTCTAGGTTTACTCTCTTCTGCTGAAAABAAA 3794
|||||

Db 3778 CCTCTAGTTTTACTCTCTTTGCTGAAAAAAA 3809
RESULT 8
US-09-427-154-1
; Sequence 1, Application US/09427154
; Patent No. 6589725
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68292-DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/427,154
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-427-154-1
Query Match 89.2%; Score 3386; DB 3; Length 3394;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 404 GGTTTTGGCGGGAAGACGTAGTTGTAATATTTTGGCTTCAGAAATGCTGCAAGTGTCCAAGCA 463
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Qy 524 GTCAATCTCTTTTGGCAATGCTGAGACCCCAATGCTCGAGATTAATGGAATTAATCT 583
Db 121 GTCAATCTCTTTTGGCAATGCTGAGACCCCAATGCTCGAGATTAATGGAATTAATCT 180
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Db 241 GGAGCTGAGCCAACTCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCCA 300
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Db 301 TCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCAGG 360
Qy 764 AGTGGCAATGAAGAAAATGATGGCTCTACTCACACCATTTAAATGTCACTGCCACGCA 823
Db 361 AGTGGCAATGAAGAAAATGATGGCTCTACTCACACCATTTAAATGTCACTGCCACGCA 420
Qy 824 AGTGATGGCAAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATT 883
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Db 481 GTACAGCTGTTACTGCAACATGGAGCTGATGCTCCATGCTAAAGATTAAGTGTCTGGTA 540
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Db 541 CCATTACACAATGCTCTCTTATGCTCATTAAGTAACTGAACCTTTTGGTCAAGCAT 600
Qy 1004 GGTGCTGTGTAAATGCAATGGACTTTGGCAATTTCACTCTCTTTCATGAGGCAAGTCTCT 1063
Db 601 GGTGCTGTGTAAATGCAATGGACTTTGGCAATTTCACTCTCTTTCATGAGGCAAGTCTCT 660
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661	Db	AAGAACAGGGTTGAAGTATGTTCTCTTCTCTTAAAGTTATGGTGAGACCCAAACATGCTCT	720
1124	Qy	AATTTGTCACAAATAAAAGTGCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAGAAATTA	1183
721	Db	AATTTGTCACAAATAAAAGTGCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAGAAATTA	780
1184	Qy	GCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAAGCTGATTTACTCGA	1243
781	Db	GCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAAGCTGATTTACTCGA	840
1244	Qy	ATCAAAAAACATCTCTCTCTGGAAATGGTGAAATTTCAAGCATCTCTCAAAACATGAAACA	1303
841	Db	ATCAAAAAACATCTCTCTCTGGAAATGGTGAAATTTCAAGCATCTCTCAAAACATGAAACA	900
1304	Qy	GCATTGCAATTTGCTGCTGCAATCTCCATATCCCAAAAGAAGCAAAATATGTGAACCTGTG	1363
901	Db	GCATTGCAATTTGCTGCTGCAATCTCCATATCCCAAAAGAAGCAAAATATGTGAACCTGTG	960
1364	Qy	CTAAGAAAAAGGAGCAAAACATCAATGAAAAAGACTAAAGAAATTTCTTGACTCTCTGCACGTG	1423
961	Db	CTAAGAAAAAGGAGCAAAACATCAATGAAAAAGACTAAAGAAATTTCTTGACTCTCTGCACGTG	1020
1424	Qy	GCATCTGAGAAAGCTCAATAATGATGTTGTTGAAGTAGTGGTGAAAAATGAAGCAAAAGGTT	1483
1021	Db	GCATCTGAGAAAGCTCAATAATGATGATGTTGTTGAAGTAGTGGTGAAAAATGAAGCAAAAGGTT	1080
1484	Qy	AATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATCTGGTCACTTA	1543
1081	Db	AATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATCTGGTCACTTA	1140
1544	Qy	CAAACTTCGCCCTTACTCTCTGAGCTATGGGGTGTGATCCTTAACATTAATATCCCTTCAGGGC	1603
1141	Db	CAAACTTCGCCCTTACTCTCTGAGCTATGGGGTGTGATCCTTAACATTAATATCCCTTCAGGGC	1200
1604	Qy	TTTTACTGCTTTACAGATGGGAAATGAAATATGTACAGCAATCTCTCCAAGAGGGTATCTCA	1663
1201	Db	TTTTACTGCTTTACAGATGGGAAATGAAATATGTACAGCAATCTCTCCAAGAGGGTATCTCA	1260
1664	Qy	TTAGGTAATTTACAGAGGCAGACAGCAATTTGCTGGAACTGCAAGGCTGGAGATGTGCA	1723
1261	Db	TTAGGTAATTTACAGAGGCAGACAGCAATTTGCTGGAACTGCAAGGCTGGAGATGTGCA	1320
1724	Qy	ACTGTAAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCA	1783
1321	Db	ACTGTAAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCA	1380
1784	Qy	TCTACACCACTTCAATTTGACGTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCTA	1843
1381	Db	TCTACACCACTTCAATTTGACGTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCTA	1440
1844	Qy	CAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGGAGGCCCTTGTAACCTTTGCACAATGCA	1903
1441	Db	CAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGGAGGCCCTTGTAACCTTTGCACAATGCA	1500
1904	Qy	TGTTCTTTATGGACATTAATGAAGTTGCAGAACTTCTGTTTAAACATGAGCAGTAGTTAAT	1963
1501	Db	TGTTCTTTATGGACATTAATGAAGTTGCAGAACTTCTGTTTAAACATGAGCAGTAGTTAAT	1560
1964	Qy	GTAGCTGAATTTATGAAATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGAA	2023
1561	Db	GTAGCTGAATTTATGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGAA	1620
2024	Qy	ATTTGCAAACTTCTGCTCCAGCATGGTGAGACCTTACCAAAAAACACAGGATGGAAT	2083
1621	Db	ATTTGCAAACTTCTGCTCCAGCATGGTGAGACCTTACCAAAAAACACAGGATGGAAT	1680
2084	Qy	ACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGAGAT	2143
1681	Db	ACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGAGAT	1740
2144	Qy	GCAGCTTTGCTAGATGCTGCCAAGAGGGTTGTTTAGCCAGAGTGAAAGATGTTCTTCT	2203

Db	1741	GCAGCTTTGCTAGATGCTCCCAAGAAAGGTTGTTTAGCCAGAGTGAAGAAGTTGTCTTCT	1800
Qy	2204	CCCTGATAATGTAAATTCGCGCATACCCAAGGCAGACATTCAACACCTTTACATTTAGCA	2263
Db	1801	CCCTGATAATGTAAATTCGCGCATACCCAAGGCAGACATTCAACACCTTTACATTTAGCA	1860
Qy	2264	GCTGGTTATAAATTTGAAGTTGCAGAGTATTTGTTTAAACACACGGAGCTGATGTAAT	2323
Db	1861	GCTGGTTATAAATTTAGAAAGTTGCAGAGTATTTGTTTAAACACACGGAGCTGATGTAAT	1920
Qy	2324	GCCCAAGACAAAGGAGCTTATTTCTTTTACATAAATGCAGCATCTTACGGCATGTAGAT	2383
Db	1921	GCCCAAGACAAAGGAGAGCTTATTTCTTTTACATAAATGCAGCATCTTACGGCATGTAGAT	1980
Qy	2384	GTAGCAGCTCTACTAATAAAGTATAATGATGTGTCAATGCCACGCACAAAATGGGCTTTC	2443
Db	1981	GTAGCAGCTCTACTAATAAAGTATAATGATGTGTCAATGCCACGCACAAAATGGGCTTTC	2040
Qy	2444	ACA CTTTTCGACGAAGCAGCCAAAAGGAGCGAACACAGCTTTGTCTTTGTTGCTAGCC	2503
Db	2041	ACACCTTTCGACGAAGCAGCCAAAAGGAGCGAACACAGCTTTGTGCTTTGTTGCTAGCC	2100
Qy	2504	CATGGAGCTGACCCGACTCTTAAANAATCAGGAAGGACAAACACTTTAGATTTTTC	2563
Db	2101	CATGGAGCTGACCCGACTCTTAAANAATCAGGAAGGACAAACACTTTAGATTTTTC	2160
Qy	2564	GCGGATGATGTCAGCGCTCTTCTGACAGCAGCATTGCCCCCATCTGCTCTGCCCTCTTGT	2623
Db	2161	GCGGATGATGTCAGCGCTCTTCTGACAGCAGCATTGCCCCCATCTGCTCTGCCCTCTTGT	2220
Qy	2624	TACAAGCCTCAAGTGTCTCAATGGTGTGAGAAGCCAGAGGCCACTCGAGATGCTCTCTCT	2683
Db	2221	TACAAGCCTCAAGTGTCTCAATGGTGTGAGAAGCCAGAGGCCACTCGAGATGCTCTCTCT	2280
Qy	2684	TGAGTTCATCTAGCCCATCAAGCCTTTCTGACGACGACAGTCTTGACAACTTATCTGGG	2743
Db	2281	TCAGGTCATCTAGCCCATCAAGCCTTTCTGACGACGACAGTCTTGACAACTTATCTGGG	2340
Qy	2744	AGTTTTTTCAGACTGTCTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGTCCTCCAGTTTG	2803
Db	2341	AGTTTTTTCAGACTGTCTTCATTTAGTTAGTTTCAAGTGGAAACAGAGGTCCTCCAGTTTG	2400
Qy	2804	GAGAAAAGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGGA	2863
Db	2401	GAGAAAAGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGGA	2460
Qy	2864	CTTGAGCACCCTAATGATATATTTTGAGAGAGAACAGATCACTTTTGATGTATTAGTTGAG	2923
Db	2461	CTTGAGCACCCTAATGATATATTTTGAGAGAGAACAGATCACTTTTGATGTATTAGTTGAG	2520
Qy	2924	ATGGGSCAACAGGAGCTGAAGGAGTTGGAATCAATGCTTATGSGACATAGGCAACAAC	2983
Db	2521	ATGGGSCAACAGGAGCTGAAGGAGTTGGAATCAATGCTTATGSGACATAGGCAACAAC	2580
Qy	2984	ATTAAAGGAGTCGAGAGACTTATCTCCGAGCAACAAGGTCCTTAAACCATATTTAACTTTG	3043
Db	2581	ATTAAAGGAGTCGAGAGACTTATCTCCGAGCAACAAGGTCCTTAAACCATATTTAACTTTG	2640
Qy	3044	AACACCTCTGGTAGTGGAAACAATTTTATAGATCTGTCTCTGTATGATAAAGAGTTTCAG	3103
Db	2641	AACACCTCTGGTAGTGGAAACAATTTTATAGATCTGTCTCTGTATGATAAAGAGTTTCAG	2700
Qy	3104	TCGTTCGAGGAGAGATGCAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAGGT	3163
Db	2701	TCGTTCGAGGAGAGATGCAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAGGT	2760
Qy	3164	GGAATCTTCAACAGATACAAATATTTCTCAAGATTTCAGAAAGTTTGTAAACAAGAACTATGG	3223
Db	2761	GGAATCTTCAACAGATACAAATATTTCTCAAGATTTCAGAAAGTTTGTAAACAAGAACTATGG	2820
Qy	3224	GAAAGATACCTCACCCGAGAAAGAAAGTTTCTGAGAAAGAAACCAACCAATGCCAATGAA	3283

Db 2821 GAAAGATACACTACCGGAGAAAGAGTTCTTGAAGAAACCAACCATGCCAATGAA 2880
Qy 3284 CGAATGCTATTTCATGGGTCTCTTTTGTGAATGCAATTTATCCAAAAGGCTTTGATGAA 3343
Db 2881 CGAATGCTATTTCATGGGTCTCTTTTGTGAATGCAATTTATCCAAAAGGCTTTGATGAA 2940
Qy 3344 AGGCATGGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTCC 3403
Db 2941 AGGCATGGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTCC 3000
Qy 3404 AAAAGCAATCAATATGATATGAAATGGAGAGGTACTGGGTCTCCAGTTCACAAAGAC 3463
Db 3001 AAAAGCAATCAATATGATATGAAATGGAGAGGTACTGGGTCTCCAGTTCACAAAGAC 3060
Qy 3464 AGATCTTGTACATTTGCCACAGCAGCTGCTCTTTTGCOCGGTAACTTTGGGAAAGTCT 3523
Db 3061 AGATCTTGTACATTTGCCACAGCAGCTGCTCTTTTGCOCGGTAACTTTGGGAAAGTCT 3120
Qy 3524 TTCTGTCAGTTCAAGTGAATGGCAATGGCAGATTTCTCTCCAGGTCACTCAGTCACT 3583
Db 3121 TTCTGTCAGTTCAAGTGAATGGCAGATTTCTCTCCAGGTCACTCAGTCACT 3180
Qy 3584 GGTAGGCCAGTGAATGGCTAGCATTTAGCTGAATATGTTTATACAGAGGAGAACAG 3643
Db 3181 GGTAGGCCAGTGAATGGCTAGCATTTAGCTGAATATGTTTATACAGAGGAGAACAG 3240
Qy 3644 GCTTATCTCAGTATTTAAATTTACTTACCAGATTTAGGCTGAAGGTATGGTGCATGGA 3703
Db 3241 GCTTATCTCAGTATTTAAATTTACTTACCAGATTTAGGCTGAAGGTATGGTGCATGGA 3300
Qy 3704 TAAATAGTATTTAAGAACTAAATTCATCTGAACCTTAAATATCAAAAGCAGAGTGGC 3763
Db 3301 TAAATAGTATTTAAGAACTAAATTCATCTGAACCTTAAATATCAAAAGCAGAGTGGC 3360
Qy 3764 CTCTACGTTTACTCTTCTGCTGAAAAAATAA 3797
Db 3361 CTCTACGTTTACTCTTCTGCTGAAAAAATAA 3394

RESULT 9
US-09-982C-3
; Sequence 3, Application US/09350982C
; Patent No. 6455290
; GENERAL INFORMATION:
; APPLICANT: Berthelsen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Isacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Relate
; TITLE OF INVENTION: Same
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4512
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primers
; NAME/KEY: misc.feature
; LOCATION: (1124)..(1124)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc.feature
; LOCATION: (2672)..(2672)
; OTHER INFORMATION: n is any nucleic acid
US-09-982C-3

Query Match 89.1%; Score 3382.8; DB 3; Length 4512;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3381; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 403 AGGTTTGGGGGAAAGACGATAGTTGAATATTTCTTCAGAAATGGTGCAGTGTCCAAAGC 462

Db 220 AGGTTTGGGGGAAAGACGATAGTTGAATATTTGCTTCAGAAATGGTGCAGAAATGTCCAAGC 279
Qy 463 ACGTGATGATGGGGGCTTATTCCTCTTCAATATGCAATGCTCTTTTGGTCAATGCTGAAGT 522
Db 280 ACGTATGATGGGGGCTTATTCCTCTTCAATATGCAATGCTCTTTTGGTCAATGCTGAAGT 339
Qy 523 AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAAATTTGGAATTTATAC 582
Db 340 AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAAATTTGGAATTTATAC 399
Qy 583 TCCTCTCCATGAAGCTCAATTTAAAGGAAAGATTTGATTTTGTGCTTGTCTGTTTACAGCA 642
Db 400 TCCTCTCCATGAAGCTCAATTTAAAGGAAAGATTTGATTTTGTGCTTGTCTGTTTACAGCA 459
Qy 643 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCC 702
Db 460 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCC 519
Qy 703 ATCTGCCAAAGCAGTGGTCTTACTGGTGAATATGAAGAAAGATGAACTCTTAGAAAGTCCAG 762
Db 520 ATCTGCCAAAGCAGTGGTCTTACTGGTGAATATGAAGAAAGATGAACTCTTAGAAAGTCCAG 579
Qy 763 GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGC 822
Db 580 GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGC 639
Qy 823 AAGTATGAGGAGCAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGAT 882
Db 640 AAGTATGAGGAGCAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGAT 699
Qy 883 TGTACAGCTGTTACTGCAACATGGAGCTGATGCTCATGCTAAAGATAAAGTGAATCTGGT 942
Db 700 TGTACAGCTGTTACTGCAACATGGAGCTGATGCTCATGCTAAAGATAAAGTGAATCTGGT 759
Qy 943 ACCAATTACACAANTGCCCTGTTCTTATGCTCATTTAAGATTAACCTAATTTTGGTCAAGCA 1002
Db 760 ACCAATTACACAANTGCCCTGTTCTTATGCTCATTTAAGATTAACCTAATTTTGGTCAAGCA 819
Qy 1003 TGGTGCCTGTGTAATGCAATGGCAATTTGGCAATTTCACTCTCTTCATGAGGAGCTTC 1062
Db 820 TGGTGCCTGTGTAATGCAATGGCAATTTGGCAATTTCACTCTCTTCATGAGGAGCTTC 879
Qy 1063 TAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAGTTATGGTGCAGACCCCACTGCT 1122
Db 880 TAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAGTTATGGTGCAGACCCCACTGCT 939
Qy 1123 CAATTGTCACAATAAAGTGTCTATAGACTTGGCTCCACACCACTGTTAAAGAAAGATTT 1182
Db 940 CAATTGTCACAATAAAGTGTCTATAGACTTGGCTCCACACCACTGTTAAAGAAAGATTT 999
Qy 1183 AGCATATGAATTTAAAGGCCACTGTTTGTGCTGCAAGCTGCAGAGAGCTGATGTTACTCG 1242
Db 1000 AGCATATGAATTTAAAGGCCACTGTTTGTGCTGCAAGCTGCAGAGAGCTGATGTTACTCG 1059
Qy 1243 AATCAAAAAACATCTCTCTCTGGAATTTGGTGAATTTCAAGCATCTCTCAACACATGAAC 1302
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Qy 1303 AGCATATGCTGCTGCTGCTCATCTCCATATCCCAAGAAAGCAATATCTGAACTGTT 1362
Db 1120 AGCANTGCATTTGCTGCTGCTCATCTCCATATCCCAAGAAAGCAATATGTTGAATCTGTT 1179
Qy 1363 GCTAAGAAAAAGGAGCAACATCAATGAAAAAGACTTAAAGAAATTTCTTGACTCTCTGCAAGT 1422
Db 1180 GCTAAGAAAAAGGAGCAACATCAATGAAAAAGACTTAAAGAAATTTCTTGACTCTCTGCAAGT 1239
Qy 1423 GGCATCTGAGAAAGCTCATTAATGATGTTTGAAGTAGTGTGAAACATGAAGCAAGGT 1482
Db 1240 GGCATCTGAGAAAGCTCATTAATGATTTTGTGAAGTAGTGTGAAACATGAAGCAAGGT 1299
Qy 1483 TAATGCTCTGATTAATCTTGGTCTGAGCTTCTCTACACAGAGCTCATATTTGCTGCTCATCT 1542

Db 1300 TAAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTGCATCT 1359
Qy 1543 ACAAACTTGGCGCTTACTCTTCTAGCTATGGGTGATCTTAACATATATATCCCTTCAGGG 1602
Db 1360 ACAAACTTGGCGCTTACTCTTCTAGCTATGGGTGATCTTAACATATATATCCCTTCAGGG 1419
Qy 1603 CTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCCAAAGAGGGTATCTC 1662
Db 1420 CTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCCAAAGAGGGTATCTC 1479
Qy 1663 ATTAGGTAAATTCAGAGGAGACAGACAATTTGCTGGAAGCTGCAAAAGCTGAGATGTGGA 1722
Db 1480 ATTAGGTAAATTCAGAGGAGACAGACAATTTGCTGGAAGCTGCAAAAGCTGAGATGTGGA 1539
Qy 1723 AACTCTAAAAAATCTGTACTGTTTCAAGTGTCACTGAGAGACATTTGAAGGGCGTCA 1782
Db 1540 AACTCTAAAAAATCTGTACTGTTTCAAGTGTCACTGAGAGACATTTGAAGGGCGTCA 1599
Qy 1783 GTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT 1842
Db 1600 GTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT 1659
Qy 1843 ACAGCATGGAGCTGATGTGCTATGCTTAAAGATAAAGAGGCTTGTACCTTTGCACAATGC 1902
Db 1660 ACAGCATGGAGCTGATGTGCTATGCTTAAAGATAAAGAGGCTTGTACCTTTGCACAATGC 1719
Qy 1903 ATGTTCTTATGGACATTAAGTGTGCAAGTCTTCTGTTAAACATGAGCAGTAGTTAA 1962
Db 1720 ATGTTCTTATGGACATTAAGTGTGCAAGTCTTCTGTTAAACATGAGCAGTAGTTAA 1779
Qy 1963 TGTAGCTGATTTATGGAAATTTTACACCTTTTACGAAGCAGCAGCAAAAGGAAATATGA 2022
Db 1780 TGTAGCTGATTTATGGAAATTTTACACCTTTTACGAAGCAGCAGCAAAAGGAAATATGA 1839
Qy 2023 AATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAAA 2082
Db 1840 AATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAAA 1899
Qy 2083 TACTCTTTGGATCTGTTTAAAGATGGAGATACAGATTTCAAGATCTGCTTAGGGGAGA 2142
Db 1900 TACTCTTTGGATCTGTTTAAAGATGGAGATACAGATTTCAAGATCTGCTTAGGGGAGA 1959
Qy 2143 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTGTGCTTC 2202
Db 1960 TGCAGCTTTGCTAGATGCTGCCAAGAGTGTGTTAGCCAGAGTGAAGAGTGTGCTTC 2019
Qy 2203 TCCTGATTAATGTAATTCGCGGATACCCAGGAGACATTCACCAACCTTTACATTTAGC 2262
Db 2020 TCCTGATTAATGTAATTCGCGGATACCCAGGAGACATTCACCAACCTTTACATTTAGC 2079
Qy 2263 AGCTGGTTTAAATTTAGAGTTGCAAGTATTTGTTTACCAACCGAGCTGATGTGAA 2322
Db 2080 AGCTGGTTTAAATTTAGAGTTGCAAGTATTTGTTTACCAACCGAGCTGATGTGAA 2139
Qy 2323 TGCCCAAGCAAAAGGAGACTTATTTCTTTTACATAATGAGCATCTTACGGGCATGTAGA 2382
Db 2140 TGCCCAAGCAAAAGGAGACTTATTTCTTTTACATAATGAGCATCTTACGGGCATGTAGA 2199
Qy 2383 TGTAGCAGCTCTATAATAAGTATAATGCTCAATGCTCAATGCCAGCAAAATGGGCTTT 2442
Db 2200 TGTAGCAGCTCTATAATAAGTATAATGCTCAATGCTCAATGCCAGCAAAATGGGCTTT 2259
Qy 2443 CACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACAGCTTTGCTTTGCTTTGCTAGC 2502
Db 2260 CACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACAGCTTTGCTTTGCTTTGCTAGC 2319
Qy 2503 CCAATGAGCTGACCCGACTCTTTAAAAATCAGGAAGCAACCACTTTAGATTTAGTTTC 2562
Db 2320 CCAATGAGCTGACCCGACTCTTTAAAAATCAGGAAGCAACCACTTTAGATTTAGTTTC 2379
Qy 2563 AGCGGATGATGTACGCTCTTTTGACAGCAGCCCAATGCCCATCTGCTGCCCTCTTG 2622
Db 2380 AGCGGATGATGTACGCTCTTTTGACAGCAGCCCAATGCCCATCTGCTGCCCTCTTG 2439

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Db 2440 TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAACCCAGAGCCACTGTCAGATGCTCTCTC 2499
Qy 2683 TTTAGGTCCTACTAGCCCATCAAGCCTTTCTGACGACGAGTCTTGAACAATCTATCTGG 2742
Db 2500 TTTAGGTCCTACTAGCCCATCAAGCCTTTCTGACGACGAGTCTTGAACAATCTATCTGG 2559
Qy 2743 GAGTTTTTCAGAACTGTCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGCTTCCAGTTT 2802
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Qy 2803 GGAGAAAAGAGAGTCTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGCAATCTTGG 2862
Db 2620 GGAGAAAAGAGAGTCTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGCAATCTTGG 2679
Qy 2863 ACTTGAGCACCTAATGATATATTTGAGAGAGAAACAGATCACTTTTGGATGATTAGTTGA 2922
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Qy 3043 GAACACCTCTGGTAGTGGAAACAATTTCTTATAGATCTGTCTCTGATGATAAGAGTTTCA 3102
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Qy 3103 GTCTGTGGAGAAAGATGCAAGTACAGTTTCGAGAGCAGACAGATGGAGTCTGCGAG 3162
Db 2920 GTCTGTGGAGAAAGATGCAAGTACAGTTTCGAGAGCAGAGATGGAGTCTGCGAG 2979
Qy 3163 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAAGAACTATG 3222
Db 2980 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAAGAACTATG 3039
Qy 3223 GGAAAGATACACTCACCGGAGAAAAGTGTGTGAAGAAAACCAACCATGCCAATGA 3282
Db 3040 GGAAAGATACACTCACCGGAGAAAAGTGTGTGAAGAAAACCAACCATGCCAATGA 3099
Qy 3283 ACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTTATCCACAAGGCTTTGATGA 3342
Db 3100 ACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTTATCCACAAGGCTTTGATGA 3159
Qy 3343 AAGCATGCTGATAGTGTGATGTTTGGAGCTGGCAATTTATTTTGTGAAAACTCTTC 3402
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Qy 3403 CAAAAGCAATCAATATGTATATGGAATTTGGAGGAGTACTGGGTTCCAGTTCAAAAAGA 3462
Db 3220 CAAAAGCAATCAATATGTATATGGAATTTGGAGGAGTACTGGGTTCCAGTTCAAAAAGA 3279
Qy 3463 CAGATCTTGTATCAATTTGCCACAGGAGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3522
Db 3280 CAGATCTTGTATCAATTTGCCACAGGAGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3339
Qy 3523 TTTCTCTGAGTTTCAAGTGCATATGAAAATGGCACTTCTCTCCAGTCACTCACTCAGTCAC 3582
Db 3340 TTTCTCTGAGTTTCAAGTGCATATGAAAATGGCACTTCTCTCCAGTCACTCACTCAGTCAC 3399
Qy 3583 TGGTAGGCCAGTGTAAATGGCCTTAGCATTTAGCTGAAATATGTTATTTACAGAGAGAAACA 3642
Db 3400 TGGTAGGCCAGTGTAAATGGCCTTAGCATTTAGCTGAAATATGTTATTTACAGAGAGAAACA 3459
Qy 3643 GGCTTATCTGAGTATTTTAAATTTACTTACAGATTTAGGGCTGAAGGTATGGTCTGATGG 3702
Db 3460 GGCTTATCTGAGTATTTTAAATTTACTTACAGATTTAGGGCTGAAGGTATGGTCTGATGG 3519

Qy 3703 ATAAATAGTATTTTAAAGAACTAATTCCTCACTGAACCTAAATCATCAAGCAGCACTGG 3762
Db |||||
Qy 3520 ATAAATAGTATTTTAAAGAACTAATTCCTCACTGAACCTAAATCATCAAGCAGCACTGG 3579
Db |||||
Qy 3763 CCTCTACGTTTACTCCTTTGCTGAAAAAAA 3794
Db |||||
Qy 3580 CCTCTACGTTTACTCCTTTGCTGAAAAAAA 3611
Db |||||
RESULT 10
US-09-350-982C-4
; Sequence 4, Application US/09350982C
; Patent No. 6455290
; GENERAL INFORMATION:
; APPLICANT: Berthelsen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Isacchi, Antonella
; APPLICANT: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Rela
; TITLE OF INVENTION: Same
; TITLE OF INVENTION: Same
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primers
; NAME/KEY: CDS
; LOCATION: (1)..(3498)
; NAME/KEY: misc feature
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (1102)..(1102)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (2650)..(2650)
; OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-4

Query Match 86.7%; Score 3291.8; DB 3; Length 3498;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3290; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Qy 403 AGGTTTTGGGCGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAGTGTCCAAAGC 462
Db |||||
Qy 198 AGGTTTTGGGCGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAGTGTCCAAAGC 257
Db |||||
Qy 463 ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGCAATGCTCTTTTGGTCAATGCTGAAGT 522
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RESULT 11
US-09-972-115A-1
; Sequence 1, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
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; SEQ ID NO 1
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US-09-972-115A-1

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; Sequence 3, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Platyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972.115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
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; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
; LOCATION: (562)..(562)
; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
; LOCATION: (614)..(614)
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; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
; LOCATION: (619)..(619)
; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
; LOCATION: (632)..(632)
; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
; LOCATION: (637)..(637)
; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
; LOCATION: (680)..(680)
; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
; LOCATION: (682)..(682)
; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
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;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	
;	NAME/KEY: misc feature	
;	LOCATION: (1971)..(1971)	
;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	
;	NAME/KEY: misc feature	
;	LOCATION: (2000)..(2000)	
;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	
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;	NAME/KEY: misc feature	
;	LOCATION: (2180)..(2180)	
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;	NAME/KEY: misc feature	
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;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	
;	NAME/KEY: misc feature	
;	LOCATION: (2289)..(2289)	
;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	
;	NAME/KEY: misc feature	
;	LOCATION: (2316)..(2316)	
;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	
;	NAME/KEY: misc feature	
;	LOCATION: (2359)..(2674)	
;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	
;	NAME/KEY: misc feature	
;	LOCATION: (2977)..(2977)	
;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	
;	NAME/KEY: misc feature	
;	LOCATION: (2291)..(2291)	
;	OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put
;	OTHER INFORMATION: in to provide alignment.	

US-09-972-115A-3

Query Match	78.2%;	Score 2968.2;	DB 3;	Length 4297;
Best Local Similarity	88.3%;	Prod. No. 0;		
Matches 3020;	Conservative 7;	Mismatches 381;	Indels 12;	Gaps 2;
Qy	384	CCCTCTGGCTTTATCATTAAGTGTTCGGCGGAAGAGCTAGTTGAATATTTGCTTCGAA	443	
Db	476	CCCCGCTGCACTTCCCGCANGTTTTGGCGGGAAGACTTANTTAAATATTTGCTTCANA	535	
Qy	444	ATGGTGCAAGTGTCCAAGCACGTCGATGATGGGGGCTTATTCCTCTTCAATAATGCATGCT	503	
Db	536	ATGGTGCAATGTTCANACAGTGATNATGGGGGCTTATTCCTCTTCATNAATGCATGCT	595	
Qy	504	CTTTTGGTCATGCTGAAGTAGTCAATCTCTCTTTTGGCAGCATGGTGCAGACCCCAATGCTC	563	
Db	596	CTTTTGGTCMTGCTRAAANTATCNATCTCTCTTTTGCNACATNGTGCANAMCCCAATGCTC	655	
Qy	564	GAGATAATTGGAAATTATCTCCTCTCCATGAAAGCTGCAATTTAAAGGAAAGATTGATGTTT	623	
Db	656	GAGATAATTGGAAATTATCTCCTCNCNATGAAGCTGCAATTTAAAGGAAAGATTGANNTT	715	
Qy	624	GCATTGTGCTGTTACAGCATCGAGCTGAGCCCAACCATCCGAAATACAGATCGAAGGACAG	683	
Db	716	GCATTGTGCTGTTACAGCATCGAGCTGAGCCCAACCATCCGAAATACAGATCGAAGGACAG	775	
Qy	684	CATTGGATTTAGCAGATCCATCTGCGAAAGCAGTGCTTACTGGTGAATATGAAGAAAGATG	743	

776	Db	 CATTGGATTTAGCAGATTCCAATCTGCCAAAGCAGTCTTACTGGTGAATATAAGAAAGATG	835
744	Qy	 AACTCTTTAGAAAGTGCCAGGAGTGGCAATCAAGAAAAAATGATGGCTCTACTCACACCAT	803
836	Db	 AACTCTTTAGAAAGTGCCAGGAGTGGCAATGAGAAAAAATGATGGCTCTACTCACACCAT	895
804	Qy	 TAAATGTCAAATGCCACGCAAGTGATGGCAGAAAGTCAAATCCAAATACATTTTGGAGCAG	863
896	Db	 TAAATGTCAAATGCCACGCAAGTGATGGCAGAAAGTCAAATCCAAATACATTTTGGCAGCAG	955
864	Qy	 GATATAACAGGATAAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTA	923
956	Db	 GATATAACAGGATAAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTA	1015
924	Qy	 AAGATAAGCTGATCTGGTACCATTACAAATGCTCTTCTTATGGTCAATATCAAGTAA	983
1016	Db	 AAGATAAGCTGATCTGGTACCATTACAAATGCTCTTCTTATGGTCAATATCAAGTAA	1075
984	Qy	 CTGAACCTTTTGGTCAAGCATGGTGCCTGTGTAAATGCAATGGACTCTGTGGCAATTCAC	1043
1076	Db	 CTGAACCTTTTGGTCAAGCATGGTGCCTGTGTAAATGCAATGGACTCTGTGGCAATTCAC	1135
1044	Qy	 CTCTTCAATGAGCAGCTTCTTAAGAACAGGGTTGAAGTATGTTCTCTTCTCTTAAGTTATG	1103
1136	Db	 CTCTTCAATGAGCAGCTTCTTAAGAACAGGGTTGAAGTATGTTCTCTTCTCTTAAGTTATG	1195
1104	Qy	 GTGCAGACCCAAACACTGCTCAAATTTGTCCAAATAAAGTGCTATAGACTTGGCTCCACAC	1163
1196	Db	 GTGCAGACCCAAACACTGCTCAAATTTGTCCAAATAAAGTGCTATAGACTTGGCTCCACAC	1255
1164	Qy	 CACAGTTTAAAGAAAGATTAGCATATGAATTTTAAAGGCCACTCGTGTCTGCAAGCTGCAC	1223
1256	Db	 CACAGTTTAAAGAAAGATTAGCATATGAATTTTAAAGGCCACTCGTGTCTGCAAGCTGCAC	1315
1224	Qy	 GAGAGCTGATGTTTACTCGAATCAAAAAACAATCTCTCTCTGGAAAAATGGTGAATTTCAAG	1283
1316	Db	 GAGAGCTGATGTTTACTCGAATCAAAAAACAATCTCTCTCTGGAAAAATGGTGAATTTCAAG	1375
1284	Qy	 ATCTCTAAACACATGAACACAGCATTTGCTGTGCTGCAATCTCCATATCCCAAAAAGAA	1343
1376	Db	 ATCTCTAAACACATGAACACAGCATTTGCTGTGCTGCAATCTCCATATCCCAAAAAGAA	1435
1344	Qy	 AGCAATATGTGAATCTGTTCTAAGAAAAAGGAGCAAAATCAATGAAAAAGACTAAAGAAT	1403
1436	Db	 AGCAATATGTGAATCTGTTCTAAGAAAAAGGAGCAAAATCAATGAAAAAGACTAAAGAAT	1495
1404	Qy	 TCTTTGACTCTCTGCAAGTGGCATCTGAGAAAGCTCAATATGATGTTGTTGAAGTAGTGG	1463
1496	Db	 TCTTTGACTCTCTGCAAGTGGCATCTGAGAAAGCTCAATATGATGTTGTTGAAGTAGTGG	1555
1464	Qy	 TGAAACATGAAGCAAAAGGTTAAATGCTCTGCAATATCTTTGGTCAGACTTCTCTACACAGAG	1523
1556	Db	 TGAAACATGAAGCAAAAGGTTAAATGCTCTGCAATATCTTTGGTCAGACTTCTCTACACAGAG	1615
1524	Qy	 CTGCATATTTGGTGCATCTCAAAACCTGCGCCCTTACTCTGAGCTATGGGTGTGATCCTA	1583
1616	Db	 CTGCATATTTGGTGCATCTCAAAACCTGCGCCCTTACTCTGAGCTATGGGTGTGATCCTA	1675
1584	Qy	 ACATATATCCCTTCAGGGCTTTTACTGCTTTTACAGATGGGAAATGAAAAATGTACAGCAAC	1643
1676	Db	 ACATATATCCCTTCAGGGCTTTTACTGCTTTTACAGATGGGAAATGAAAAATGTACAGCAAC	1735
1644	Qy	 TCCTCCAAAGGGTATCTCAATTAAGTTAAATTCAGAGGAGACAGCAATTCCTGGAAGCTG	1703
1736	Db	 TCCTCCAAAGGGTATCTCAATTAAGTTAAATTCAGAGGAGACAGCAATTCCTGGAAGCTG	1795
1704	Qy	 CAAAGGCTGAGATGTCCAAACTGTAAAAAAAATGTGTACTGTTTCAGAGTGTCAACTGCA	1763
1796	Db	 CAAAGGCTGAGATGTCCAAACTGTAAAAAAAATGTGTACTGTTTCAGAGTGTCAACTGCA	1855
1764	Qy	 GAGACATTTGAAGGGCGTCACTCTACACCATTCAATTTTGCAGCTGGGTATAACAGAGTGT	1823

Db 1856 GAGACATTGAAGGGCGTCAGTCTACACACTTCAATTTTGCAGCTGGGTATTAACAGAGTGT 1915
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Db 1916 CCGTGGTGAATATCTGCTACAGCATGAGAGCTGATGTGCATGCTTAAGATAAAGAGNGGCC 1975
Qy 1884 TTGTACCTTTGCACATGCAATGCTTTCTATGACATATTAAGAGTTGCAGAACTTCTTTGTTA 1943
Db 1976 TTGTACCTTTGCACATGCAATGCTTTCTATGACATATTAAGAGTTGCAGAACTTCTTTGTTA 2035
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Db 2036 AACATGGAGCAGTGTAAATGCTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAG 2095
Qy 2004 CAGCAAAAGGAAATATGAATTTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCA 2063
Db 2096 CAGCAAAAGGAAATATGAATTTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCA 2155
Qy 2064 AAAAAACAGGATGGAAATATCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTC 2123
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Qy 2424 CCACGGACAAATGGCTTTTCACTTTGCGAGAGAGCCCAAGGAGCAACAGC 2483
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Qy 2544 CACCTTTAGATTTAGTTTTCAGCGGATGATGTACAGCGCTCTTTCTGACAGCAGCCATGCC 2603
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Qy 2604 CATCTGCTCTGCCCTCTTTGTTAAGCCCTCAAGTGTCTCAATGGTGTGAGAGCCAGGAG 2663
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RESULT 13
US-09-196-387-1
; Sequence 1, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4134 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-196-387-1

Query Match 47.8%; Score 1813.4; DB 3; Length 4134;
Best Local Similarity 72.3%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 891; Indels 27; Gaps 2;

QY 383 TCCCTCTGCTTTATCATTAAGTTTGGCGGAAAGACGTAGTTGAATATTGCTTCAG 442
DB 657 TCTCCCTGCACTTCGCTGCAGGTTTGGAGGAAGGATGTTGTAGAACACATTACTACAG 716
QY 443 AATGGTGAAGTGTCCAGCAGTGTATGATGGGGCTTTATTCCTTTCATATATCATGC 502
DB 717 ATGGGTGCTAATGTGCAGCTGTGATGAGGTCTCATCCCGCTTCATAATGCCGTG 776
QY 503 TCTTTTGGTCACTGCTGAAGTAGTCAATCTCTTTGGCAGATGGTGCAGACCCCAATGCT 562
DB 777 TCTTTTGGCCATGCTGAGGTTGTGAGTCTGTTATTTGTGCAAGGAGCTGATCCAAATGCC 836
QY 563 CGAGATAATTGGAATTATCTCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATGTT 622
DB 837 AGGGATAACTGGAACATATACACTCTGCATGAAGCTGCTATTAAAGGGAAGATCGATGTG 896
QY 623 TGCATTGCTCTGTACAGCATGGAGTGGCCAAACCCGGAATACAGATGGAGGACA 682
DB 897 TGCATTGCTCTGTGAGCAGCGAGCTGACCCAAACATTCGGAACACTGATGGGAATCA 956
QY 683 GCATTGGATTAGCAGATCCATCTGCAAGCAGTGTCTTACCTGGTGAATATAAGAAAGAT 742
DB 957 GCCTGGACCTGGCAGATCTTTCAGCAAAAGCTGCTTACAGGTGATACAGAAAGAC 1016
QY 743 GAACCTTTAGAAAGTGCAGGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCAACA 802
DB 1017 GAACCTCTAGAAGCTGTAGGAGTGTGTAATGAAGAAAAAATAATGGCTTTTACTGACTCT 1076
QY 803 TTAATGTCAATGCCACCAAGTGTGACAGAAAGTCAATCCATTACATTGGCAGCA 862
DB 1077 CTAATATGTAATTTGCCATGCAAGTGTATGGCGAAAGTGCAGCTCTTTTACATCTAGCAG 1136
QY 863 GGATATAACAGAGTAAAGATTGTACAGCTGTTTACTGCAACATGGAGCTGATGTCATGCT 922

1137 GGCTACAAACAGAGTTTGAATAGTTTCAGCTTCTTCAGCATGGTGTGATGTTTCATGCA 1196
923 AAAGATAAAGGTGATCTGGTACCATTACACATGCTGTTCTTATGTTGCTCATTTATGAAGTA 982
1197 AAAGACAAGGTGGACTTGTGCTCTTCATATATGATGTTTCATATGGAATATGATGAAGTC 1256
983 ACTGAACCTTTTGGTCAAGCATGGTCCCTGTGTAAATGCAATGCAATGTTGGCAATTCACCT 1042
1257 ACAGAACTGCTACTAAAGCATGGAGCTTGTGTATATGCAATGATGCTCTGGCAGATTACT 1316
1043 CCTCTTCATGAGGCGACTTCTAAGAACAGGGTGAAGTATGTTCTTCTCTTCTTAAAGTTAT 1102
1317 CCACCTGACGAGGCTGCTTCCAAAGAACCGTGTAGAAGTCTGCTCTTGTGTTACTTAGCCAT 1376
1103 GGTGAGACCCCAACACTGCTCAATTTGTACAAATAAAGTGTATAGACTTGGCTGCCACA 1162
1377 GGCCTGATCTTACGTTAGTCACTGCAATGGCAAAAGTGTGTGGATATGCTTCCAACT 1436
1163 CCACAGTTTAAAGAAAGATTAGCATATGAATTTAAAGGCCACTCGTTGTGTCGAAGTCGA 1222
1437 CCGAGCTTTAGGAGAGATTGACTTATGAATTTAAAGGTCTCTTACTACAGCAGCC 1496
1223 CGAGAACTGATGTTTACTCGAATCAAAAAACATCTCTCTCGAAAAATGGTGAATTTCAAG 1282
1497 AGAGAAGCAGACTTAGCTTAAAGTTTAAAAAACAACCTCGCTCTGGAATCATTAATTTCAA 1556
1283 CATCTCAACACATGAACAGCATGATGTTGCTGCTGTCATCTCCATATCCCAAAAGA 1342
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1343 AAGCAATATGTGAATCTGTGTAAGAAAAAGAGCAAAACATCAATGAAAGAAATCAAGAA 1402
1617 AAACAAGTGACAGAAATTTGTTACTTAGAAAAGAGCAATGTTTAATGAAAAAATAAAGAT 1676
1403 TTTCTTGACTCTCTGACGTGGCATCTGAGAAAGCTCATTAATGATGTTGTTGAAGTAGTG 1462
1677 TTTATGATCTCCCTGCAATGTTGACGCCGAAAGAGCCCAATGATGTCATGGAAGTTCTG 1736
1463 GTGAAACATGAAGCAAGGTTAATGCTCTGGAATATCTTGTGTCAGACTTCTCTACACAGA 1522
1737 CATAGCATGGCGCAAGATGAATGCACTGGACACCTTTGGTGCAGACTGCTTTGTCATAGA 1796
1523 GCTGCATATTGTGGTCACTTCAAAACCTGCGCTCTCTGAGCTATGGGTGATGCTCT 1582
1797 GCGCCCTTAGCAGGCCACTGCGAGACCTTGCCTCTCTGCTGAGTTACGGCTCTGACCCC 1856
1583 AACATTATATCCCTTCAGGGCTTTTACTGCTTTTACAGATGGGAAATGAAATATGACAGCA 1642
1857 TCCATCATCTCTTACAAAGGCTTACAGCAGCAGATGGGCAATGAAAGCAGTGCAGCAG 1916
1643 CTCTCCAAAGAGGTATCTCATTTAGGTAAATTCAGAGGAGCAGACAAATTCGTGGAAGCT 1702
1917 ATTCTGAGTGAGAGTACACCTATACGTACTTCTGATGTTGATATTCGACTCTTTAGAGGCA 1976
1703 GCAGAGGCTGAGAGTGTGAAACCTGTAAGAACTGTGCTACTGTTTCAGAGTGTCAACTGSC 1762
1977 TCTAAGCTGGAGACTTGGAAACTGTGAACAACTTTGAGCTCTCAAAATGTAATGTG 2036
1763 AGAGACATTGAAGGGCGTCAGTCTACACCACTTCAATTTTTCAGAGTGGGTATACAGAGTG 1822
2037 AGAGACTTTAGAGGGCGCGCATTTCCAGCCCTTACACTTTCGAGCAGAGGCTTACAAACCGGTG 2096
1823 TCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTCATGCTGCTAAAGATAAGAGGC 1882
2097 TCTGTGTGAGAGTACTCTGTACACCAAGTGCAGTGTCCATGCGCAAAAGCAAGGGTGGC 2156
1883 CTGTGACTTTGCACAATGTCATGTTCTTATGACATTAATGAGTTGCAAGACTCTCTGTT 1942
2157 TTGTGCCCCCTTCAATAATGCTGTTTCATATGACACTATGAGTGGCTGAGCTTTTAGTA 2216
1943 AAACATGAGCAGTAGTTAATGTTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCA 2002

Db 2217 AGGCATGGGCTTCTGTCAATGTGGCGCACTTATGGAAATTTACCCCTCTCCATGAAGCA 2276
Qy 2003 GCACAAAGGAAATATGAAATTTGCAAACTTCTGTCCAGCATGTGGCAGACCCCTACC 2062
Db 2277 GCAGCTAAGGAAAGTATGAAATCTGCAAGCTCCTTTTAAAAACATGGAGCAGATCCAAC 2336
Qy 2063 AAAAAACAGGATGGAATTAACCTCTTGGATCTTGTAAAGATGGAGATACAGATATT 2122
Db 2337 AAAAAAGAACAGAGATGGAATATACACCTTTGGATTTGGTAAAGGAGGACACAGATATT 2396
Qy 2123 CAAGATCTGTTAGGGAGATGAGCTTGTAGATGCTGCAAGAGAGGGTGTGTTAGCC 2182
Db 2397 CAGGACTTACTGAAGGGGATGCTGCTTGTGTGATGCTGCAAGAGAGGGTGTGCTGGCA 2456
Qy 2183 AGAGTGAAGAAAGTTGTCTTCTCTGATTAATGTAATTTGCCCGCATGCCAAGGCGAGCAT 2242
Db 2457 AGAGTGCAGAAAGCTCTGTACCCAGAGAAATATCAACTGCAGAGACACCCAGGGCAGAAAT 2516
Qy 2243 TCAACACCTTTACATTTAGCAGCTGGTTATATAATTTAGAAAGTTGCAGATATTGTTA 2302
Db 2517 TCAACCCCTCTGCACTGGCAGCAGGCTATATAATTAACCTGGAAGTAGCTGAATATCTTCTA 2576
Qy 2303 CAACAGGAGCTGATGTAATGCCCAAGACAAAGAGGAGCTTATTTCTTTACATAATGCA 2362
Db 2577 GAGCATGAGCTGATGTAATGCCCAAGCAGCAAGGGTGTAAATTCCTTCTCATATGCG 2636
Qy 2363 GCATCTTACGGGCATGTAGATGTAGCAGCTCTACTAATAAAGTATAATGCAATGTGTCAT 2422
Db 2637 GCATCTTATGGCATGTTGACATAGCGGCTTTATGATAAAATACACACGTGTGTAAT 2696
Qy 2423 GCCAGGCAAAATGGGCTTTACACCTTTGCAGAGCAGCCCAAGGGAGCAGACAG 2482
Db 2697 GCAACAGATAAGTGGGCGCTTACTCCCCCTCATGAAGCAGCCCAAGAAAGGAGCGCAG 2756
Qy 2483 CTTTGTGCTTTGTGTAGCCCATGGAGCTGACCGACTCTTAAATAATCAGGAAGGACAA 2542
Db 2757 CTGTGGCCCTCTCTAGCGGATGGTGCAAGCCCCACCATGAAGACCAAGAGGCGCAG 2816
Qy 2543 ACACCTTTAGATTTAGCGGATGATGTAGCGCTCTTCTGACAGCAGCCATGCC 2602
Db 2817 ACGCTCTGGATCTGGCAACAGCTGACGATATCAGAGCTTTGCTGATAGATGCCATGCC 2876
Qy 2603 CCATCTGCTGCGCTCTGTGTACAGGCTCAAGTGCTCAATGGTGTGAGAGGCCAGGA 2662
Db 2877 CCAGAGGCTTACCTACCTGTTTTAAACCTCAGG-----CTACT 2915
Qy 2663 GCCACTGCAGATGCTCTCTCTTCAAGTCCATCAAGCTTCTGACAGCCAGC 2722
Db 2916 GTAGTGAGTGCTCTCTGATCTCACAGCATCCACCCCTCTCGCTCTCGGCTGCCAGC 2975
Qy 2723 AGTCTTGAACAATTATCTGGGAGTTTTTCAAGCTGTCTTCAGTAGTTAGTTCAAGTGA 2782
Db 2976 AGCATAGACAACCTCACTGGCCCTTTAGCAGAGTTGGCGGTAGGAGGAGCCTCCAATGCA 3035
Qy 2783 ACAGAGGTGCTCCAGTTTGGAGNAAG-----GAGTTCCAGGAGTAGATTTAGC 2836
Db 3036 GGGATGCGCGCGGGAAACAGAAAGGAAGAGAGAGTTGCTGGTCTTGAATGAAT 3095
Qy 2837 ATAACCTCAATTCGTAAGGAATCTTGGACTGAGCACCTTAATGGATATATTTGAGAGAGAA 2896
Db 3096 ATCAGCCAAATTTCAAAAAGCCTTGGCCCTTGAACCTTCGGGATATCTTTGAACAGAA 3155
Qy 2897 CAGATCACTTTGGATGTATTAGTTAGATGGGCAACAGGAGCTGAAGAGATGGAAATC 2956
Db 3156 CAGATTACACTAGATGTGTGGCTGATATGGGTATGAAGAGTTGAAAGAAATAGGCATC 3215
Qy 2957 AATGCTTATGACATAGGACCAAACTAATTAAGAGTCCGAGAGACTTATCTCCGGCAA 3016
Db 3216 AATGCATATGGGACCGGCCCAAAATTAATCAAGAGGATAGAAAGACTTTAGGTGGACAA 3275
Qy 3017 CAAGGCTTAAACCCATATTAATCTTGAACACCTCTGGTAGTGGAACTTTCTATAGAT 3076
Db 3276 CAAGGCACCAATCCTTATTTGACTTTTCACTGTGTATATCAGGGAACGATTTGCTGAT 3335

Qy 3077 CTGTCTCTGATGATGAATAAGAGTTTCACTCTGTGGAGGAAGAGATGCAAGTACAGTTTGA 3136
Db 3336 CTTGCTCAGAAGATAAAGAAATATCACTCACTGGGAAGAGAGATGCAAGTACTATTTCGA 3395
Qy 3137 GAGCACAGAGATGAGGTCTATGCAAGTGGAAATCTTCAACAGATACAAATATTCTCAAGATT 3196
Db 3396 GAACACAGAGATGGTGTGTAATCTGGCGGATCTTCAACAGATACAAATGTCTTCGAATT 3455
Qy 3197 CAGAAGGTTTGTAAACAAGAACTATGGGAAGATACACTCACCGGAGAAAAAGAGTTTCT 3256
Db 3456 CAAAAAGTTGTCAACAAGAAAGTTTGAGGAGCGGTTCTGCCACCCAGACAGAAAGTGTCT 3515
Qy 3257 GAAGAAAAACCAACCAATGCCAATGAACGAATGCTATTTTCATGGGTCTCCTTTTGTGAT 3316
Db 3516 GAGGAGAAATCACACCAATCAATGAGCGCATGTTGTTTTCATGGTTCTCCTTTTCAATTAAT 3575
Qy 3317 GCATTTATCCACAAGGCTTTGATGAAAGGCATGCGTACATAGGTGTATGTTTGGAGCT 3376
Db 3576 GCCATTTATTCATAAAGGTTTGTAGCGCATGCAATACATAGGAGAAATGTTTGGGCCC 3635
Qy 3377 GGCAATTTATTTGCTGAAAACTCTTCCAAAAGCAATCAATATGATATGGAATTTGGAGGA 3436
Db 3636 GGGATTTATTTGCTGAAAACTCTCTCAAAAAGCAACCAATATGTTTATGGAATTTGGAGGA 3695
Qy 3437 GGTACTGGGTGTCAGTTTCAAAAGACAGATCTTGTTCATTTGCCACAGGAGCTGCTC 3496
Db 3696 GGAACAGGCTGCCCTACACACAGGACAGGTCATGCTATATATGTACAGACAAATGCTC 3755
Qy 3497 TTTTGGCGGTAACTTTGGGAAGTCTTTCTGAGTTCAGTGCATGCAATGAAAAATGECAT 3556
Db 3756 TTCTGTAGTGAGCCCTTGGGAATCTTCTGAGTTTAGCATTGAAAAATGGCCAC 3815
Qy 3557 TCTCTCCAGTCACTCACTGTCAGTCACTGGTAGGCCAGTGTAAATGGCTTAGCATTTAGCT 3616
Db 3816 GCGCTCCAGGGCACCACTCACTGTTGTTAGACCGAGCGTCAATGGCTGGCATATGCT 3875
Qy 3617 GAATATGTTTACAGAGGAGAACAGCTTATCTGAGTATTTAATTTACTTACCAGATT 3676
Db 3876 GAATATGTCATCTACAGAGGAGAACAGGCAATACCCAGATATCTTATCATTACAGATC 3935
Qy 3677 ATGAGGCTCTGAAG 3689
Db 3936 ATGAAGCCAGAG 3948

RESULT 14

US-09-841-835-1
; Sequence 1, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841.835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

Db	1377	GGCGCTGATCTCTACGTTAGTCAACTGCCATGGCAAAAGTGTGTGATATGGCTCCAAC	1436
Qy	1163	CCACAGTTAAAAAGAAAGATTAGCATATGAATTTAAAGGGCCACTCGTTGTCTGCAAGCTGCA	1222
Db	1437	CCGGAGCTTAGGGAGAGATTGACTTATGAATTTAAAGTCACTTCTTTACTTACAAGCAGCC	1496
Qy	1223	CGAAGAGCTGATGTTACTCGAATCAAAAAACATCTCTCTCTGGAATGGTGAATTTCAAG	1282
Db	1497	AGAGAAGCAGACTTAGCTAAAGTTAAAAAAAACACTCGCTCTGGAATCATTAATTTCAAA	1556
Qy	1283	CATCTCTMAACACATGAACAGCATTTGCATTTGCTGTGTCATCTCCATATCCCAAAAGA	1342
Db	1557	CAACCGAGTCTCATGAACAGACACTGCACTGTGCTGTGCGCTCTCTCGCATCCCAACGT	1616
Qy	1343	AAGCAAAATATGTGAACCTGTTGCTTAAGAAAAAGAGCAAAACATCAATAAAAAGACTAAAGAA	1402
Db	1617	AAACAAGTGACAAATTTGTTACTTTAGAAAAGGAGCAATCTTAATGAAAAAATAAAGAT	1676
Qy	1403	TTCTTGACTCTCTGCACTGGGCATCTGAAGAAAGCTCATATAATGATGTTGTGAAGTAGTG	1462
Db	1677	TTCATGACTCCCCTGCATGTTGCAGCCGAAGAGCCCAATAATGATGTCATGGAAGTTCTG	1736
Qy	1463	GTGAACATGAACAAAGGTTAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGA	1522
Db	1737	CATAAGCATGGGCCCAAGATGAATGCACCTGGACACCCTTGGTCAGACTGCTTTGCAATAGA	1796
Qy	1523	GCTGCATATTGTGGTCACTCTACAAACTCGCGCTACTCTCTGAGCTATGGGTGTGATCCT	1582
Db	1797	GCGCCCTAGCAGCCACCTGCAGACTCGCGCTCTCTGCTGAGTTACGGCTCTGACCC	1856
Qy	1583	AACATTATATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAA	1642
Db	1857	TCCATCATCTCTTTACAAGCTTCACAGCAGCACAGATGGGCAATGAAGCAGTGCAGCAG	1916
Qy	1643	CTCCTCCAAGAGGGTATCTCATTTAGTAAATTCAGAGGCAGACAGCAATTTGCTGGAAGCT	1702
Db	1917	ATTCTGAGTGAGAGTACACCTATACGTACTCTCTGATGTTGATTTATCGACTCTTTAGAGCA	1976
Qy	1703	GCAAGGCTGGAGATGTCGAAACTGTFAAAAAAAGCTGTACTGTTTCAGAGTGTCAACTGC	1762
Db	1977	TCTAAAGCTGGAGACTTGGAACTGTGAAGCAACTTTGCAGCTCTCAAAATGTGAATTTGT	2036
Qy	1763	AGAGACATTTGAAGGGCGTCAGTCTACACCACTTCATTTTGCAGCTGGGTATACAGAGTG	1822
Db	2037	AGAGACTTAGAGGCGCGCAATCCACGCCCTTACACTTCGACAGGGCTACAAACCGCTG	2096
Qy	1823	TCCGTGGTGGAAATATCTGCTACAGCATGAGCTGATGTGCAATGCTTAAAGATAAGAGGC	1882
Db	2097	TCTGTTGTAGTACCTGCTACACCAAGGTGCGATGTCCATGTCCTCAAGAACAAAGGGTGGC	2156
Qy	1883	CTTGTAACCTTGCACAAATGCATGCTCTTATGGACATTAATGAAGTTCAGAACTTCTTGTT	1942
Db	2157	TTGGTCCCCCTTCATAATGCCTGTTCATATGACACTATGAGTGGCTGAGCTTTTAGTA	2216
Qy	1943	AAACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACTTTTACATGAAGCA	2002
Db	2217	AGGCATGGGGCTTCTGTCAATGTGGCGGACTTATGGAAATTTACCCCTCTCCATGAAGCA	2276
Qy	2003	GCAGCAAAAAGGAAAAATATGAATTTTGCAAACTTCTGCTCCAGCATGGTGAGACCCCTACC	2062
Db	2277	GCAGCTTAAAGGAAGATATGAATATCTGCAAGCTCCTTTTAAAAACATGGAGCAGATCCAACT	2336
Qy	2063	AAAAAAAACAGGATGGAATATCTCTTTTGGATCTGTTTAAAGTGGAGATACAGATATT	2122
Db	2337	AAAAAGAACAGAGATGGAATATACCTTTTGGATTTTGGTAAAGGAAGGAGACACAGATATT	2396
Qy	2123	CAAGATCTGTTAGGGGAGATGCAAGCTTTTGCTAGATGCTGCCAAGAAAGGGTGTGTTAGCC	2182
Db	2397	CAGEACTTACTGNAAGGGATGCTGCTTTTGTGGATGCTGCCAAGAAAGGGCTGCCTGGCA	2456
Qy	2183	AGAGTGAAGAAGTTGCTTCTCTCTGATAATGTAAATTTGCCGCGATACCCAAGGCAGACAT	2242

Db 2457 AGAGTGAGAGGCTCTGTATCCCGAGAGAAATATCACTGCGAGAGACACCCAGGGGCGAGAAAT 2516
Qy 2243 TCACACCTTTTACATTTAGCAGCTGGTTATAATAATTTAGAAAGTGCAGAGTATTTGTTA 2302
Db 2517 TCACACCTCTGACCTGGCAGCAGGCTATAATAAACCTTGAAGTAGCTGAATATCTTCTA 2576
Qy 2303 CAACACGAGCTGATGTGAATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCA 2362
Db 2577 GAGCATGGAGCTGATGTAAATGCCCGAGGACAAAGGGTGTAAATTCCTCTTCAATAATGCG 2636
Qy 2363 GCATCTTACGGGATGTAGATGTAGAGCTCTACTATAAAGATATAATGATGTGTCAT 2422
Db 2637 GCATCTTATGGGCAATGTGACATAGCGCTTTATGTATTAATAACAACAGCTGTGTAAAT 2696
Qy 2423 GCCACGACAAATGGGCTTTTACACCTTTGACGAAGCAGCCCAAAAGGAGGACGAACACAG 2482
Db 2697 GCAACAGATAGTGGGCGTTTACTCCCTCCATGAAGCAGCCACAGAAAGGAGGAGCGAG 2756
Qy 2483 CTTTGTGCTTTGCTAGCCCATGGAGCTGACCGGACTCTTAAATAATCAGGAAGGACAA 2542
Db 2757 CTGTGCGCTCTCTCTAGCGCATGCTGCAAGCCCAACCATGAAAGAACCCAGGAAGGCCAG 2816
Qy 2543 ACACCTTTAGATTTAGTTTCAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCC 2602
Db 2817 ACGCTCTGGATCTGGCAACAGCTGACGATATCAGAGCTTTGCTGATAGATGCCATGCC 2876
Qy 2603 CCATCTGCTCTGCCCTCTTTGTATCAAGCCTCAAGTGTCTCAATGCTGTGAGAAAGCCACGGA 2662
Db 2877 CCAGAGGCTTACCTACTCTGTTTAAACCTCAGG-----CTACT 2915
Qy 2663 GCCACTGAGATGCTCTCTCTTCAAGTCCATCTAGCCCATCAAGCCCTTTCTGACGAGC 2722
Db 2916 GTAGTGTGCTCTCTCTGATCTCACAGCATCCACCCCTCCTGCCCTCGGCTGCCAGC 2975
Qy 2723 AGTCTTGACAACTTATCTGGGAGTTTTTCAGAACTGCTCTTCAAGTAGTTAGTTCAAGTGA 2782
Db 2976 AGCATAGACAACTTCACTGGGCCCTTTAGCAGATTTGGCCGTAGGAGGAGCCTCCTAATGCA 3035
Qy 2783 ACAGAGGCTGCTCCAGTTTGGAGAAAG-----GAGGTTCCAGGAGTAGATTTTAGC 2836
Db 3036 GGGGATGGCGCGCGGGAACAGAAAGGAGGAGGAGTGTGCTGTTCATCAAT 3095
Qy 2837 ATAACTCAATTCGTAAGAACTTTGGACTTGGACACCTAATGGATATATTGAGAGAGAA 2896
Db 3096 ATCAGCCAAATTTCTAAAGAGCCTTTGGCTTTGAACACCTTCGGGATATCTTTGAAACAGAA 3155
Qy 2897 CAGATCACTTTGGATGTATTAGTTGAGATGGGCAAGGAGCTGAAGGAGATTGGAATC 2956
Db 3156 CAGATTACATAGATGTGTGGCTGATATGGGTCTATGAGTTGAAAGAAATAGGCATC 3215
Qy 2957 AATGCTTATGACATAGGCACAAACTAATTAAGGAGTTCGAGAGACTTATCTCCGACAA 3016
Db 3216 AATGCATATGGCACCGCCACAAATTAATCAAGGAGTAGAAGACTCTTAGTGGACAA 3275
Qy 3017 CAAGGCTTAACCCATATTTAACTTTGAA CACCTCTGGTAGTGGAACAA TTTCTATAGAT 3076
Db 3276 CAAGGCCCAATCCTTATTTGACTTTTCACTGTGTTAATCAGGGAAAGATTTTCTGGAT 3335
Qy 3077 CTGTCTCTGATGATAAGAGTTTCAGTCTGTGAGGAGGAGATGCAAGTACAGTTTCA 3136
Db 3336 CTTGCTCCAGAAAGATAAGAAATATCAGTCACTGGAAGAGAGATGCAAGTACTATTTCGA 3395
Qy 3137 GAGCACAGAGATGAGGCTCATGCAAGTGGAACTTTCAACAGATACAATTTCTCAAGATT 3196
Db 3396 GAAACACAGAGATGGTGGTAAATGCTGGCGCATCTTCAACAGATACAATGTCTATTCGAAT 3455
Qy 3197 CAGAAAGTTTGAACAGAAACTATGGAAAGATACACTCAACCGGAGAAAGAGTTTCT 3256
Db 3456 CAAAAGTTGTCAACAGAAAGTTGAGGAGCGGTTCTGCCACCGACAGAAAGAGTTGCT 3515
Qy 3257 GAAGAAACCAACCACTGCAATGAAAGATGCTATTTTCAATGGTCTCTCTTTTGTGAAT 3316
Db 3516 GAGGAGAAATCAACCACTCAATGAGCGCATGTGTTTCAATGGTTCTCTTTTCAATTAAT 3575

Qy 3317 GCAATATTCACAAAGCCTTTGATGAAAGCATGCGTACATAGTGTGTATGTTGGAGCT 3376
Db 3576 GCCATTTATTCATAAAGGTTTGTAGCGCAGCATGCATACATAGGAGGAATGTTTGGGGCC 3635
Qy 3377 GGCATTTATTTCTGTAAGAACTCTTCCAAAGCAATCAATATATGTATGGAATTTGGAGGA 3436
Db 3636 GGGATTTATTTGCTGAAAACTCTCTCAAAGCAACCAATATGTTTATGGAATTTGGAGGA 3695
Qy 3437 GGTACTGGGTGTCCAGTTTCAAAAGACAGATCTTTGTATCACTTTGCCACAGCAGCTGCTC 3496
Db 3696 GGAACAGGCTGCCCTACACACAAAGGACAGGTCATGCTATATATGTACAGACAAATGCTC 3755
Qy 3497 TTTTCCGGGTAACTTTGGGAAAGTCTTTCTCGAGTTTCAGTGCATGAAATGGCACAT 3556
Db 3756 TTCTGTAGATGACCTTTGGGAAATCTTTCTGAGTTTAGCACCAATGAAATGGCCAC 3815
Qy 3557 TCTCTCCAGGTATCATCTCAGTCACCTAGTGGTGGCCAGTGTAAATGGCTAGCATTTAGCT 3616
Db 3816 GCGCTCCAGGACCACTCAGTCATTTGGTAGACCGAGCGTCAATGGCTGGCATATGCT 3875
Qy 3617 GAATATGTTTATTTACAGAGGAGAACAGGCTTTATCTCAGTATTTTAAATTTACTTACCAGATT 3676
Db 3876 GAATATGTCATCTACAGAGGAGAACAGGCATACCCAGATATCTTATCATCTTACCAGATC 3935
Qy 3677 ATGAGGCTGAAG 3689
Db 3936 ATGAAGCCAGAAG 3948

RESULT 15

US-09-972-115A-7
; Sequence 7, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972.115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-115A-7

Query Match 47.8%; Score 1813.4; DB 3; Length 4134;
Best Local Similarity 72.3%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 891; Indels 27; Gaps 2;

Qy 383 TCCCTCTGGCTTTATCATTTAAGGTTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAG 442
Db 657 TCTCCCTCGACTTCGCTGCAGGTTTTTGGAAAGGAGATGTTGTAGAACACTTACTACAG 716
Qy 443 AATGGTCAAGTGTCCAAAGCACGTGATGATGGGGCCCTTATTCCTCTTCAATATGCAATGC 502
Db 717 ATGGGTCTAATGTCCACGCTCGTGTGATGAGGAGTCTCATCCGCTTCAATAATGCTGT 776
Qy 503 TCTTTTGGTCAATGCTGAAGTAGTCAATCTCCTTTTGGACATGTTGCGAGACCCCAATGCT 562
Db 777 TCTTTTGGCCATGCTGAGGTTGTAGTCTGTATTGTGCCAAGGAGCTGTATCCCAATGCC 836
Qy 563 CGAGATAATTTGGAATTTATCTCTCTCATGAGCTGCAATTTAAAGGAAAGATGATGTT 622

837	DB	AGG	ATTA	CTG	GA	AACT	ATAT	CAC	CTCT	GC	ATG	AA	CG	CTG	CTATTAA	AGG	GA	AG	ATCG	ATG	GTG	896															
623	QY	TG	CA	TTG	TG	CTG	TTT	CA	G	CA	TG	GA	CTG	AG	CTG	AG	CA	ACC	ATCC	GA	AA	TAC	AG	ATCG	AA	G	CA	CA	682								
897	DB	TG	CA	TTG	TG	CTG	TTT	CA	G	CA	TG	GA	CTG	AG	CTG	AG	CA	ACC	ATCC	GA	AA	TAC	AG	ATCG	AA	G	CA	CA	956								
683	QY	G	CA	TTG	GA	TTT	A	G	CA	G	AT	CC	CA	T	GC	CA	A	A	G	C	G	T	CTT	A	C	T	G	T	GA	AA	742						
957	DB	G	CC	CT	G	G	CA	CTG	G	CA	G	AT	CC	CA	T	GC	CA	A	A	G	C	T	CTT	A	C	T	G	T	GA	AA	1016						
743	QY	G	AA	CT	CTT	A	G	AA	CTG	G	CA	G	AT	CC	CA	T	GC	CA	A	A	G	C	T	CTT	A	C	T	G	T	GA	AA	802					
1017	DB	G	AA	CT	CTT	A	G	AA	CTG	G	CA	G	AT	CC	CA	T	GC	CA	A	A	G	C	T	CTT	A	C	T	G	T	GA	AA	1076					
803	QY	T	T	AA	AT	G	T	C	A	CTG	C	G	CA	G	AT	CC	CA	T	GC	CA	A	A	G	C	T	CTT	A	C	T	G	T	GA	AA	862			
1077	DB	C	T	AA	AT	G	T	C	A	CTG	C	G	CA	G	AT	CC	CA	T	GC	CA	A	A	G	C	T	CTT	A	C	T	G	T	GA	AA	1136			
863	QY	G	G	A	T	A	A	C	A	G	A	T	T	G	T	A	C	A	A	G	T	G	T	T	A	C	A	A	G	T	G	T	GA	AA	922		
1137	DB	G	G	C	T	A	C	A	C	A	G	A	T	T	G	T	A	C	A	A	G	T	G	T	T	A	C	A	A	G	T	G	T	GA	AA	1196	
923	QY	A	A	G	A	T	A	A	G	T	G	A	T	T	G	T	A	C	A	A	G	T	G	T	T	A	C	A	A	G	T	G	T	GA	AA	982	
1197	DB	A	A	G	A	T	A	A	G	T	G	A	T	T	G	T	A	C	A	A	G	T	G	T	T	A	C	A	A	G	T	G	T	GA	AA	1256	
983	QY	A	C	T	G	A	A	CTTTT	T	G	G	T	C	A	A	G	A	T	T	G	C	T	G	T	T	A	A	G	T	G	A	T	T	GA	AA	1042	
1257	DB	A	C	A	G	A	CT	G	T	A	C	T	A	A	G	A	T	T	G	C	T	G	T	T	A	A	G	T	G	A	T	T	GA	AA	1316		
1043	QY	C	T	CT	T	C	A	T	A	G	G	C	A	G	T	T	C	A	A	G	G	T	T	G	A	G	T	A	G	T	A	G	T	GA	AA	1102	
1317	DB	C	C	A	CT	G	C	A	C	G	A	G	G	T	T	C	A	A	G	G	T	T	G	A	G	T	A	G	T	A	G	T	GA	AA	1376		
1103	QY	G	G	T	G	C	A	G	C	C	A	C	A	G	T	T	G	C	A	A	T	T	G	C	A	A	T	T	G	C	A	A	T	GA	AA	1162	
1377	DB	G	G	C	G	CT	G	A	T	C	T	A	G	T	C	A	A	T	T	G	C	A	A	T	T	G	C	A	A	T	T	GA	AA	1436			
1163	QY	C	C	A	G	TTT	A	A	A	A	G	A	A	G	A	T	T	A	A	G	G	C	A	C	T	G	T	T	A	A	G	G	A	T	GA	AA	1222
1437	DB	C	G	G	A	G	CTT	A	G	G	A	G	A	T	T	G	A	A	G	G	A	T	T	G	A	A	G	A	T	T	GA	AA	1496				

QY	1703	GCAAAGCGCTGGAGATGTGAAAACTGTTHAAAATAAACTGTGTACTGTTCAGAGTGTCAACTGC	1762
DB	1977	TCTAAAGCTCTGGAGACTTTGGAAACCTGTGAAGACAACCTTTTGCAAGCTCTCAAAATGTGAATTGT	2036
QY	1763	AGACACATTGAAGGGCGTAGTGTACACACACTTTCATTTTCCAGCTGGTATTAACAGAGTG	1822
DB	2037	AGAGCTTTAGAGGGCGGGCATTTCCAGCCCTTACATTTTCGACGAGGCTTCAACC GGCTG	2096
QY	1823	TCCGTGTGGAAATATCTGTCTACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGGAGGC	1882
DB	2097	TCTGTGTAGAGTACCTGCTACACCACGGTCCGATGTCCATGCCAAGAACAAGGGTGGC	2156
QY	1883	CTTGTA CTTTTGCAAAATGANTGTTCTTATGGACATTAATGAAGTTGAGAACCTTCTTGTT	1942
DB	2157	TTGTGCCCCCTTATAAATGCGCTGTTCATATGGACACTATGAGGTGGCTGAGCTTTTAGTA	2216
QY	1943	AAACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACTTTTACATGAAGCA	2002
DB	2217	AGGCATGGGGCTTCTGTCAATGTGGCGGACTTATGGAAATTTACCCCTCTCCCATGAAGCA	2276
QY	2003	GCAGCAAAAGGAAAAATATGAAATTTGCCAACTTCTGCTCCAGCATGGTCAGACCCCTACC	2062
DB	2277	GCAGCTAAAGGAAGTATGAATCTGCAGCTCCTCTTTTAAAA CATGGAGCAGATCCA ACT	2336
QY	2063	AAAAAAAACAGGATGGAATA TCTCTTTTGGATCTTGTTTAAAGATGGAGATACAGATATT	2122
DB	2337	AAAAAGAACAGAGATGGAATA TACCTTTTGGATTTTGTGTAAGGAAGGAGACACAGATATT	2396
QY	2123	CAAGATCTGCTTAGGGAGATGACGCTTTGCTAGATGCTGCCAAGAGGGCTTTTAGCC	2182
DB	2397	CAGACTTACTGTAAAGGGGATGTGCTTTGTTGGATGCTGCCAAGGAAGGCTGCCTGGCA	2456
QY	2183	AGAGTGAAGAAGTTGTCTTCTCTGATAATGTAAATTTGCCCGCATATCCC AAGCAGACAT	2242
DB	2457	AGAGTCGAGAAGCTCTGTATCCCAGAGATATCAATGTCAGACACACCCAGGGCAGNAAT	2516
QY	2243	TCAA CACTTTACATTTAGCAGCTGGTTATPAATTAATTTAGAAGTTGACAGTATTGTTTA	2302
DB	2517	TCAACCCCTCTGCACCTGGCAGCAGGCTATAATAA CTTGGAAGTAGCTGAATATCTCTA	2576
QY	2303	CAACACGGAGCTGATGTGAATGCCAAGACAAAGGAGGACTTATTCCTTTACATATGCA	2362
DB	2577	GAGCATGGAGCTGATGTATAATGCCAAGGACAAGGGGTGGTTAAATTCCTCTTCAATAATGG	2636
QY	2363	GCATCTTTACGGCATGPAGATGTAGCAGCTCTACTAATAAAGTATAATGCATGTGTCAAT	2422
DB	2637	GCATCTTTATGGCATGTTGACATAGCGCTTTATTGATAAANAATCAACACTGTGTAAAT	2696
QY	2423	GCCA CGGACAAATGGGCTTTTCA CACTTTTGACGAAGCAGCCCCAAAGGAGCAACACAG	2482
DB	2697	GCAACAGATAAGTGGGCGTTTACTCTCCCTCCATGTAAGCAGCCCCAGAAAGGAGCGCAG	2756
QY	2483	CTTTGTGCTTTGTTGTAGGCCATGGAGCTGACCCGACTCTTAAAAATCAGGAAGGACAA	2542
DB	2757	CTGTGCGCCCTCTCTCTAGCGCATGTGTGCAGACCCCCACCATGAAGAACCAGGAAGGCAG	2816
QY	2543	ACACCTTTTAGATTTAGTTTTCAGCGGATGATGT CAGGGCTCTCTTGACAGCAGCCATGSCCC	2602
DB	2817	ACGGCTCTGGATCTGGCAA CAGCTGACGATATCAGAGCTTTGCTGATAGATGCCATGCC	2876
QY	2603	CCATCTGCTCTGGCCCTCTGTTTACAAGCCCTCAAGTGTCTCAATGGTGTGAAGCCCGGAG	2662
DB	2877	CCAGAGGCCCTTACCTACCTGTTTTAAACCTCAG-----CTACT	2915
QY	2663	GCACATCGAGATGCTCTCTCTT CAGGTCCATCTAGGCCCATCAAGCCCTTCTGAGCCAGC	2722
DB	2916	GTAGTGAGTGCCTCTCTGATCTCACAGCATCCACGCCCTCTCTCGGCTCGGCTGCAGC	2975
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DB	2976	AGCATAGCAACCTCACTGCGCCCTTTTAGCAGAGTTGGCGTAGGAGAGCCTCCAATGCA	3035

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 17:00:29 ; Search time 3854.36 Seconds
(without alignments)
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Title: US-10-616-101-1

Perfect score: 3797

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
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- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3797	100.0	3797	10	US-10-616-101-1
2	3393.4	89.4	3816	10	US-10-616-101-2
3	3388.8	89.2	4275	3	US-09-972-115A-5
4	3388.8	89.2	4275	6	US-10-163-587A-14
5	3387.2	89.2	4127	7	US-10-199-937-100
6	3387.2	89.2	4406	7	US-10-199-937-106
7	3387.2	89.2	4992	7	US-10-199-937-134
8	3387.2	89.2	5002	7	US-10-199-937-132
9	3387.2	89.2	5075	8	US-10-302-172-556
10	3387.2	89.2	6018	3	US-09-849-602-11
11	3387.2	89.2	6189	10	US-10-898-653-5
12	3297	85.8	3400	3	US-09-509-196A-1
13	3296.2	86.8	3508	7	US-10-199-937-1
14	2969.6	78.2	4493	3	US-09-972-115A-1
15	2968.2	78.2	4297	3	US-09-972-115A-3
16	2439.8	64.3	2371	7	US-10-199-937-92
17	2439.8	64.3	3353	7	US-10-199-937-88

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19	1813.4	47.8	3984	7	US-10-199-937-3
20	1813.4	47.8	4134	3	US-09-841-835-1
21	1813.4	47.8	4134	3	US-09-972-115A-7
22	1533.8	40.4	4435	7	US-10-252-157-342
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24	1449.6	38.2	4491	10	US-10-898-653-4
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ALIGNMENTS

RESULT 1

US-10-616-101-1
; Sequence 1, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Osovsokaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616.101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-616-101-1

Query Match	100.0%	Score 3797;	DB 10;	Length 3797;
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Matches 3797;	Conservative	0;		
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QY 3781 TTGCTGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3797
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RESULT 2
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; Sequence 2, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Osobovskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616.101
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-616-101-2

Query Match 89.4%; Score 3393.4; DB 10; Length 3816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 422 AGGTTTTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 481
QY 463 AGTGATGATGGGGGCTTTTCTCTTCAATAATGATGCTCTTTTGGTCATGCTGAGT 522
Db 482 AGTGATGATGGGGGCTTTTCTCTTCAATAATGATGCTCTTTTGGTCATGCTGAGT 541
QY 523 AGTCAATCTCTTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 582
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QY 643 TGGAGCTGAGCCACCATCCGAATACAGATGGAAGGACAGCATTTGATTTAGCAGATCC 702
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; Sequence 5, Application US/09972115A
; Publication No. US20030032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Platiyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
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; PRIOR APPLICATION NUMBER: US 60/128,577
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; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4275
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(3781)
; OTHER INFORMATION:
US-09-972-115A-5

Query Match 89.2%; Score 3388.8; DB 3; Length 4275;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4

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; Publication No. US20030096263A1
; GENERAL INFORMATION:
; APPLICANT: Oliveira, Marcos
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10163,587A
; PRIORITY FILING DATE: 2003-01-10
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; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5778
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3501)
; OTHER INFORMATION:
US-10-163-587A-14

Query Match 89.2%; Score 3388.8; DB 6; Length 5778;
Best Local Similarity 99.9%; Pred No. 0;
Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 403 AGGTTTTGGCGGAAAGAGTGTAGTTGAATATTTGCTCAGATGTTGCAAGTGTCCAAGC 462
DB 198 AGGTTTTGGCGGAAAGAGTGTAGTTGAATATTTGCTCAGATGTTGCAAGTGTCCAAGC 257

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DB 258 ACGTGATGATGGGGCCCTTATTCTCTTTCATAATGTCATGCTCTTTTGGTCACTGCTGAAGT 317
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Db 3558 CCTCTACGTTTTTACTCCCTTTGCTGAAAAAAA 3589
RESULT 5
US-10-199-937-100
; Sequence 100, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866736559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 4127
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3508)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (3509)..(4127)
US-10-199-937-100
Query Match 89.2%; Score 3387.2; DB 7; Length 4127;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTGGCGGAAAGAGCTAGTTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAAGC 462
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QY 3523 TTTCTCAGTTCAGTGCATGAAATGGACACATCTCTTCCAGGTCATCTCAGTCAC 3582
DB 3328 TTTCTCAGTTCAGTGCATGAAATGGACACATCTCTTCCAGGTCATCTCAGTCAC 3387
QY 3583 TGGTAGCCCAAGTAAATGSCCTAGCATTTAGCTGAAATATGTTATTTTACAGAGAGAAACA 3642
DB 3388 TGGTAGCCCAAGTAAATGSCCTAGCATTTAGCTGAAATATGTTATTTTACAGAGAGAAACA 3447
QY 3643 GGCTTATCTCGAGTATTTAATTTACTTACCAGATTTATGAGGCTTGAAGGTATGGTCGATGG 3702
DB 3448 GGCTTATCTCGAGTATTTAATTTACTTACCAGATTTATGAGGCTTGAAGGTATGGTCGATGG 3507
QY 3703 ATAAATAGTATTTTAAAGAACTAAATTCCTGAGTAACTTAAATCATCAAGAGCAGATGG 3762
DB 3508 ATAAATAGTATTTTAAAGAACTAAATTCCTGAGTAACTTAAATCATCAAGAGCAGATGG 3567
QY 3763 CCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA 3794
DB 3568 CCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA 3599

RESULT 6
US-10-199-937-106
; Sequence 106, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: MCelligott, David L.
; TITLE OF INVENTION: TANKTRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; PRIOR FILING DATE: 2002-07-22
; PRIOR FILING DATE: 2000-06-28
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 4406

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(3787)
US-10-199-937-106

Query Match 89.2%; Score 3387.2; DB 7; Length 4406;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	403	AGGTTTGGCGGAAGAGCGTAGTGAATATTGCTTCAGAAATGCGCAAGTGTCCAAGC	462
DB	487	AGGTTTGGCGGAAGAGCGTAGTGAATATTGCTTCAGAAATGCGCAAGTGTCCAAGC	546
QY	463	AGTGATGATGGGGGCTTATTCCTCTTCAATATGATGCTCTTTGGTCATGCTGAAGT	522
DB	547	AGTGATGATGGGGGCTTATTCCTCTTCAATATGATGCTCTTTGGTCATGCTGAAGT	606
QY	523	AGTCAATCTCCTTTTGGGACATGGTGACAGACCCCAATGCTCGAGATAATTTGGAATTTATAC	582
DB	607	AGTCAATCTCCTTTTGGGACATGGTGACAGACCCCAATGCTCGAGATAATTTGGAATTTATAC	666
QY	583	TCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATTTGCTATGCTGTTCACAGCA	642
DB	667	TCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATTTGCTATGCTGTTCACAGCA	726
QY	643	TGGAGCTGAGCCACCAATCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCC	702
DB	727	TGGAGCTGAGCCACCAATCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCC	786
QY	703	ATCTGCGCAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTAAAGAAAGTCCAG	762
DB	787	ATCTGCGCAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTAAAGAAAGTCCAG	846
QY	763	GAGTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATTAATGTCAACTGCCACGC	822
DB	847	GAGTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATTAATGTCAACTGCCACGC	906
QY	823	AGTGATGGCAGAAAGTCAATCCATTACATTTGGCAGCAGGATATACAGAGTAAGAT	882
DB	907	AGTGATGGCAGAAAGTCAATCCATTACATTTGGCAGCAGGATATACAGAGTAAGAT	966
QY	883	TGTACAGCTGTACTGCAACATGGAGCTGATGCTCAATGCTTAAAGATAAGAGTGAATCTGCT	942
DB	967	TGTACAGCTGTACTGCAACATGGAGCTGATGCTCAATGCTTAAAGATAAGAGTGAATCTGCT	1026
QY	943	ACCATTTACACAAATGCTGTTTATGGTCAATATGAAGTAACTGAACTTTTGGTCAAGCA	1002
DB	1027	ACCATTTACACAAATGCTGTTTATGGTCAATATGAAGTAACTGAACTTTTGGTCAAGCA	1086
QY	1003	TGGTGCCTGTGTAATGCAATGGACTTGGCAATTCATCTCTTCATGAGGCGAGCTTC	1062
DB	1087	TGGTGCCTGTGTAATGCAATGGACTTGGCAATTCATCTCTTCATGAGGCGAGCTTC	1146
QY	1063	TAAAGAACAGGGTGAAGTATGTTCTCTCTTAAAGTATGGTCAGACCCCAACACTGCT	1122
DB	1147	TAAAGAACAGGGTGAAGTATGTTCTCTCTTAAAGTATGGTCAGACCCCAACACTGCT	1206
QY	1123	CAATTGTCACAATAAAGTGCTATAGACTTGGCTCCACACACAGTTTAAAGAAAGATT	1182
DB	1207	CAATTGTCACAATAAAGTGCTATAGACTTGGCTCCACACACAGTTTAAAGAAAGATT	1266
QY	1183	AGCATATGAATTTAAGGCCACTCGTGTGCAAGCTGCAGAGCTGATGTTACTCG	1242
DB	1267	AGCATATGAATTTAAGGCCACTCGTGTGCAAGCTGCAGAGCTGATGTTACTCG	1326
QY	1243	AATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCAAAACATGAAAC	1302
DB	1327	AATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCAAAACATGAAAC	1386
QY	1303	AGCATTGCAATGTGCTGCTATCCCATATCCCAAGAAAGCAAAATATGTGAATCTGTT	1362

DB	1387	AGCATTGCAATGTGCTGCTGCAATCCCATATCCCAAGAAAGCAAAATATGTGAATCTGTT	1446
QY	1363	GCTAAGAAAGGAGCAACATCAATGAAAGACTAAAGAAATCTTTGACTCTCTCGACCT	1422
DB	1447	GCTAAGAAAGGAGCAACATCAATGAAAGACTAAAGAAATCTTTGACTCTCTCGACCT	1506
QY	1423	GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACCATGAAGCAAGGT	1482
DB	1507	GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACCATGAAGCAAGGT	1566
QY	1483	TAATGCTCTGGAAATCTTTGGTCAGACTTCTCTACAGAGCTGCATATTTGGTCAATCT	1542
DB	1567	TAATGCTCTGGAAATCTTTGGTCAGACTTCTCTACAGAGCTGCATATTTGGTCAATCT	1626
QY	1543	ACAAACCTGCCGCCCTACTCTGAGCTATGGGTGTCATCTTAACATATATCCCTTCAGGG	1602
DB	1627	ACAAACCTGCCGCCCTACTCTGAGCTATGGGTGTCATCTTAACATATATCCCTTCAGGG	1686
QY	1603	CTTTACTGCTTTTACAGATGGGAAATGTAACAGAACTCTCTCCAAAGAGGGTATCTC	1662
DB	1687	CTTTACTGCTTTTACAGATGGGAAATGTAACAGAACTCTCTCCAAAGAGGGTATCTC	1746
QY	1663	ATTAGGTAATTCAGAGGAGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGCA	1722
DB	1747	ATTAGGTAATTCAGAGGAGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGCA	1806
QY	1723	AACGTAAAGAACTGTCTACTGTTTACAGAGTCTCAACTGCAGAGACATTTGAAGGGCGTCA	1782
DB	1807	AACGTAAAGAACTGTCTACTGTTTACAGAGTCTCAACTGCAGAGACATTTGAAGGGCGTCA	1866
QY	1783	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1842
DB	1867	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1926
QY	1843	ACAGATGGAGCTGATGTCATGCTTAAAGATAAGAGGAGGCTTTGACCTTTGCACAAATGC	1902
DB	1927	ACAGATGGAGCTGATGTCATGCTTAAAGATAAGAGGAGGCTTTGACCTTTGCACAAATGC	1986
QY	1903	ATGTTCTTATGGACATTAAGTTTGCAGAACTCTCTTAAACATGAGCAGTAGTTAA	1962
DB	1987	ATGTTCTTATGGACATTAAGTTTGCAGAACTCTCTTAAACATGAGCAGTAGTTAA	2046
QY	1963	TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022
DB	2047	TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2106
QY	2023	AATTTGCAAACTTCTGCTCCAGACTGGTGCAGACCTTACCAAAAAAAGAGGATGGAAA	2082
DB	2107	AATTTGCAAACTTCTGCTCCAGACTGGTGCAGACCTTACCAAAAAAAGAGGATGGAAA	2166
QY	2083	TACTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAGA	2142
DB	2167	TACTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAGA	2226
QY	2143	TGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTCTTC	2202
DB	2227	TGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTCTTC	2286
QY	2203	TCCTGATTAATGTAATTTGCCCGGATACCCAGGCGAGACATTCACACCTTTACATTTAGC	2262
DB	2287	TCCTGATTAATGTAATTTGCCCGGATACCCAGGCGAGACATTCACACCTTTACATTTAGC	2346
QY	2263	AGCTGGTTTATTAATTTAGAAAGTTTGCAGAGTATTTGTTTACAAACAGGAGCTGATGTAA	2322
DB	2347	AGCTGGTTTATTAATTTAGAAAGTTTGCAGAGTATTTGTTTACAAACAGGAGCTGATGTAA	2406
QY	2323	TGCCCAAGCAAAAGGAGGACTTATTTCTTTTACATAATGCAGCATCTTACGGGCGATGTAGA	2382
DB	2407	TGCCCAAGCAAAAGGAGGACTTATTTCTTTTACATAATGCAGCATCTTACGGGCGATGTAGA	2466
QY	2383	TGTAGCAGCTCTACTAATAAAGTAAATGCAATGCTCAATGCCAGCAAAATGGGCTTT	2442
DB	2467	TGTAGCAGCTCTACTAATAAAGTAAATGCAATGCTCAATGCCAGCAAAATGGGCTTT	2526

Db 3533 ACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGATTAAGTTGA 3592
Qy 2923 GATGGGACAAAGAGCTGAAGAGATTTGGAAATCAATGCTTTATGGACATAGGCACAAACT 2982
Db 3593 GATGGGACAAAGAGCTGAAGAGATTTGGAAATCAATGCTTTATGGACATAGGCACAAACT 3652
Qy 2983 AATTAAAGGAGTCAGAGACTTATCTCGGACAAAGAGCTTTAAACCCATATTAACTTTT 3042
Db 3653 AATTAAAGGAGTCAGAGACTTATCTCGGACAAAGAGCTTTAAACCCATATTAACTTTT 3712
Qy 3043 GAACACCTCTGCTAGTGAAACAAATCTTTATAGATCTGCTCTCATGATGATAAGAGTTTCA 3102
Db 3713 GAACACCTCTGCTAGTGAAACAAATCTTTATAGATCTGCTCTCATGATGATAAGAGTTTCA 3772
Qy 3103 GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATG 3162
Db 3773 GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATG 3832
Qy 3163 TGGAAATCTTCAACAGATACAAATATCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3222
Db 3833 TGGAAATCTTCAACAGATACAAATATCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3892
Qy 3223 GGAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAAACCAACCAATGCAATGA 3282
Db 3893 GGAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAAACCAACCAATGCAATGA 3952
Qy 3283 ACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTAACCAAAAGGCTTTGATGA 3342
Db 3953 ACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTAACCAAAAGGCTTTGATGA 4012
Qy 3343 AAGGATCGGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTGGTGAATCTCTTC 3402
Db 4013 AAGGATCGGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTTGGTGAATCTCTTC 4072
Qy 3403 CAAGAGCAATCAATATGATATGAAATGGAAGAGGTACTGGGTTCCAGTTTCAACAAGA 3462
Db 4073 CAAGAGCAATCAATATGATATGAAATGGAAGAGGTACTGGGTTCCAGTTTCAACAAGA 4132
Qy 3463 CAGATCTTTGTACATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3522
Db 4133 CAGATCTTTGTACATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 4192
Qy 3523 TTTCTCGAGTTTCAGTGAATGAAATGGGACATCTCTCTCCAGGTCACTCAGTCAAC 3582
Db 4193 TTTCTCGAGTTTCAGTGAATGAAATGGGACATCTCTCTCCAGGTCACTCAGTCAAC 4252
Qy 3583 TGGTAGGCCAGGTGAAATGGCCTAGCATAGCTGAATATGTTATTTACAGAGAGAAACA 3642
Db 4253 TGGTAGGCCAGGTGAAATGGCCTAGCATAGCTGAATATGTTATTTACAGAGAGAAACA 4312
Qy 3643 GGCTTATCTCAGTATTTAAATTTACTTACCAGATATGAGGCTGAAGGTATGGTCGATGG 3702
Db 4313 GGCTTATCTCAGTATTTAAATTTACTTACCAGATATGAGGCTGAAGGTATGGTCGATGG 4372
Qy 3703 ATAAATAGTTATTTAAGAAACTAATTCACCTGAACCTAAATCATCAAGCAGCAGTGG 3762
Db 4373 ATAAATAGTTATTTAAGAAACTAATTCACCTGAACCTAAATCATCAAGCAGCAGTGG 4432
Qy 3763 CCTCTACGTTTCTCTCTTTGCTGAAGAAAA 3794
Db 4433 CCTCTACGTTTCTCTCTTTGCTGAAGAAAA 4464

RESULT 8

US-10-199-937-132
; Sequence 132, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKRASE2 MATERIALS AND METHODS

; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 5002
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (229)..(4383)
US-10-199-937-132

Query Match 89.2%; Score 3387.2; DB 7; Length 5002;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTGGGCGGAAAGACGCTAGTTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAGC 462
Db 1083 AGGTTTTGGGCGGAAAGACGCTAGTTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAGC 1142
Qy 463 ACGTGATGATGGGGCCCTTATTCCTCTTCATATATGCAATGCTCTTTTGGTCAATGCTGAAGT 522
Db 1143 ACGTGATGATGGGGCCCTTATTCCTCTTCATATATGCAATGCTCTTTTGGTCAATGCTGAAGT 1202
Qy 523 AGTCMACTCTCTTTTGGACATGGTGCAGACCCCAATGCTCGAGATAAATGGAAATTATAC 582
Db 1203 AGTCMACTCTCTTTTGGACATGGTGCAGACCCCAATGCTCGAGATAAATGGAAATTATAC 1262
Qy 583 TCCTCTCATTGAAGCTCAATTTAAAGGAAAGATGATGTTTGCAATGCTGCTGTTTACAGCA 642
Db 1263 TCCTCTCATTGAAGCTCAATTTAAAGGAAAGATGATGTTTGCAATGCTGCTGTTTACAGCA 1322
Qy 643 TGGAGCTGAGCCAAACCATCCGAAATA CAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 702
Db 1323 TGGAGCTGAGCCAAACCATCCGAAATA CAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 1382
Qy 703 ATCTGCCAAAGCAGTGTCTTACTGTGTAATATAAGAAAGATGAACTCTTAGAAAGTGCAG 762
Db 1383 ATCTGCCAAAGCAGTGTCTTACTGTGTAATATAAGAAAGATGAACTCTTAGAAAGTGCAG 1442
Qy 763 GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCATTAATGTCAACTGCCACGC 822
Db 1443 GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCATTAATGTCAACTGCCACGC 1502
Qy 823 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGAT 882
Db 1503 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGAT 1562
Qy 883 TGTACAGCTGTACTGCAACATGGAGCTGATGTCATGCTTAAAGATTAAGATTAAGGTGATCTCGT 942
Db 1563 TGTACAGCTGTACTGCAACATGGAGCTGATGTCATGCTTAAAGATTAAGATTAAGGTGATCTCGT 1622
Qy 943 ACCATTACAAATGCCCTGTTCTTATGCTCATTAAGAGTAACCTGAACTTTTGGTCAAGCA 1002
Db 1623 ACCATTACAAATGCCCTGTTCTTATGCTCATTAAGAGTAACCTGAACTTTTGGTCAAGCA 1682
Qy 1003 TGGTGCCTGTGTAATGCAATGGAGCTTTGTGGCAATCACTCTCTTCATGAGGAGCTTC 1062
Db 1683 TGGTGCCTGTGTAATGCAATGGAGCTTTGTGGCAATCACTCTCTTCATGAGGAGCTTC 1742
Qy 1063 TAAGAACAGGGTTCAAGTATGTTCTCTCTTAAAGTTATGTTGTCAGACCCCAACACTGCT 1122
Db 1743 TAAGAACAGGGTTCAAGTATGTTCTCTCTTAAAGTTATGTTGTCAGACCCCAACACTGCT 1802
Qy 1123 CAATTGTCACAATAAAAGTGTATAGACTTTGGCTCCCAACACACACAGTTTAAAGAAAGATT 1182
Db 1803 CAATTGTCACAATAAAAGTGTATAGACTTTGGCTCCCAACACACACAGTTTAAAGAAAGATT 1862

1183 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAAGCTGATGTTACTCG 1242
1184 |||||
1863 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAAGCTGATGTTACTCG 1922
1864 |||||
1243 AATCAAAAACATCTCTCTCTGGAATGTTGGAATTTCAAGCATCTCTCAACACATGAAGAC 1302
1244 |||||
1923 AATCAAAAACATCTCTCTCTGGAATGTTGGAATTTCAAGCATCTCTCAACACATGAAGAC 1982
1924 |||||
1303 AGCATGCAATGCTGCTGCAATCTCCATATCCCAAGAAAGCAATATGTTGAACTGTT 1362
1304 |||||
1983 AGCATGCAATGCTGCTGCAATCTCCATATCCCAAGAAAGCAATATGTTGAACTGTT 2042
1984 |||||
1363 GCTAAGAAAGGAGCAAAACATCAATGAAAGAGCTAAGAAATTTCTGACCTCTCTGCAAGT 1422
1364 |||||
2043 GCTAAGAAAGGAGCAAAACATCAATGAAAGAGCTAAGAAATTTCTGACCTCTCTGCAAGT 2102
2044 |||||
1423 GGATCTGAGAAAGCTCAATAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT 1482
1424 |||||
2103 GGATCTGAGAAAGCTCAATAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT 2162
2104 |||||
1483 TAATGCTCTGGTAATCTTGGTGCAGACTTCTCTACACAGCTGCAATATGTTGGTCACTC 1542
1484 |||||
2163 TAATGCTCTGGTAATCTTGGTGCAGACTTCTCTACACAGCTGCAATATGTTGGTCACTC 2222
2164 |||||
1543 ACAAACTCTGCGCTACTCTGAGCTATGGGTGATCCTTAACATATATATCCCTTCAGGG 1602
1544 |||||
2223 ACNAACTCTGCGCTACTCTGAGCTATGGGTGATCCTTAACATATATATCCCTTCAGGG 2282
2224 |||||
1603 CTTTACTGCTTTTACAGATGGGAAATGAAATGATGATACAGCAACTCTCTCAAGAGGGTATCTC 1662
1604 |||||
2283 CTTTACTGCTTTACAGATGGGAAATGAAATGATGATACAGCAACTCTCTCAAGAGGGTATCTC 2342
2284 |||||
1663 ATTAGTAATTCAGAGGACAGACAAATGCTGGAAGCTGCAGAGCTGCAGAGTGTGCA 1722
1664 |||||
2343 ATTAGTAATTCAGAGGACAGACAAATGCTGGAAGCTGCAGAGCTGCAGAGTGTGCA 2402
2344 |||||
1723 AACTGTAAAAAACTGTGACTGTTCCAGAGTGTCAACTGCAGAGACATTTGAAGGGGGTCA 1782
1724 |||||
2403 AACTGTAAAAAACTGTGACTGTTCCAGAGTGTCAACTGCAGAGACATTTGAAGGGGGTCA 2462
2404 |||||
1783 GTCTACACACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT 1842
1784 |||||
2463 GTCTACACACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT 2522
2464 |||||
1843 ACAGCATGAGCTGATGTCATGCTTAAGATAAAGAGGCGCTTGTACCTTTGCACATGC 1902
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2523 ACAGCATGAGCTGATGTCATGCTTAAGATAAAGAGGCGCTTGTACCTTTGCACATGC 2582
2524 |||||
1903 ATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTGTTTAAACATGGAGCAGTAGTTAA 1962
1904 |||||
2583 ATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTGTTTAAACATGGAGCAGTAGTTAA 2642
2584 |||||
1963 TGTAGCTGATTTATGGAATTTTACCTTTTACATGAAGCAGCAGCAAAAAGGAAAATATGA 2022
1964 |||||
2643 TGTAGCTGATTTATGGAATTTTACCTTTTACATGAAGCAGCAGCAAAAAGGAAAATATGA 2702
2644 |||||
2023 AATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAAA 2082
2024 |||||
2703 AATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAAA 2762
2704 |||||
2083 TACTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTCTCTTATGGGGAGA 2142
2084 |||||
2763 TACTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTCTCTTATGGGGAGA 2822
2764 |||||
2143 TGCAGCTTTTGTAGTGTCTGCAAGAGGGTGTGTTTATGAGCAGATGAAGTGTGCTTTC 2202
2144 |||||
2823 TGCAGCTTTTGTAGTGTCTGCAAGAGGGTGTGTTTATGAGCAGATGAAGTGTGCTTTC 2882
2824 |||||
2203 TCGTGAATATGTAATGTCGGGATACCCAGGAGACATTCGAAACCTTTTATTTAGC 2262
2204 |||||
2883 TCGTGAATATGTAATGTCGGGATACCCAGGAGACATTCGAAACCTTTTATTTAGC 2942
2884 |||||

2263 AGCTGGTTATATAATTTAGAAAGTTGCAGAGTATTTGTTTACACACGAGAGCTGATGTGAA 2322
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2943 AGCTGGTTATATAATTTAGAAAGTTGCAGAGTATTTGTTTACACACGAGAGCTGATGTGAA 3002
2944 |||||
2323 TGCCCAAGACAAAGAGAGACTTTATTCCTTTTACATTAATGAGCATCTTACGGGATGTAGA 2382
2324 |||||
3003 TGCCCAAGACAAAGAGAGACTTTATTCCTTTTACATTAATGAGCATCTTACGGGATGTAGA 3062
3004 |||||
2383 TGTAGCAGCTCTACTTAATAAGTATAATGCTGTCATGTCACGAGCAAAATGGGCTTTT 2442
2384 |||||
3063 TGTAGCAGCTCTACTTAATAAGTATAATGCTGTCATGTCACGAGCAAAATGGGCTTTT 3122
3064 |||||
2443 CACACCTTTTGCAAGAGCAGCCCAAAAGGAGCAACACAGCTTTTGTGCTTTGTTGCTAGC 2502
2444 |||||
3123 CACACCTTTTGCAAGAGCAGCCCAAAAGGAGCAACACAGCTTTTGTGCTTTGTTGCTAGC 3182
3124 |||||
2503 CCATGGAGCTGACCCGACTCTTTAAAAATTCAGGAAGGACAAACACCTTTTATGATTTAGTTTC 2562
2504 |||||
3183 CCATGGAGCTGACCCGACTCTTTAAAAATTCAGGAAGGACAAACACCTTTTATGATTTAGTTTC 3242
3184 |||||
2563 AGCGCATGATGTCAGGCTCTTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTTG 2622
2564 |||||
3243 AGCATGATGTCAGGCTCTTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTTG 3302
3244 |||||
2623 TTACAAGCCTCAAGTGTCTCAATGTTGTGAGAGCCAGAGCCACTGCAAGATGCTCTCTC 2682
2624 |||||
3303 TTACAAGCCTCAAGTGTCTCAATGTTGTGAGAGCCAGAGCCACTGCAAGATGCTCTCTC 3362
3304 |||||
2683 TTTCAAGTCTCATCTAGCCCATCAAGCCTTTCTGACGCGAGCATCTTGAACAATTTATCTGG 2742
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3363 TTTCAAGTCTCATCTAGCCCATCAAGCCTTTCTGACGCGAGCATCTTGAACAATTTATCTGG 3422
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2743 GAGTTTTTTCAGAACTGCTTCTCAAGTAGTTAGTTTCAAGTGAACAGAGGGTCTTCCAGTTT 2802
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3483 GGAGAAAAGAGGAGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGG 3542
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2863 ACTTGAGCACTTAATGGAATATATTTTGAGAGAGAAACAGATCACTTTGGATGATTTAGTTGA 2922
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3543 ACTTGAGCACTTAATGGAATATATTTTGAGAGAGAAACAGATCACTTTGGATGATTTAGTTGA 3602
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2923 GATGGGACACAGAGCTGAGAGGATTTGGATCAATGCTTTATGACATAGGCACAAACT 2982
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3603 GATGGGACACAGAGCTGAGAGGATTTGGATCAATGCTTTATGACATAGGCACAAACT 3662
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2983 AATTAAGGAGTCGAGAGACTTATCTCCGGACAAACAGGCTCTTAAACCATATTTAACTTT 3042
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3663 AATTAAGGAGTCGAGAGACTTATCTCCGGACAAACAGGCTCTTAAACCATATTTAACTTT 3722
3664 |||||
3043 GAACACCTCTGTTAGTGGAACAATTTCTTATAGATCTGCTCTGATGATTAAGAGTTTCA 3102
3044 |||||
3723 GAACACCTCTGTTAGTGGAACAATTTCTTATAGATCTGCTCTGATGATTAAGAGTTTCA 3782
3724 |||||
3103 GTCTGTGGAGAGAGATGCAAGGTACAGTTCGAGAGCAGAGATGGAGGTCATGCGAG 3162
3104 |||||
3783 GTCTGTGGAGAGAGATGCAAGGTACAGTTCGAGAGCAGAGATGGAGGTCATGCGAG 3842
3784 |||||
3163 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAAACTATG 3222
3164 |||||
3843 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAAACTATG 3902
3844 |||||
3223 GGAAGAATACCTCAACAGAGAAAGAGTTTCTGAAGAAACCAACCACTTGCCTTGA 3282
3224 |||||
3903 GGAAGAATACCTCAACAGAGAAAGAGTTTCTGAAGAAACCAACCACTTGCCTTGA 3962
3904 |||||
3283 AGCAATGCTATTTTCAATGGGTCTCTCTTGTGAATCAATTTATCCAAAGGGTTTGA 3342
3284 |||||
3963 AGCAATGCTATTTTCAATGGGTCTCTCTTGTGAATCAATTTATCCAAAGGGTTTGA 4022
3964 |||||
3343 AAGGCATGCGTACATAGGTGGTATGTTTTGGAGCTGGCATTTATTTTGTGTAACCACTTTC 3402
3344 |||||

1603 QY CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCTC 1662
1650 Db CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCTC 1709
1663 QY ATTAGGTAAATCAGAGGCGAGACAGACAATTCGTGGAAAGCTGCAAAAGGCTGGAGATGTGGA 1722
1710 Db ATTAGGTAAATCAGAGGCGAGACAGACAATTCGTGGAAAGCTGCAAAAGGCTGGAGATGTGGA 1769
1723 QY AACTGTAAAAAATCTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCA 1782
1770 Db AACTGTAAAAAATCTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCA 1829
1783 QY GTCTACACCACTTCATTTTTCAGAGTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGCT 1842
1830 Db GTCTACACCACTTCATTTTTCAGAGTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGCT 1889
1843 QY ACAGATGGAGCTGATGTGCATGCTTAAGATTAAGAGGAGGCTTTGACCTTTGCACAATGC 1902
1890 Db ACAGATGGAGCTGATGTGCATGCTTAAGATTAAGAGGAGGCTTTGACCTTTGCACAATGC 1949
1903 QY ATGTTCTTTATGACATTAATGAAGTTGCAGAACTTCTGTTTAAACATGGAGCAGTAGTTAA 1962
1950 Db ATGTTCTTTATGACATTAATGAAGTTGCAGAACTTCTGTTTAAACATGGAGCAGTAGTTAA 2009
1963 QY TGTAGCTGATTTATGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
2010 Db TGTAGCTGATTTATGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2069
2023 QY AATTTGCAAACTTCGTCCAGCATGGTGCAGACCTTACCAAAAAAAGAGGATGGAAA 2082
2070 Db AATTTGCAAACTTCGTCCAGCATGGTGCAGACCTTACCAAAAAAAGAGGATGGAAA 2129
2083 QY TACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAGA 2142
2130 Db TACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAGA 2189
2143 QY TGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTCTTC 2202
2190 Db TGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTCTTC 2249
2203 QY TCCTGATTAATGTAATTCGCGGATFACCAAGGAGACATTCACACCTTTACATTTAGC 2262
2250 Db TCCTGATTAATGTAATTCGCGGATFACCAAGGAGACATTCACACCTTTACATTTAGC 2309
2263 QY AGCTGGTTATTAATTTAGAGTTGTCAGAGTATTTGTTTACACCGAGCTGATGTGAA 2322
2310 Db AGCTGGTTATTAATTTAGAGTTGTCAGAGTATTTGTTTACACCGAGCTGATGTGAA 2369
2323 QY TGCCCAAGACAAAGGAGACTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAGA 2382
2370 Db TGCCCAAGACAAAGGAGACTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAGA 2429
2383 QY TGTAGCAGCTCTACTAATAAGTATAATGCAATGTGCAATGTCACCGGACAAATGGGCTTT 2442
2430 Db TGTAGCAGCTCTACTAATAAGTATAATGCAATGTGCAATGTCACCGGACAAATGGGCTTT 2489
2443 QY CACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACAGCTTTGCTTTGTTGCTAGC 2502
2490 Db CACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACAGCTTTGCTTTGTTGCTAGC 2549
2503 QY CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTAGATTAGTTTC 2562
2550 Db CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTAGATTAGTTTC 2609
2563 QY AGCGGATGATGTACGGCTCTTTCTGACAGCAGCCATGCCCCCATCTGCTGCCCTCTTG 2622
2610 Db AGCGGATGATGTACGGCTCTTTCTGACAGCAGCCATGCCCCCATCTGCTGCCCTCTTG 2669
2623 QY TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGAGCCACTGCAGATGCTCTC 2682
2670 Db TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGAGCCACTGCAGATGCTCTC 2729
2683 QY TTCAGGTCATCTAGCCCATCAAGCCTTTCTGACGCGCAGCTTTGACAACTTATCTGG 2742

2730 Db TTCAGGTCATCTAGCCCATCAAGCCTTTCTGACGCGAGAGTCTTGACAACTTATCTGG 2789
2743 QY GAGTTTTTCAGAACTGCTTCAGTAGTTAGTTCAAGTGAACAGAGGCTGCTTCAGTTT 2802
2790 Db GAGTTTTTCAGAACTGCTTCAGTAGTTAGTTCAAGTGAACAGAGGCTGCTTCAGTTT 2849
2803 QY GGAGAAAAGGAGGTTCCAGGAGTAGATTTTAGCAATACTCAATTCGTAAGGAATCTTGG 2862
2850 Db GGAGAAAAGGAGGTTCCAGGAGTAGATTTTAGCAATACTCAATTCGTAAGGAATCTTGG 2909
2863 QY ACTTGAGCACCTAATGGATATATTGGAGAGAAACAGATCACTTTTGGATGTAATTAGTGA 2922
2910 Db ACTTGAGCACCTAATGGATATATTGGAGAGAAACAGATCACTTTTGGATGTAATTAGTGA 2969
2923 QY GATGGGCGCAAGGAGCTGAAGGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 2982
2970 Db GATGGGCGCAAGGAGCTGAAGGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 3029
2983 QY AATTAAAGGAGCTCAGAGACTTATCTCCGGAACAACAGGCTCTTAACCCATATTTAACTTT 3042
3030 Db AATTAAAGGAGCTCAGAGACTTATCTCCGGAACAACAGGCTCTTAACCCATATTTAACTTT 3089
3043 QY GAACACCTCTCGTAGTGGAAACAATTTCTTATAGATCTGTCTCTCGATGATAAGAGTTTCA 3102
3090 Db GAACACCTCTCGTAGTGGAAACAATTTCTTATAGATCTGTCTCTCGATGATAAGAGTTTCA 3149
3103 QY GTCTGTGGAGAAAGATGCAAAAGTACAGTTTCGAGAGCACAGATGGAGTTCATGCAGG 3162
3150 Db GTCTGTGGAGAAAGATGCAAAAGTACAGTTTCGAGAGCACAGATGGAGTTCATGCAGG 3209
3163 QY TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3222
3210 Db TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3269
3223 QY GGAAGATFACACTCAACCGAGAGAAAGAGTTTCTGAAGAAAACCAACACCATGCCAATGA 3282
3270 Db GGAAGATFACACTCAACCGAGAGAAAGAGTTTCTGAAGAAAACCAACACCATGCCAATGA 3329
3283 QY ACGAATGCTATTTTCAATGGGCTCTCTTTTGTGAATGCAATTCACAAAGGCTTTGATGA 3342
3330 Db ACGAATGCTATTTTCAATGGGCTCTCTTTTGTGAATGCAATTCACAAAGGCTTTGATGA 3389
3343 QY AAGCATGCGTACATAGGTGCTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTTTC 3402
3390 Db AAGCATGCGTACATAGGTGCTATGTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTTTC 3449
3403 QY CAAAAGCAATCAATATGTAATGGAATTTGGAGGAGTACTGGGTGTCAGTTTCACAAAGA 3462
3450 Db CAAAAGCAATCAATATGTAATGGAATTTGGAGGAGTACTGGGTGTCAGTTTCACAAAGA 3509
3463 QY CAGATCTTTGTACATTTGCCACAGGAGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3522
3510 Db CAGATCTTTGTACATTTTCCACAGGAGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3569
3523 QY TTTCTCGAGTTTCAAGTGAATGAAAATGGCAATTCCTCCAGTCACTCACTCAGTCAC 3582
3570 Db TTTCTCGAGTTTCAAGTGAATGAAAATGGCAATTCCTCCAGTCACTCACTCAGTCAC 3629
3583 QY TGGTAGGCCAGTGTAAATGGCCTTAGCATTAAGTGAATATGTTTATACAGAGGAGAAACA 3642
3630 Db TGGTAGGCCAGTGTAAATGGCCTTAGCATTAAGTGAATATGTTTATACAGAGGAGAAACA 3689
3643 QY GGCCTATCTGAGTATTTAATTTACTTACAGATTTATGAGGCTGAGGATGTTGCTGATGG 3702
3690 Db GGCCTATCTGAGTATTTAATTTACTTACAGATTTATGAGGCTGAGGATGTTGCTGATGG 3749
3703 QY ATAAATAGTATTTTAAAGAACTAATCCACTGAACCTTAAATCATCAAGCAGCAGTGG 3762
3750 Db ATAAATAGTATTTTAAAGAACTAATCCACTGAACCTTAAATCATCAAGCAGCAGTGG 3809
3763 QY CCTCTACGTTTACTCTCTTGTGTAAGAAAAA 3794

Db	3810	CCTCTACGTTTACTCCTTTGCTGAAAAAAA	3841	
RESULT 10				
US-09-849-602-11				
; Sequence 11, Application US/09849602				
; Publication No: US20030165834A1				
; GENERAL INFORMATION:				
; APPLICANT: Scanlan, Matthew J.				
; APPLICANT: Old, Lloyd J.				
; APPLICANT: Stockert, Elisabeth				
; APPLICANT: Chen, Yao-Teeng				
; TITLE OF INVENTION: Colon Cancer Antigen Panel				
; FILE REFERENCE: L0461/7105 (JRV)				
; CURRENT APPLICATION NUMBER: US/09/849,602				
; CURRENT FILING DATE: 2001-05-04				
; NUMBER OF SEQ ID NOS: 30				
; SOFTWARE: PatentIn version 3.0				
; SEQ ID NO 11				
; LENGTH: 6018				
; TYPE: DNA				
; ORGANISM: Homo sapien				
US-09-849-602-11				
Query Match 89.2%; Score 3387.2; DB 3; Length 6018;				
Best Local Similarity 99.9%; Pred. No. 0;				
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	403	AGGTTTTGGGGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGTCCAAAGC	462	
Db	418	AGGTTTTGGGGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAATGTCCAAAGC	477	
Qy	463	ACGTGATGATGGGGCCTTATTCCTCTTCAATAATGCAATGCTCTTTTGGTCATGCTGAAGT	522	
Db	478	ACGTGATGATGGGGCCTTATTCCTCTTCAATAATGCAATGCTCTTTTGGTCATGCTGAAGT	537	
Qy	523	AGTCAATCTCTTTTGGACATGGTGAGACCCCAATGCTCGAGATAATTTGGAAATTATAC	582	
Db	538	AGTCAATCTCTTTTGGACATGGTGAGACCCCAATGCTCGAGATAATTTGGAAATTATAC	597	
Qy	583	TCCTCTCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCAATTTGCTGTTTACAGCA	642	
Db	598	TCCTCTCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCAATTTGCTGTTTACAGCA	657	
Qy	643	TGGAGCTGAGCCAAACCATCCGAATACAGATGGAAGGACAGCATTTGGAATTAGCAGATCC	702	
Db	658	TGGAGCTGAGCCAAACCATCCGAATACAGATGGAAGGACAGCATTTGGAATTAGCAGATCC	717	
Qy	703	ATCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCAG	762	
Db	718	ATCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCAG	777	
Qy	763	GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGC	822	
Db	778	GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGC	837	
Qy	823	AAGTGATGGCAGAAAGTCAATCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGAT	882	
Db	838	AAGTGATGGCAGAAAGTCAATCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGAT	897	
Qy	883	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTTAAAGATAAGGTGATCTGGT	942	
Db	898	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTTAAAGATAAGGTGATCTGGT	957	
Qy	943	ACCAATTACCAATGCCTGCTTATGGTCAATTTAAGTAATCACTGAACTTTTGGTCAAGCA	1002	
Db	958	ACCAATTACCAATGCCTGCTTATGGTCAATTTAAGTAATCACTGAACTTTTGGTCAAGCA	1017	
Qy	1003	TGGTGCCTGTGTAATGCAATGAGACTTGTGGCAATTCACCTCTTCATGAGGAGCTTC	1062	
Db	1018	TGGTGCCTGTGTAATGCAATGAGACTTGTGGCAATTCACCTCTTCATGAGGAGCTTC	1077	
Qy	1063	TAAGAACAGGGTTGAAGTATGTTCTTCTTCTTAAAGTTATGGTGCAGACCCCAACTGCT	1122	

Db	1078	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGCAGACCCCAACTGCT	1137	
Qy	1123	CAATTGTCACAATAAAAGTCTATAGACTTTGGCTCCACACCAAGTAAAGAAAGATT	1182	
Db	1138	CAATTGTCACAATAAAAGTCTATAGACTTTGGCTCCACACCAAGTAAAGAAAGATT	1197	
Qy	1183	AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAGCTGATGTTACTCG	1242	
Db	1198	AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAGCTGATGTTACTCG	1257	
Qy	1243	AATCAAAAAACATCTCTCTGGAATATGGTGAATTTCAAGCATCTCTCAACACACATGAAAC	1302	
Db	1258	AATCAAAAAACATCTCTCTGGAATATGGTGAATTTCAAGCATCTCTCAACACACATGAAAC	1317	
Qy	1303	AGCATTCGATTTGCTGCTGCAATCTCATATCCCAAGAAAGCAAAATATGTGAATGTT	1362	
Db	1318	AGCATTCGATTTGCTGCTGCAATCTCATATCCCAAGAAAGCAAAATATGTGAATGTT	1377	
Qy	1363	GCTAAGAAAAAGGAGCAAAACATCAATGAAGAGCTTAAAGAAATTTCTTGACTCTCTGCAAGT	1422	
Db	1378	GCTAAGAAAAAGGAGCAAAACATCAATGAAGAGACTTAAAGAAATTTCTTGACTCTCTGCAAGT	1437	
Qy	1423	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAGGT	1482	
Db	1438	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAGGT	1497	
Qy	1483	TAATGCTCTGGAATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGTCATCT	1542	
Db	1498	TAATGCTCTGGAATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGTCATCT	1557	
Qy	1543	ACAAACCTGCGCCTACTCTGAGCTATGGGTGATCCTTAAACATTTATCCCTTCAGGG	1602	
Db	1558	ACAAACCTGCGCCTACTCTGAGCTATGGGTGATCCTTAAACATTTATCCCTTCAGGG	1617	
Qy	1603	CTTTACTGCTTTACAGATGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCTC	1662	
Db	1618	CTTTACTGCTTTACAGATGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCTC	1677	
Qy	1663	ATTAGGTAATTCAGAGCAGACAGACAAATTTGCTGGAAGCTGCAAAAGCTGGAGATGCGA	1722	
Db	1678	ATTAGGTAATTCAGAGCAGACAGACAAATTTGCTGGAAGCTGCAAAAGCTGGAGATGCGA	1737	
Qy	1723	AACGTAAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCA	1782	
Db	1738	AACGTAAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCA	1797	
Qy	1783	GTCTACACCACTTCATTTTGCAGCTGGGTATFAACAGAGTGTCCGTGGTGAATATCTGCT	1842	
Db	1798	GTCTACACCACTTCATTTTGCAGCTGGGTATFAACAGAGTGTCCGTGGTGAATATCTGCT	1857	
Qy	1843	ACAGCATGGAGCTGATGTCATGCTTAAAGATAAAGAGGGCTTGTACTCTTTGCAATATGC	1902	
Db	1858	ACAGCATGGAGCTGATGTCATGCTTAAAGATAAAGAGGGCTTGTACTCTTTGCAATATGC	1917	
Qy	1903	ATGTTCTTATGGACATTTAAGTTGAGAACTTCTTTTAAACATGGAGCAGTAGTTAA	1962	
Db	1918	ATGTTCTTATGGACATTTAAGTTGAGAACTTCTTTTAAACATGGAGCAGTAGTTAA	1977	
Qy	1963	TGTAAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022	
Db	1978	TGTAAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2037	
Qy	2023	AATTTGCAAACTTCTGCTCCAGCATGTGTGAGACCCCTTACCAAAAAAACAGGGATGGA	2082	
Db	2038	AATTTGCAAACTTCTGCTCCAGCATGTGTGAGACCCCTTACCAAAAAAACAGGGATGGA	2097	
Qy	2083	TACTCCTTTGGATCTTCTTAAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGAGA	2142	
Db	2098	TACTCCTTTGGATCTTCTTAAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGAGA	2157	
Qy	2143	TGCAGCTTTGCTAGATCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAAAGTTGCTTTC	2202	

Db 2158 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTTGTTTAGCCAGAGTGAAGAGTGTGCTTC 2217
Qy 2203 TCCTGATATGTAATTTGCGCGATACCCAGGCGAGACATTCACACCTTTTACATTTAGC 2262
Db 2218 TCTGATATGTAATTTGCGCGATACCCAGGCGAGACATTCACACCTTTTACATTTAGC 2277
Qy 2263 AGCTGGTTATATAATTTTAGAAGTTGCGAGATATTTGTTTACAACACGGAGCTGATGTGAA 2322
Db 2278 AGCTGGTTATATAATTTTAGAAGTTGCGAGATATTTGTTTACAACACGGAGCTGATGTGAA 2337
Qy 2323 TGCCCAAGCAAAAGGAGGATTTATTCCTTTTACATATGAGCATCTTACGGGCATGTAGA 2382
Db 2338 TGCCCAAGCAAAAGGAGGATTTATTCCTTTTACATATGAGCATCTTACGGGCATGTAGA 2397
Qy 2383 TGTTAGCAGCTCTACTAAATAAGATATAATGATGTGTCATGTCACCGACAAATGGGCTTT 2442
Db 2398 TGTTAGCAGCTCTACTAAATAAGATATAATGATGTGTCATGTCACCGACAAATGGGCTTT 2457
Qy 2443 CACACCTTTTGCA CGAAGCAGCCCAAAAGGAGCGAAACACAGCTTTTGTGCTTTGCTAGC 2502
Db 2458 CACACCTTTTGCA CGAAGCAGCCCAAAAGGAGCGAAACACAGCTTTTGTGCTTTGCTAGC 2517
Qy 2503 CCATGGAGCTGACCGGATCTCTTTTAAATAATCAGGAAGGACAAACACCTTTTAGATTTAGTTTC 2562
Db 2518 CCATGGAGCTGACCGGATCTCTTTTAAATAATCAGGAAGGACAAACACCTTTTAGATTTAGTTTC 2577
Qy 2563 AGCGATGATGTGAGCGCTCTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTTG 2622
Db 2578 AGCAGATGATGTGAGCGCTCTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTTG 2637
Qy 2623 TTACAAGCCTCAAGTGCTCAATGGTGTCGAGAGCCAGGAGCCACTGCGAGATGCTCTCTC 2682
Db 2638 TTACAAGCCTCAAGTGCTCAATGGTGTCGAGAGCCAGGAGCCACTGCGAGATGCTCTCTC 2697
Qy 2683 TTCAAGGCTCAAGTGCTCAATGGTGTCGAGAGCCAGGAGCCACTGCGAGATGCTCTCTC 2742
Db 2698 TTCAAGGCTCAAGTGCTCAATGGTGTCGAGAGCCAGGAGCCACTGCGAGATGCTCTCTC 2757
Qy 2743 GAGTTTTTTCAGAACTGCTCTTCAAGTGTAGTTCAAGTGGAACAGAGGGTCTTCCAGTTT 2802
Db 2758 GAGTTTTTTCAGAACTGCTCTTCAAGTGTAGTTCAAGTGGAACAGAGGGTCTTCCAGTTT 2817
Qy 2803 GGAGAAAAGAGGTTTCCAGGAGTAGATTTTACGCACTCAATTCGTAAGGAATCTTGG 2862
Db 2818 GGAGAAAAGAGGTTTCCAGGAGTAGATTTTACGCACTCAATTCGTAAGGAATCTTGG 2877
Qy 2863 ACTTGAGCACTTAATGGATATATTTGAGAGAAACAGATCACTTTGGATGTATTTAGTTGA 2922
Db 2878 ACTTGAGCACTTAATGGATATATTTGAGAGAAACAGATCACTTTGGATGTATTTAGTTGA 2937
Qy 2923 GATGGGCAACAGGAGCTGAAGGAGATTTGGAATCAATGCTTATGACATAGGCACAACT 2982
Db 2938 GATGGGCAACAGGAGCTGAAGGAGATTTGGAATCAATGCTTATGACATAGGCACAACT 2997
Qy 2983 AATTAAGGAGTCCGAGACTTATCTCCGCAACAAAGGCTTTAAACCCATATTTAACTTT 3042
Db 2998 AATTAAGGAGTCCGAGACTTATCTCCGCAACAAAGGCTTTAAACCCATATTTAACTTT 3057
Qy 3043 GAACACCTCTGTTAGTGGAACTTTCTTATAGATCTGTCCTCTGATGATAAAGAGTTTCA 3102
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Qy 3103 GTCTGGGAGGAGATGCAAGTACAGTTGAGGACACAGATGAGGAGTCAATGAGG 3162
Db 3118 GTCTGGGAGGAGATGCAAGTACAGTTGAGGACACAGATGAGGAGTCAATGAGG 3177
Qy 3163 TCGAATCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3222
Db 3178 TCGAATCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3237
Qy 3223 GGAAAGATACACTCAACCGGAGAAAGAGTTTCTGAAGAAAACCAACCATGCCAATGA 3282
Db 3238 GGAAAGATACACTCAACCGGAGAAAGAGTTTCTGAAGAAAACCAACCATGCCAATGA 3297

Qy 3283 ACGAATGCTATTTTCAATGGGCTCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 3342
Db 3298 ACGAATGCTATTTTCAATGGGCTCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 3357
Qy 3343 AAGCATCGGTACATAGGTGTATGTTTGGAGCTGGCAATTTATTTTGTGTAATACTTTTC 3402
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Qy 3403 CAAAGCAATCAATATGATATGGAATTTGGAGGAGGTACTGGGTGTCCAGTTTCAAAAGA 3462
Db 3418 CAAAGCAATCAATATGATATGGAATTTGGAGGAGGTACTGGGTGTCCAGTTTCAAAAGA 3477
Qy 3463 CAGATCTTTGTATCATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3522
Db 3478 CAGATCTTTGTATCATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3537
Qy 3523 TTTCTCGAGTTCAAGTGTCAATGGAATAATGGCAATTTCTCTCCAGGTCACTCACTGATCAC 3582
Db 3538 TTTCTCGAGTTCAAGTGTCAATGGAATAATGGCAATTTCTCTCCAGGTCACTCACTGATCAC 3597
Qy 3583 TGGTAGGCCCTAGTGTAAATGGCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAAC 3642
Db 3598 TGGTAGGCCCTAGTGTAAATGGCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAAC 3657
Qy 3643 GGCTTATCTCGAGTATTTAAATTTACTTACAGATTTAGGGCTGAAGGTATGTCGATGG 3702
Db 3658 GGCTTATCTCGAGTATTTAAATTTACTTACAGATTTAGGGCTGAAGGTATGTCGATGG 3717
Qy 3703 ATAAATAGTTATTTTAAAGAACTAATTTCCACTGAACCTTAAATATCAAAAGCAGCAGTGG 3762
Db 3718 ATAAATAGTTATTTTAAAGAACTAATTTCCACTGAACCTTAAATATCAAAAGCAGCAGTGG 3777
Qy 3763 CCTCTACGTTTACTCTCTTCTGCTGAAAAAAA 3794
Db 3778 CCTCTACGTTTACTCTCTTCTGCTGAAAAAAA 3809

RESULT 11

US-10-898-653-5
; Sequence 5, Application US/10898653
; Publication No. US20050143370A1
; GENERAL INFORMATION:
; APPLICANT: Helleday et al
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: J660-046
; CURRENT APPLICATION NUMBER: US/10/898,653
; CURRENT FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 6189
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-898-653-5

Query Match 89.2%; Score 3387.2; DB 10; Length 6189;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTCGGCGGAAAGACGTAGTTGGAATAATTTGCTTCAGAAATGTCAGAGTGTCAAAGC 462
Db 577 AGGTTTTCGGCGGAAAGACGTAGTTGGAATAATTTGCTTCAGAAATGTCAGAAATGTCAAAGC 636
Qy 463 ACGTGATCATGGGGCCCTTATTCCTCTCAATATGCAATGCTCTTTTGGTCACTGCTGAAGT 522
Db 637 ACGTGATCATGGGGCCCTTATTCCTCTCAATATGCAATGCTCTTTTGGTCACTGCTGAAGT 696
Qy 523 AGTCAATCTCTTTTGGACATGGTGACAGCCCAATGCTCGAGATAATTTGGAATTTATAC 582
Db 697 AGTCAATCTCTTTTGGACATGGTGACAGCCCAATGCTCGAGATAATTTGGAATTTATAC 756
Qy 583 TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTTGATGTTTGCATTTGCTGTTCACAGA 642

Db 757 TCCTCTCCATGAAGCTGCATTAAGGAAGATTGATGTTTGCATTTGCTGTTACAGCA 816
Qy 643 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGGAAGACAGCATTTGATTTAGCAGATCC 702
Db 817 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGGAAGACAGCATTTGATTTAGCAGATCC 876
Qy 703 ATCTGCCAAGCAGTCTTACTGCTGATATATAAGAAAGATGAACCTCTAGAAAGTCCAG 762
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Qy 763 GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGCTCAACTGCCACGC 822
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Qy 823 AAGTGATGGCAGAAAGTCAACTCCATTTACATTTTGGCAGCAGGATATACAGAGTAAAGAT 882
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RESULT 12
US-09-509-196A-1
; Sequence 1, Application US/09509196A
; Patent No. US20020037582A1

GENERAL INFORMATION:
; APPLICANT: DALY, Roger J.
; APPLICANT: SUTHERLAND, Robert L.
; TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 1871-129
; CURRENT APPLICATION NUMBER: US/09/509,196A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: P09388
; PRIOR FILING DATE: 1997-09-23
; PRIOR APPLICATION NUMBER: PCT AU98/00795
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3400
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-509-196A-1

Query Match 86.8%; Score 3297; DB 3; Length 3400;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3303; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 482 ATTCTCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAAGTAGTCAATCTCTCTTTTGGCA 541
Db 1 ATTCTCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAAGTAGTCAATCTCTCTTTTGGCA 60
QY 542 CATGGTCAGACCCCAATGCTCGAGATAATTGGAATTTATCTCTCTCCATGAAGCTGCA 601
Db 61 CATGGTCAGACCCCAATGCTCGAGATAATTGGAATTTATCTCTCTCCATGAAGCTGCA 120
QY 602 ATTAAGGAAAGATTGATGTTTGGCATTTGCTGCTTTACAGCATGCGTGGCCACCATC 661
Db 121 ATTAAGGAAAGATTGATGTTTGGCATTTGCTGCTTTACAGCATGCGTGGCCACCATC 180
QY 662 CGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCCATCTGCCAAAGCAGTGT 721
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QY 782 ATGATGCTCTTACTCACACCATTAATAATGCTCAACGCAAGTGTAGGCGAGAAAGTCA 841
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QY 842 ACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTACTGCAA 901
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Db 421 CATGGAGCTGATGCTTCATGCTTAAAGATTAAGGTGATCTGGTACCAATTACAAATGCTGT 480
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Db 481 TCTTATGCTCATTTAGTAAGTAAGTCTTGGTCAAGCATGCTGCTGTTAAATGCA 540
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QY 1202 CACTCGTTGCTGCAAGCTGCAACGAGAGCTGATGTTACTCGAATCAAAAAACATCTCTCT 1261

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RESULT 13
US-10-199-937-1
; Sequence 1, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3508)
US-10-199-937-1

Query Match 86.8%; Score 3296.2; DB 7; Length 3508;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3298; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 403 AGGTTTTCGGCGGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAGTGTCCAGC 462
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Job time : 3863.36 secs

Job time : 3863.36 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 17:00:26 ; Search time 754.113 Seconds
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Title: US-10-616-101-1

Perfect score: 3797

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3026960 seqs, 1061187768 residues

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Listing first 45 summaries

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- 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3387.2	89.2	3815	US-11-266-748A-23602	Sequence 23602, A
2	3387.2	89.2	6189	US-11-266-748A-23750	Sequence 23750, A
3	1813.4	47.8	4134	US-11-266-748A-29428	Sequence 29428, A
4	1794.8	47.3	8901	US-11-266-748A-22929	Sequence 22929, A
5	663.8	17.5	675	US-11-266-748A-251004	Sequence 251004, A
6	663.8	17.5	675	US-11-266-748A-311521	Sequence 311521, A
7	570	15.0	594	US-11-266-748A-39554	Sequence 39554, A
8	535.6	14.1	929	US-11-266-748A-152365	Sequence 152365, A
9	535.6	14.1	564	US-11-266-748A-189602	Sequence 189602, A
10	533.6	14.1	564	US-11-266-748A-55144	Sequence 55144, A
11	533.6	14.1	564	US-11-266-748A-217436	Sequence 217436, A
12	515.6	13.6	668	US-11-266-748A-165504	Sequence 165504, A
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14	503.2	13.3	1000	US-11-266-748A-116071	Sequence 116071, A
15	503.2	13.3	1000	US-11-266-748A-158235	Sequence 158235, A
16	503.2	13.3	1000	US-11-266-748A-221377	Sequence 221377, A
17	503.2	13.3	1000	US-11-266-748A-286109	Sequence 286109, A
18	503.2	13.3	1000	US-11-266-748A-337538	Sequence 337538, A
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20	503.2	13.3	1000	US-11-266-748A-467527	Sequence 467527, A
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22	336.8	8.9	566	US-11-266-748A-463378	Sequence 463378, A

ALIGNMENTS

RESULT 1

US-11-266-748A-23602
; Sequence 23602, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnson, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 23602
; LENGTH: 3815
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23602

Query Match 89.2%; Score 3387.2; DB 8; Length 3815;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 403 AGGTTTGGGCGGAAGACGTAGTGTGATTTGTTTCAGATGTTGCAAGTGTCCAGC 462
DB 337 AGGTTTGGGCGGAAGACGTAGTGTGATTTGTTTCAGATGTTGCAAGTGTCCAGC 396

Sequence 8589, Ap
Sequence 3203, Ap
Sequence 272728,
Sequence 33245,
Sequence 380066,
Sequence 463445,
Sequence 174653,
Sequence 246075,
Sequence 56688, A
Sequence 3160, Ap
Sequence 794, App
Sequence 32152, A
Sequence 32784, A
Sequence 25093, A
Sequence 23775, A
Sequence 3622, Ap
Sequence 22278, A
Sequence 1815, Ap
Sequence 1819, Ap
Sequence 2096, Ap
Sequence 7246, Ap
Sequence 65708, A

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DB 397 ACGTGATGATGGGGCCTTATTCCTCTCTCAATAATGCGATGCTCTTTTGGTCATGCTGAAGT 456
QY 523 AGTCAATCTCTTTTGGGACATGCTGCGAGACCCCAATGCTCGAGATAATTTGGAATTATAC 582
DB 457 AGTCNACTCTTTTGGGACATGCTGCGAGACCCCAATGCTCGAGATAATTTGGAATTATAC 516
QY 583 TCCTCTCCATGAAGCTGCAATTAAGGAAGATGATGTTTGGCATGCTGCTTTACAGCA 642
DB 517 TCCTCTCCATGAAGCTGCAATTAAGGAAGATGATGTTTGGCATGCTGCTTTACAGCA 576
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DB 577 TGGAGCTGAGCCACCAACCATCCGAATACAGATGGGAGGACAGCATTTAGCAGATCC 636
QY 703 ATCTGCCAAAGCAGTGTCTACTGCTGAAATTAAGAAAGATGAACTCTTTAGAAAGTGCCAG 762
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QY 763 GAGTGGCAATGAAGAAATAATGATGGCTCTACTCACCAATTAATGTCAACTGCCACGC 822
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Db 3697 CCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA 3728

RESULT 2

US-11-266-748A-23750
; Sequence 23750, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23750
; LENGTH: 6189
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23750

Query Match 89.2%; Score 3387.2; DB 8; Length 6189;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAGC 462
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Db 3816 GGGCTTCAGGCGACCACTCACTGATTTGGTAGACCGAGGTCATGGGCTGGCATATGCT 3875
Qy 3617 GAATATGTTATTTACAGAGGAAACAGGCTTATCTCTGAGTATTTAAATTTACTTACCAGATT 3676
Db 3876 GAAATATGTCATCTACAGAGGAAACAGGATACCCAGAGTATCTTATCACTTACCAGATC 3935
Qy 3677 ATGAGGCTGAAG 3689
Db 3936 ATGAAGCCAGAG 3948

RESULT 4

US-11-266-748A-22929
; Sequence 22929, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PENDING FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22929
; LENGTH: 8901
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-22929

Query Match 47.3%; Score 1794.8; DB 8; Length 8901;
Best Local Similarity 72.5%; Pred. No. 0;
Matches 2365; Conservative 0; Mismatches 872; Indels 27; Gaps 2;
Qy 432 ATTTGCTTCAGATGGTGCAGTGTCCAGCAGCTGATGATGGGGGCTTATTCCTCTTC 491

Db 2 ACTTACTACAGATGGGTGCTAAATGTCACGCTGATGATGGAGGTCTCATCCGCTTC 61
Qy 492 ATAATGATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCTTTTGGGACATGGTGAG 551
Db 62 ATAATGCTGCTTTTGGCCATGCTGAGGTGTGAGTCTGTTATTTGTCGAAGAGCTG 121
Qy 552 ACCCAATGCTCGAGATAATTTGGAAATATATCTCTCTCCATGAAGCTGCAATTTAAAGGAA 611
Db 122 ATCCAAATGCCAGGATAATCTGGAACTATACACCTCTGCAATGAAGCTGCTATTTAAAGGGA 181
Qy 612 AGATTGATGTTTGCATTTGCTGTTTACAGCATGAGCTGAGCCCAACCATCCGAATAACAG 671
Db 182 AGATCGATGTTGCTGCTGCTGTCGAGCAGGAGCTGACCCAAACATTCGGAACACTG 241
Qy 672 ATGGAAGACAGCATTTGGATTTAGCATCCATCTGCCAAGCAGTGTCTTACTGGTGAAT 731
Db 242 ATGGGAATCAGCCCTGGACCTGGCAGATCTTTCAGCAAAAGCTGTCTTACAGGTGAAT 301
Qy 732 ATAAGAAGATGAATCTTTAGAAAGTGCAGAGTGGCAATGAAGAAATAATGATGGCTC 791
Db 302 ACAAGAAGACGAATCTCTAGAGCTGCTAGAGTGGTAATGAAGAAATAATGATGGCTT 361
Qy 792 TACTCACACCATTTAAATGTTCAACTGCCACGCAAGTGTGCGAGAAAGTCAACTCCATTAC 851
Db 362 TACTGACTCTCTTAAATGTTGAATTTGCCATGCAAGTGTGGCGGAAAGTCTGCTCTTTAC 421
Qy 852 ATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTTACTGCAACATGGAGCTG 911
Db 422 ATCTAGCAGCGGGCTACAAACAGAGTTCGAATAGTTTCAGCTTCTTCTTTCAGCATGGTGTG 481
Qy 912 ATGTCCATGCTTAAAGATAAAGGTGATCTGTGTACCATTACACAAATGACCTGTTCTTATGTC 971
Db 482 ATGTTTCATGCAAAAGACAAAGGTGAGCTTGTGCTCTTCATATGATGCTATGATGAGAC 541
Qy 972 ATTATGAAGTAACTGAACTTTTGGTCAAGCATGGTGTGCTGTGTAATGCAATGGAATGTT 1031
Db 542 ATTATGAAGTCAACAGAACTGCTACTTAAAGCATGGAGCTTGTGTTAATGCCATGGATCTCT 601
Qy 1032 GGAATTCACCTCTTTCATGAGGAGGCTTCTAAGAACAGGTTGGAAGTATGTTCTCTTC 1091
Db 602 GGCAGTTTACTTCCACTGCGAGGCTGCTTCCAAAGAACCGTGTAGAAAGTGTGCTCTTTGT 661
Qy 1092 TCTTAAAGTTATGTTGCGAGACCAACACTGCTCAATTTGTACAAATAAAAGTGTATAGACT 1151
Db 662 TACTTAGCCATGGCGCTGATCTAGCTTAGTCACTGCTGCGCAAAAGTGTGCTGTGGATA 721
Qy 1152 TGGCTCCACACACACAGTTTAAAGAAAGATTAGCATATGAATTTTAAAGGCCACCTGTTGC 1211
Db 722 TGGCTCCAACTCCGGAGCTTAGGGAGAGATTGACTTTATGAATTTTAAAGGTCAATCTTTAC 781
Qy 1212 TGAAGTGCACGAGAGGCTGATGTTTACTGCAATCAAAACATCTCTCTCTGGAATGG 1271
Db 782 TACAAGCAGCAGAGAGAGCAGACTTAGCTTAAAGTTTAAAGAAACACTGCTCTGGAATCA 841
Qy 1272 TGAATTTCAAGCATCTTCAACACATGAACAGACTTGCATTTGCTGCTCATCTCCAT 1331
Db 842 TTAATTTCAACAAACCCGAGTCTCATGAAACAGCACTGCACTGTGCTGTGCTCTCTGCG 901
Qy 1332 ATCCCAAAAGAAAGCAATATGTGAATCTTGTGCTTAAAGAAAGGAGCAACATCAATGAAA 1391
Db 902 ATCCCAACGTAAACAGTGAACAGATTGTTACTTAGAAAGGAGCAATGTTAATGAAA 961
Qy 1392 AGACTAAAGAAATCTTGACTCTCTGACGTGGCATCTGAGAAAGCTCATTAATGATGTTG 1451
Db 962 AAAATAAAGATTTTCATGACTCCCTGCTGATGTTGCGAGCGAAAGAGCCCATTAATGTGCA 1021
Qy 1452 TTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGAATAATCTTCTGTCAGACTT 1511
Db 1022 TGAAGTTTCTGCATGAAGCATGGCGCCAGATGAATGCACTGGACACCCCTTGTGTCAGACTG 1081
Qy 1512 CTCTACACAGAGCTGCATATTTGTGCTCATCTACAAACCTGCGGCTACTCTCTGAGCTATG 1571

Db 1082 CTTTGCATAGAGCGCCCTAGCAGGCCACCTGCAGACCTGCCGCTCTCTGCTGAGTTACG 1141
Qy 1572 GGTGTGATCCCTAAACATTATATATCCCTTCAGGCTTTTATCTGCTTTTACAGATGGAAATGAAA 1631
Db 1142 GCTCTGACCCCTCCATCATCTCTCTTACAGGCTTACAGCAGCAGATGGCAATGAAG 1201
Qy 1632 ATGTACAGCAACTCTCCAGAGGGTATCTCATTTAGTAAATTCAGAGCAGACAGACAAT 1691
Db 1202 CAGTGCAGCAGATTCTGAGTGAGAGTACACCTATACGTACTTCTGTGATTTATCGAC 1261
Qy 1692 TGCTGGAACTGCAAGGCTCGAGATGCGAAACTGTAAATAAACTGTACTGTTCAGA 1751
Db 1262 TCTTAGAGGCATCTTAAGCTGGAGCTTGGAACTGTGAGCACTTTGACGCTCMAA 1321
Qy 1752 GTGTCAACTGCAGAGACATTAAGGGGCTAGTCTTACACCACTTCATTTTGCAGCTGGT 1811
Db 1322 ATGTGAATTGAGAGACTTAGAGGCGCGCACTTCAAGCCCTTACACTTCGCAGCAGGCT 1381
Qy 1812 ATACAGAGTGTCCGTGGTGAATATCTGTACAGCATGGAGCTGATGTCATGCTAAAG 1871
Db 1382 ACAACCGGCTGTCTGTGTAGAGTACCTGTCTACACCAAGCTGCGGCTGTCATGCCAAAG 1441
Qy 1872 ATAAAGAGGCTTGTACTTTGACCAATGATGTTCTTATGGACATTTAGAGTTCGAG 1931
Db 1442 ACAAGGTGGCTTGTGTCCTTCAATATGCTGTTCAATGGACACTATGAGGTGCTG 1501
Qy 1932 AACTTCTTTTAAACATGGAGCAGTGTAAATAGTGTGATTTATGGAATTTTACACTT 1991
Db 1502 AGCTTTTGTAGTAAAGCATGGGCTTCTGTCAATGTGGGGGACTTATGGAAATTTTACCCTC 1561
Qy 1992 TACATGAGCAGCAGCAAGGAAATATGAAATTTGCCAACTTCTGCTCCAGCATGGT 2051
Db 1562 TCCATGAGCAGCAGCTAAAGGAAATGATGAAATCTGCAAGCTCTTTTAAACATGGAG 1621
Qy 2052 CAGACCTTACCAAAAAAACAAGGATGAAATATCTCTTGGATCTTGTAAAGATGGAG 2111
Db 1622 CAGATCCAACTTAAAGNACAGAGATGGAATATACCTTTGGATTTGGTAAAGNAGAG 1681
Qy 2112 ATACAGATATTCAAGATCTGCTTATGGGAGATGAGCTTTGCTAGATGCTGCCAAGAG 2171
Db 1682 ACACAGATATTCCAGACTTACTGAAAAGGGATGCTGCTTTGTTGGATGCTGCCAAGAG 1741
Qy 2172 GTTCTTATGACAGATGAGAGTGTCTTCTCTGATATGTAATTTGCCGATACCC 2231
Db 1742 GCTCCCTGGCAAGATGAGAGTCTGTATCCCAAGAGATATCAACTGACAGACACCC 1801
Qy 2232 AAGCAGACATTTCAACACTTTTACATTTAGCAGCTGGTTATATAATTTAGAAGTTGAG 2291
Db 1802 AGGCAGAAATTTCAACCCCTCTGCACCTGGCAGCAGGCTATATAAATCTGGAAGTAGCTG 1861
Qy 2292 AGTATTTGTTAAACACGGAGCTGATGTGAATGCCCAAGACAAAGGAGACTTATTCCTT 2351
Db 1862 AATATCTTCTAGAGCATGGAGCTGATGTAAATGCCCAAGGAGGGTGTAAATTCCTC 1921
Qy 2352 TACATAATGAGCATCTTACGGCATGTAGATGTAGCAGCTCTACTAATAAGTATATG 2411
Db 1922 TTTAATAATGCGGCATCTTATGGGCATGTGTACATAGCGGCTTATGATATAAATACAA 1981
Qy 2412 CATGTGTCAATGCCAGCAAAATGGGCTTTTACACACTTTTGCAGAAAGCAGCCCAAGG 2471
Db 1982 CGTGTATAATGCAACAGATTAAGTGGGGTCTTCTCCCTCCATGAGCAGCCCAAGAG 2041
Qy 2472 GACGAAACAGCTTTGTGTTGTGTAGCCCATGGAGCTGACCCGACTTTTAAATC 2531
Db 2042 GAAGGACGAGCTGTGGCCCTCTCTCTAGCGCATGTGTGAGACGCCCAACCATGAAGAAC 2101
Qy 2532 AGGAGGACAAACCTTTAGATTTTGTTCAGGGGATGATGTCAGGCTCTTCTGACAG 2591
Db 2102 AGGAAGGACAGAGCCCTTGTGATCTGGCAACAGCTGAGCATATCAGAGCTTTGCTGATAG 2161
Qy 2592 CAGCATGCCCCCATCTGCTCTGCCCTCTTGTAAAGCCCTCAAGTGTCTCAATGGTGA 2651
Db 2162 ATGCCATGCCCCCAGAGGCGCTTACCTACTGTTTAAACCTCAGG----- 2206

Qy 2652 GAAGCCAGAGGACCACTGCAGATGCTCTCTCTTACAGTTCATCTAGGCCATCAAGCCTTT 2711
Db 2207 -----CTACTGTAGTGAGTGCCTCTCTGATCTCACCAAGCATCCACCCCTCTGCTCT 2260
Qy 2712 CTGCAGCCAGCAGTCTTTGACAACTTATCTGGAGTCTTTTTCAGAACTGTCTTTCAGTAGTTA 2771
Db 2261 CGGCTGCCAGCAGCATAGACAACTCTACTGCGCTTTTAGCAGAGTTGGCCGTAGGAGGAG 2320
Qy 2772 GTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAAG-----GAGGTTCCAGGAG 2825
Db 2321 CCTCCAAATGCAAGGGATGGCGCGCGGAAACAGAAAGAAAGGAGAGTAGTTCTGTGTC 2380
Qy 2826 TAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGGACTTTGAGCACTTAATGATATAT 2885
Db 2381 TTGACATGAATATCAGCCAAATTTCTAAAGAGCCCTTGGCCTTGAACACCTTTCGGGATATCT 2440
Qy 2886 TTGAGAGAGAACAGATCACCTTTGGATGATTAATAGTGGGGCAACAAGAGCTGAAGG 2945
Db 2441 TTGAAACAGAACAGATTACTAGATGTGTGGCTGATATGGGTCTAGNAGAGTTGAAAG 2500
Qy 2946 AGATTGGAATCAATGCTTATGGACATAGGACAAACTAAATTTAAAGGAGTCGAGAGACTTA 3005
Db 2501 AAATAGGCATCAATGCATATGGGCACCGCCACAAATTAATCAAAGGAGTAGAAAGACTCT 2560
Qy 3006 TCTCCGAGACAAAGGCTTTAAACCATATTTAACTTTGAACACCTCTGCTAGTGGAAACA 3065
Db 2561 TAGGTGACAAACAGGCAACCAATCTCTTATTTGACTTTTCACTGTGTTAACTCAGGGAACGA 2620
Qy 3066 TTCTTATAGATCTGTCTCTGATGATAAAGAGTTTCACTGTGGAGGAGAGAGATGAAA 3125
Db 2621 TTTTGTGGATCTGTCTCCAGAGATTAAGATATCACTCAGTGGAGAGAGAGATGCAAA 2680
Qy 3126 GTACAGTTTCAGAGCAGACAGAGATGGAGGTCTGAGGTGGAACTTCTCAACAGATACAATA 3185
Db 2681 GTACTATTTCAGAAACACAGAGATGGTGAATGCTGGCGGCATCTTCAACAGATACAATG 2740
Qy 3186 TTCTCAAGATTCAAGAGTTTGTAAACAAAGAACTATATGGGAAAGNATACACTCACCGAGAA 3245
Db 2741 TCATTGCAATTTCAAAAAGTTTGTCAACAAAGAAAGTTGAGGGAGCGGTTCTGCCACCGACAGA 2800
Qy 3246 AAGAAGTTCTTGAAGAAAAACCAACCATGCCAATGAACGAATGCTATTTTCATGGGTCTC 3305
Db 2801 AGGAGTGTCTGAGGAGATCAACACCATCAATGAGCGCATGTGTTTCATGCTCTC 2860
Qy 3306 CTTTGTGAATGCAATTTATCCAAAGGCTTTGATGAAAAGCATGCGTACATAGGTGGTA 3365
Db 2861 CTTTCATTAATGCCATTATTTATAAAGGTTTGTATGAGCGACATGCATACATAGGAGGAA 2920
Qy 3366 TGTGAGCTGCGCATTTATTTGCTGAAAACCTTCCAAAAGCAATCAATATGTATATG 3425
Db 2921 TGTGAGGCGCGGATTTATTTTGTCTAAAACCTCTCAAAAAGCAACAAATATGTTATG 2980
Qy 3426 GAATTGAGGAGGTACTGCGGTGTCAGTTTCAAAAAGACAGATCTTGTATACATTTGCCACA 3485
Db 2981 GAATTGAGGAGGAAACAGGCTGCCCTACACAAAGGACAGGTCACTGCTATATATGTCA 3040
Qy 3486 GGCAAGCTCTTTTGTGCGGGTAACTTGGGAAAGTCTTTCCTGAGTTTCAGTGCATATGA 3545
Db 3041 GACAAATGCTCTTCTGTGAGAGTGACCCCTTGGGAAATCTTCTGAGTTTAGCACCATGA 3100
Qy 3546 AAATGGACATTTCTCTCCAGGTCTCATCTCAGTCACTGCTAGGCCAGGCCAGTGAATGCC 3605
Db 3101 AAATGGCCCAACGCGCTTCCAGGGCACCACTCAGTCTTGGTAGACCGAGCGTCAATGGGC 3160
Qy 3606 TAGCATTAGCTGAATATGTTATTTTACAGAGAGAAACAGGCTTATCTCTGAGTATTTAATTA 3665
Db 3161 TGGCATATGCTGAATATGATCTATACAGAGAGNACAGGCATACCCAGAGATCTTATCA 3220
Qy 3666 CTTTACCAGATTATGAGCGCTGAAG 3689
Db 3221 CTTTACCAGATCATGAAGCCAGAAG 3244

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RESULT 5
US-11-266-748A-251004
; Sequence 251004, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2005-03-14
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 251004
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-251004

Query Match      17.5%; Score 663.8; DB 8; Length 675;
Best Local Similarity 99.0%; Pred. No. 1.5e-175;
Matches 668; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2417 GTCAATGCCAGCAGCAAAATGGGCTTTTCACACCTTTGCGAGAGCAGCCCAAAAGGGACGA 2476
Db 1 GTCAATGCCAGCAGCAAAATGGGCTTTTCACACCTTTGCGAGAGCAGCCCAAAAGGGACGA 60
QY 2477 ACACAGCTTTGTGCTTTGTGCTAGCCATGAGCTGACCCGACTCTTTAAATCAGGAA 2536
Db 61 ACACAGCTTTGTGCTTTGTGCTAGCCATGAGCTGACCCGACTCTTTAAATCAGGAA 120
QY 2537 GGACAAACACCTTTAGATTAGTTTTCAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCC 2596
Db 121 GGACAAACACCTTTAGATTAGTTTTCAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCC 180
QY 2597 ATGCCCCCATCTGCTCTGCCCTCTTGTGTACAGCCCTCAAGTGCTCAATGGTGTGAGAACG 2656
Db 181 ATGCCCCCATCTGCTCTGCCCTCTTGTGTACAGCCCTCAAGTGCTCAATGGTGTGAGAACG 240
QY 2657 CCAGAGGCCACTGCGAGATGCTCTCTCTTCAGTGCCATCAGCCATCAAGCCCTTTCTGCA 2716
Db 241 CCAGAGGCCACTGCGAGATGCTCTCTCTTCAGTGCCATCAGCCATCAAGCCCTTTCTGCA 300
QY 2717 GCCAGAGCTTTGACAACTTATCTGGAGTTTTCAGAACTGCTCTTCAAGTGTAGTTTCA 2776
Db 301 GCCAGAGCTTTGACAACTTATCTGGAGTTTTCAGAACTGCTCTTCAAGTGTAGTTTCA 360
QY 2777 AGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAGAGGGTTCAGGAGTAGATTATTAGC 2836
Db 361 AGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAGAGGGTTCAGGAGTAGATTATTAGC 420
QY 2837 ATAACTCAATTCGTAAGGAATCTTGGACTTTGAGCACTTAATGATATATTTGAGAGAGAA 2896
Db 421 ATAACTCAATTCGTAAGGAATCTTGGACTTTGAGCACTTAATGATATATTTGAGAGAGAA 480

US-11-266-748A-311521/c
; Sequence 311521, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2005-03-14
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 311521
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-311521

Query Match      17.5%; Score 663.8; DB 8; Length 675;
Best Local Similarity 99.0%; Pred. No. 1.5e-175;
Matches 668; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2897 CAGATCACTTTGGATGTATTAGTTGAGATGGGCAAGAGAGCTGAGAGAGATTGGAATC 2956
Db 481 CAGATCACTTTGGATGTATTAGTTGAGATGGGCAAGAGAGCTGAGAGAGATTGGAATC 540
QY 2957 AATGCTTATGACATAGGACCAAACTAATTAAGAGAGTCGAGAGACTTATCTCCGACAA 3016
Db 541 AATGCTTATGACATAGGACCAAACTAATTAAGAGAGTCGAGAGACTTATCTCCGACAA 600
QY 3017 CAAGGCTTTAAACCATATTTAACTTTGAACACCTCTGCTAGTGGAACTTCTTATAGAT 3076
Db 601 CAAGGCTTTAAACCATATTTAACTTTGAACACCTCTGCTAGTGGAACTTCTTATAGAT 660
QY 3077 CTGTCTCTCTGATGAT 3091
Db 661 CTGTCTCTCTGATGAT 675

RESULT 6
US-11-266-748A-311521/c
; Sequence 311521, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2005-03-14
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 311521
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-311521

Query Match      17.5%; Score 663.8; DB 8; Length 675;
Best Local Similarity 99.0%; Pred. No. 1.5e-175;
Matches 668; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2417 GTCAATGCCAGCAGCAAAATGGGCTTTTCACCTTTGCGAGAGCAGCCCAAAAGGGACGA 2476
Db 675 GTCAATGCCAGCAGCAAAATGGGCTTTTCACCTTTGCGAGAGCAGCCCAAAAGGGACGA 616
QY 2477 ACACAGCTTTGTGCTTTGTGCTAGCCATGAGCTGACCCGACTCTTAAATCAGGAA 2536
Db 615 ACACAGCTTTGTGCTTTGTGCTAGCCATGAGCTGACCCGACTCTTAAATCAGGAA 556
QY 2537 GGACAAACACCTTTAGATTAGTTTTCAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCC 2596
Db 555 GGACAAACACCTTTAGATTAGTTTTCAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCC 496
QY 2597 ATGCCCCCATCTGCTCTGCCCTCTTGTGTACAGCCCTCAAGTGTCTCAATGGTGTGAGAACG 2656

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Db 495 ATGCCCCCATCTGCTGCCCCCTCTGTTTCAACAGCCTCAAGTCTCAATGGTGTGAGAAGC 436
Qy 2657 CCAGAGGCCACTGAGATGCTCTCTCTTTCAGGTTCATCTAGCCCATCAAGCCTTCTTGCA 2716
Db 435 CCAGAGGCCACTGAGATGCTCTCTCTTTCAGGTTCATCTAGCCCATCAAGCCTTCTTGCA 376
Qy 2717 GCCAGGAGTCTTGACAACTTATCTGGGAGTCTTTCAGAACTGTCTTCAGTAGTTAGTTCA 2776
Db 375 GCCACCAAGTCTTGACAACTTATCTGGGAGTCTTTCAGAACTGTCTTCAGTAGTTAGTTCA 316
Qy 2777 AGTGAACAGAGGGTCTTTCAGTCTTGAGAAAAGAGGAGTTCAGGAGTAGATTTTAGC 2836
Db 315 AGTGAACAGAGGGTCTTTCAGTCTTGAGAAAAGAGGAGTTCAGGAGTAGATTTTAGC 256
Qy 2837 ATAACTCAATTCGTAAGGAATCTTGGACTTGAGCACTTAATGAATATATTTGAGAGAGAA 2896
Db 255 ATAACTCAATTCGTAAGGAATCTTGGACTTGAGCACTTAATGAATATATTTGAGAGAGAA 196
Qy 2897 CAGATCACTTTGGATGATTTAGTTGAGATGGGCACAGAGGCTGAAGGAGATTGGAATC 2956
Db 195 CAGATCACTTTGGATGATTTAGTTGAGATGGGCACAGAGGCTGAAGGAGATTGGAATC 136
Qy 2957 AATGCTTATGACATAGGCAAACTAATTAAGGAGTCGAGAGACTTATCTCCGGACAA 3016
Db 135 AATGCTTATGACATAGGCAAACTAATTAAGGAGTCGAGAGACTTATCTCCGGACAA 76
Qy 3017 CAAGGCTTTAAACCCCATTTTAACTTTGAACACCTCTGGTAGTGAACAAATTTCTTATAGAT 3076
Db 75 CAAGGCTTTAAACCCCATTTTAACTTTGAACACCTCTGGTAGTGAACAAATTTCTTATAGAT 16
Qy 3077 CTGCTCTCTGATGAT 3091
Db 15 CTGCTCTCTGATGAT 1

RESULT 7

US-11-266-748A-99554
; Sequence 99554, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99554
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-99554
; Query Match 15.0%; Score 570; DB 8; Length 594;

Best Local Similarity 99.7%; Pred. No. 3e-149;
Matches 592; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 3194 ATTCAAGAGGTTGTAAAG-AAAATATGGGAAAGATACATCACCGG-AGAAAAAGAG 3251
Db 1 ATTCAAGAGGTTGTAAAGAAAGAACTATGGAAAGATACATCACCGGAAAGAAAGAG 60
Qy 3252 TTTCTGAAGAAACCACCAACCATGCCAATGAAGAAATGCTATTTTCATGGGTCTCTCTTTG 3311
Db 61 TTTCTGAAGAAACCACCAACCATGCCAATGAAGAAATGCTATTTTCATGGGTCTCTCTTTG 120
Qy 3312 TGAATGCAATTTATCCAAAAGGCTTTGATGAAAAGGCATGGTACATAGGTGGTATGTTG 3371
Db 121 TGAATGCAATTTATCCAAAAGGCTTTGATGAAAAGGCATGGTACATAGGTGGTATGTTG 180
Qy 3372 GAGCTGGCATTTATTTTGTGAAAACCTCTTCCAAAAGCAATCAATATGATATGGAATG 3431
Db 181 GAGCTGGCATTTATTTTGTGAAAACCTCTTCCAAAAGCAATCAATATGATATGGAATG 240
Qy 3432 GAGGAGTACTGGGTGTCAGTTTCAAAAAGCAGATCTTGTACATTTGCCACAGGCAGC 3491
Db 241 GAGGAGTACTGGGTGTCAGTTTCAAAAAGCAGATCTTGTACATTTGCCACAGGCAGC 300
Qy 3492 TGCTCTTTTCCCGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGCATGAAATGG 3551
Db 301 TGCTCTTTTCCCGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGCATGAAATGG 360
Qy 3552 CACATCTCTCCAGGTTCATCAGTCACTGGTAGGCCAGGTGAAATGGCCTAGCAT 3611
Db 361 CACATCTCTCCAGGTTCATCAGTCACTGGTAGGCCAGGTGAAATGGCCTAGCAT 420
Qy 3612 TAGCTGAATATGTTATTTTACAGAGGAGAAAGGCTTATCTGAGTATTAATTAATCTTACC 3671
Db 421 TAGCTGAATATGTTATTTTACAGAGGAGAAAGGCTTATCTGAGTATTAATTAATCTTACC 480
Qy 3672 AGATTATGAGGCTTGAAGGTATGGTGCATGATGATAAATAGTATTTTAAAGAACTAAATTC 3731
Db 481 AGATTATGAGGCTTGAAGGTATGGTGCATGATGATAAATAGTATTTTAAAGAACTAAATTC 540
Qy 3732 ACTGAACCTAAATTCATCAAGAGCAGTGGCCTCTACGTTTAACTCTCTTTGCT 3785
Db 541 ACTGAACCTAAATTCATCAAGAGCAGTGGCCTCTACGTTTAACTCTCTTTGCT 594

RESULT 8

US-11-266-748A-152365/c
; Sequence 152365, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 152365
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-152365

Query Match 15.0%; Score 570; DB 8; Length 594;
Best Local Similarity 99.7%; Pred. No. 3e-149; Indels 2; Gaps 2;
Matches 592; Conservative 0; Mismatches 0;
QY 3194 ATTGAGAGGTTTGTAAACAG-AAACATATGGAAAGATACATCAACCGG-AGAAAAGAAG 3251
Db 594 ATTGAGAGGTTTGTAAACAGAAACTATGGAAAGATACATCAACCGGAGAAAAGAAG 535
QY 3252 TTTCTGAGAGAAACACACACCAATGCAATGAACGAATGCTATTTTCATGGGTCTCCTTTTG 3311
Db 534 TTTCTGAGAGAAACACACACCAATGCCAATGAACGAATGCTATTTTCATGGGTCTCCTTTTG 475
QY 3312 TGAATGCAATATCCACAAAGGCTTTTGATGAAGGCATGCGTACATAGTGTGTATGTTTG 3371
Db 474 TGAATGCAATATCCACAAAGGCTTTTGATGAAGGCATGCGTACATAGTGTGTATGTTTG 415
QY 3372 GAGCTGGCATTTATTTTGTGAAAACTCTTCCAAAGCAATCAATATATGTATGAAATTG 3431
Db 414 GAGCTGGCATTTATTTTGTGAAAACTCTTCCAAAGCAATCAATATATGTATGAAATTG 355
QY 3432 GAGGAGGTACTGGGTGTCAGTTTCAAAAGACAGATCTTTGTATACATTTTGGCCACAGGCAGC 3491
Db 354 GAGGAGGTACTGGGTGTCAGTTTCAAAAGACAGATCTTTGTATACATTTTGGCCACAGGCAGC 295
QY 3492 TGCTCTTTTGGCGGTAACTTTGGGAAAGTCTTTCTCGAGTTCAGTGCATGCAATGAAATGG 3551
Db 294 TGCTCTTTTGGCGGTAACTTTGGGAAAGTCTTTCTCGAGTTCAGTGCATGCAATGAAATGG 235
QY 3552 CACATTCCTCCAGGTCACTCAGTCAGTGTAGGCCCAAGTAAATGGCCCTAGCAT 3611
Db 234 CACATTCCTCCAGGTCACTCAGTCAGTGTAGGCCCAAGTAAATGGCCCTAGCAT 175
QY 3612 TAGCTGAATATGTTATTTACAGAGAGAACAGGCTTATCTCGAGTATTTAATTAATCTTACC 3671
Db 174 TAGCTGAATATGTTATTTACAGAGAGAACAGGCTTATCTCGAGTATTTAATTAATCTTACC 115
QY 3672 AGATTATGAGGCTCAAGGTATGTCGATGATTAATAGTATTTTAAAGAACTAATTC 3731
Db 114 AGATTATGAGGCTCAAGGTATGTCGATGATTAATAGTATTTTAAAGAACTAATTC 55
QY 3732 ACTGAACCTTAAATCATCAAGCAGCAGTGGCTCTAGCTTTTACTCCTTTTGCT 3785
Db 54 ACTGAACCTTAAATCATCAAGCAGCAGTGGCTCTAGCTTTTACTCCTTTTGCT 1

RESULT 9
US-11-266-748A-189602
; Sequence 189602, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 189602
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-189602

Query Match 14.1%; Score 535.6; DB 8; Length 929;
Best Local Similarity 74.0%; Pred. No. 1.7e-139;
Matches 679; Conservative 0; Mismatches 239; Indels 0; Gaps 0;
QY 1688 CAATTGCTGGAGCTGCAGAGGCTGAGATGTCGAAACTGTGAAACTGTAAATAACTGTACTGTT 1747
Db 12 CGACTCTTTAGAGGCATCTTAAAGCTGGAGACTTGGAAACTGTGAAAGCAACTTTGAGCTCT 71
QY 1748 CAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCACTCTACACCACTTTCATTTTGCAGCT 1807
Db 72 CAAATGTGATTTGTAGAGACTTAGAGGGCGGCATTTCCAGCCCTTACACTTTCGACGA 131
QY 1808 GGGTATAACAGAGTGTCCGTGGTGAATATCTGTACAGCATGGAGCTGTATGTCATGCT 1867
Db 132 GGCTACAAACCGTGTCTGTGTAGAGTACCTGTCTACACCAACGGTGGCGATGTCCATGCC 191
QY 1868 AAAGTAAAGAGGCTTGTACCTTTGCACATGCATGCTTCTTATGGACATTAAGAATT 1927
Db 192 AAAGACAAGGTGTGCTGGTCCCTCTTCAATATGCTGTTTATATGGACACTATGAGGTG 251
QY 1928 GCAGAACTTCTTGTAAACATGGAGCAGTGTAAATGTAGCTGATTTTATGGAAATTTTACA 1987
Db 252 GCTGAGCTTTTAGTAGGCGATGGGCTTCTGTCAATGTGGCGGACTTATGGAAATTTACC 311
QY 1988 CCTTTACATGAAGCAGCAGCAAAAGAAATATGAAATTTGCAAACTTCTGCTCCAGAT 2047
Db 312 CCTCTCATGAAGCAGCAGCTTAAAGGAAATATGAAATCTGCAAGCTCCTTTTAAAGCAT 371
QY 2048 GGTGACAGCTCTACCAAAACAGGAGTGAATATCTCTTGGATCTTGTGTTAAAGAT 2107
Db 372 GGACGAGATCCAACTTAAAGAAACAGAGATGAAATACACCTTTGGATTTGGTAAAGGAA 431
QY 2108 GGAGATACAGATATTTCAAGATCTGTTAGGGGAGATGAGCTTTTGTAGATGCTGCCAAG 2167
Db 432 GGAGACACAGATATTCAGGACTTACTGAGAGGGAGTGTCTGCTTTGGTGTGCTGCCAAG 491
QY 2168 AAGGTTTGTAGCCAGAGTGAAGAAGTTGTCTTCTCTGATTAATGTAAATTTGCGCGAT 2227
Db 492 AAGGCTGCTGGCAAGAGTGCAGAGCTCTGTACCCAGAGAAATATCAACTGCAGAGAC 551
QY 2228 ACCCAAGGCAGACATTTCAACCTTTTACATTTAGCAGCTGTTTATTAATTTAGAGTT 2287
Db 552 ACCGAGGCGAGAAATCAACCCCTCTGCACCTGGCAGCAGGCTATAATTAACCTGGAAATA 611
QY 2288 GCAGAGTATTTGTTTACAACAGGAGCTGATGTGAATGCCAAGACAAAGGAGGACTTATT 2347
Db 612 GCTGAATATCTTCTAGAGCATGGAGCTGATGTTTATGCCAGGACACAGGTTGTTTAAAT 671
QY 2348 CCTTTACATAATCAGCATCTTTACGGGCATGTAGATGTAGAGCTCTTACTATAAAGTAT 2407
Db 672 CCTCTTCATATGCGGCATCTTATGGGCATGTTGACATAGCGGCTTTTATTGATAAATAAC 731
QY 2408 AATGATGTGTCAATGCCACGACAAATGGGCTTTTACACCTTTTGCACAGACAGCCCAA 2467
Db 732 AACACGTGTGTAATGCAACAGATGAAGTGGCGCTTTACTCCCTCCCTCCATGAAGACGCCAG 791

Query Match	13.6%;	Score 515.6;	DB 8;	Length 658;
Best Local Similarity	97.6%;	Pred. No. 5.9e-134;		
Matches 518;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;
Qy	1644	TCCTCCAAAGAGGGTATCTCATTTAGGTAAATTCAGAGGCAGACAGACAATTCGTGGAGCTG	1703	
Db	23	TCCTCAAGAAGGGTATCTCATTTAGGTAAATTCAGAGGCAGACAGACAATTCGTGGAGCTG	82	
Qy	1704	CAAAAGCGTGAGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCA	1763	
Db	83	CAAAAGCGTGAGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCA	142	
Qy	1764	GAGACATTGAAGGGCGTCAGTCTACACCATTTTTCAGCTGGGTATAACAGAGTGT	1823	
Db	143	GAGACATTGAAGGGCGTCAGTCTACACCCCTTCATTTTCAGCTGGGTATAACAGAGTGT	202	
Qy	1824	CCGTGGTGGAAATATCTGCTACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCC	1883	
Db	203	CCGTGGTGGAAATATCTGCTACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCC	262	
Qy	1884	TTGTACCTTTGCAAAATGTCATGTTCTTTATGGACATTAATGAAGTTGACAGAACTTCTTGTTA	1943	
Db	263	TTGTACCTTTGCAAAATGTCATGTTCTTTATGGACATTAATGAAGTTGACAGAACTTCTTGTTA	322	
Qy	1944	AACATGAGCAGTAGTTAAATGTTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAG	2003	
Db	323	AACATGAGCAGTAGTTAAATGTTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAG	382	
Qy	2004	CAGCAAGAAGAAATATGAAATTTGCAAACTTCCTGCTCCAGCATGGTGACAGCCCTACCA	2063	
Db	383	CAGCAAGAAGAAATATGAAATTTGCAAACTTCCTGCTCCAGCATGGTGACAGCCCTACCN	442	
Qy	2064	AAAAAACAAGGATGGAATACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTC	2123	
Db	443	NNNNNNCAGGATGGAATACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTC	502	
Qy	2124	AAGATCTGCTTAGGGAGATGCAGCTTTGCTAGATGTCGCAAGAGGGTT	2174	
Db	503	AAGATCTGCTTAGGGAGATGCAGCTTTGCTAGATGTCGCAAGAGGGTT	953	

[illegible]

RESULT 15
US-11-266-748A-158235/c
; Sequence 158235, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick

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; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 158235
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-158235

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Query Match	13.3%	Score 503.2;	DB 8;	Length 1000;
Best Local Similarity	76.2%;	Pred. No. 2.3e-130;		
Matches 619;	Conservative 0;	Mismatches 193;	Indels 0;	Gaps 0;
QY	2878	GGATATATTTCAGAGAGAACAGATCACCTTTGGATGTATTAGTTTGAGATGGGGCACAAAGGA	2937	
DB	998	GGATATCTTTTGAACACAGACAGATTACCTAGATGTGTGGCTGATATGGGTCAATGAGA	939	
QY	2938	GCTGAAAGGAGATTGGAAATCAATGCTTATGACATAGGCACAAAACCTAATTAAAGGATCGA	2997	
DB	938	GTTTGAAGAAGAAATAGGCATCAATGCATATGGCCACCGCCACAAATTAATCAAGAGAGTAGA	879	
QY	2998	GAGACTTATCTCCGGACCAACAAGGCTTCAACCCATATTTAACTTTGAAACACCTCTCGTAG	3057	
DB	878	AAGACTCTTAGTGGGACAAACAGGCCAACTCTTATTTCACITTTTCACITGTTTAATCA	819	
QY	3058	TGAAACAAATCTTTATAGATCTGTCTCCTGATGATAAGAGGTTTCAGTCTGTGGAGGAAGA	3117	
DB	818	GGGACGATTTTGTCTGGATCTTGCTCCAGAAGATTAAGAATATACGTCAGTGGAAGAGA	759	
QY	3118	GATGCAAAATPACAGTTTCGAGAGCACAGAGATGAGAGTTCATGCAAGGTGGAACTTTCACACAG	3177	
DB	758	GATGCAAAATPACTATTTCGAGAACACAGAGATGGTGGTAAATGCTGGGGGCATCTTCAACAG	699	
QY	3178	ATACAAATATCTCAAGATTCCAGAAAGTTTGTACACAGAAACTATGGAAGAGATACACTCA	3237	
DB	698	ATCAATGTCAITTCGAATTCAAAAGTTGTCAACAAGAAGTTGAGGAGCGGTTCTGCGCA	639	
QY	3238	CCGGAGAAAAGAAGTTTTCGAAGAAAACCAACACCATGCCAATGAAACGAATGCTATTTTCA	3297	
DB	638	CCGACAGAGAAGTGTCTGAGGAGAATCACACCATCACAAATGAGCGCATGTGTTTCA	579	
QY	3298	TGGGTCTCCTTTTGTGNAATGCAATATTCACAAAGGCTTTGATGAAAGGCATCGGTACAT	3357	
DB	578	TGTTCTCCTTTTCATTAATGCCAATTAATCATAAAGGGTTTGATGAGCGCATGCATACAT	519	
QY	3358	AGGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACCTCTTCCAAAAGCAATCAATA	3417	
DB	518	AGGAGGNAATGTTTGGGCGGGGATTTATTTTGTGAAAACCTCTTCCAAAAGCAACCAATA	459	
QY	3418	TGTATATGGAAATGGAGAGGTAAGTGGGTCTCAGTTTCACAAAGACAGATCTTTGTATCAT	3477	
DB	458	TGTTTATGAAATTTGGAGAGGAACAGGCTGCCCTTACACAAAGGACAGGTTCATGCTATAT	399	

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Query Match	100.0%	Score 3816;	DB 3;	Length 3816;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3816;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	CGCGTGTCTCGCGCGCGGGGCGAGCCGCGGGGGCAGGGAGCCCGAGCGAGGGCGCGG	60		
1	CGCGTGTCTCGCGCGCGGGCAGCGCGGGGGCAGGGAGCCCGAGCGAGGGCGCGG	60		
61	TGGGCGCGGGCCATGGGACTCGCGCGGATCCGGTGACAGCAGGGAGCCCAAGCGGCCGGG	120		
61	TGGGCGCGGGCCATGGGACTCGCGCGGATCCGGTGACAGCAGGGAGCCCAAGCGGCCGGG	120		
121	CCCTGAGCGCGTCTTCTCGGGGGGCGCTCGCCCTCTGCTCGGGGGCGCGGGCTCTCTG	180		
121	CCCTGAGCGCGTCTTCTCGGGGGGCGCTCGCCCTCTGCTCGGGGGCGCGGGCTCTCTG	180		
181	TCCGTTTCTGCGCGCTGTTGCTGTGGCGTGTGGGCGGGCCAGGATCATGTCCGGTTCGGCG	240		
181	TCCGTTTCTGCGCGCTGTTGCTGTGGCGTGTGGGCGGGCCAGGATCATGTCCGGTTCGGCG	240		
241	CGCGCGGGGGGAGCGGCCTCTCGCGAGCGCGCGGGCCGAGGCCGTGGAGCGCGGCCGCC	300		

Db 241 GCGCCGCGGGGAGCGCGCTGCGCGAGCGCGCGCGCGGCGCGTGGAGCGCGCGCC 300
Qy 301 GAGAGCTGTTTCGAGGCGTCCGCGAACCGGGGACGTGGAAACGAGTCAAGAGCGTGGTGA 360
Db 301 GAGAGCTGTTTCGAGGCGTCCGCGAACCGGGGACGTGGAAACGAGTCAAGAGCGTGGTGA 360
Qy 361 CTGAGAAAGGTGAACAGCGCGGACAGCGCGGGGAGGAAATCCACCCCGCTGCACCTTCGCCG 420
Db 361 CTGAGAAAGGTGAACAGCGCGGACAGCGCGGGGAGGAAATCCACCCCGCTGCACCTTCGCCG 420
Qy 421 CAGGTTTTGGCGGAAAGAGCTAGTTCGAATATTTGCTTCAGAAATGGTGCAAAATGTCGAAG 480
Db 421 CAGGTTTTGGCGGAAAGAGAGCTAGTTCGAATATTTGCTTCAGAAATGGTGCAAAATGTCGAAG 480
Qy 481 CAGGTGATGATGGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGTCAATGCTGAAG 540
Db 481 CAGGTGATGATGGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGTCAATGCTGAAG 540
Qy 541 TAGTCAATCTCTTTTGGGACATGGTGAGACCCCAATGCTCGAGATAAATGGAAATATA 600
Db 541 TAGTCAATCTCTTTTGGGACATGGTGAGACCCCAATGCTCGAGATAAATGGAAATATA 600
Qy 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTGCAATGCTGTGTTACAGC 660
Db 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTGCAATGCTGTGTTACAGC 660
Qy 661 ATGGAGCTGAGCCCAACCATCCGAATACAGATGGAAGGACAGACATTTGATTTAGCAGATC 720
Db 661 ATGGAGCTGAGCCCAACCATCCGAATACAGATGGAAGGACAGACATTTGATTTAGCAGATC 720
Qy 721 CATCTGCAAGCAGTGGCTTACTGGTGAATATAGAAAGATGAATCTCTTAGAAAGTGCCA 780
Db 721 CATCTGCAAGCAGTGGCTTACTGGTGAATATAGAAAGATGAATCTCTTAGAAAGTGCCA 780
Qy 781 GGAGTGCATGAAGAAAGATGATGCTTACTCACACATTAATGTCACACTGCCACG 840
Db 781 GGAGTGCATGAAGAAAGATGATGCTTACTCACACATTAATGTCACACTGCCACG 840
Qy 841 CAAGTGTGCGAGAAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGA 900
Db 841 CAAGTGTGCGAGAAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGA 900
Qy 901 TTGTACAGCTGTTACTGCAACATGAGCTGATGCTTCAATGATGAAGTAAAGAGTGAATCGG 960
Db 901 TTGTACAGCTGTTACTGCAACATGAGCTGATGCTTCAATGATGAAGTAAAGAGTGAATCGG 960
Qy 961 TACCATTACACAATGCTGTTCTTATGTCATATGATGAAGTAAAGTGAATGTTGTCGAAGC 1020
Db 961 TACCATTACACAATGCTGTTCTTATGTCATATGATGAAGTAAAGTGAATGTTGTCGAAGC 1020
Qy 1021 ATGTGCTGTTGTAATGCAATGGAATTTGGCAATTCACCTCTTTCATGAGGAGCTT 1080
Db 1021 ATGTGCTGTTGTAATGCAATGGAATTTGGCAATTCACCTCTTTCATGAGGAGCTT 1080
Qy 1081 CTAAGAACAGGTTGAAGTATGTTCTCTCTTAAAGTATGTTGTCAGACCCACACTGC 1140
Db 1081 CTAAGAACAGGTTGAAGTATGTTCTCTCTTAAAGTATGTTGTCAGACCCACACTGC 1140
Qy 1141 TCAATTCGCAATTAAGTGTATAGACTTGGCTCCACACACACAGTAAAGAAAGAT 1200
Db 1141 TCAATTCGCAATTAAGTGTATAGACTTGGCTCCACACACAGTAAAGAAAGAT 1200
Qy 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAGCTGATGTTACTC 1260
Db 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAGCTGATGTTACTC 1260
Qy 1261 GAATCAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCTCAACACATGAAA 1320
Db 1261 GAATCAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCTCAACACATGAAA 1320
Qy 1321 CAGCATTTGCTGCTGCTCATCTCCATATCCAAAAGAACAAATATGTCGAATG 1380
Db 1321 CAGCATTTGCTGCTGCTCATCTCCATATCCAAAAGAACAAATATGTCGAATG 1380

Qy 1381 TGCTAAGAAAAGGAGCAACATCAATGAAGAAAGACTAAAGAAATTTCTTGACTCCTCTGCACG 1440
Db 1381 TGCTAAGAAAAGGAGCAACATCAATGAAGAAAGACTAAAGAAATTTCTTGACTCCTCTGCACG 1440
Qy 1441 TGGCATCTGAGAAAGCTCATAATGATGTTGCTGAAGTAGTGGTGAACATGAAGCAAGG 1500
Db 1441 TGGCATCTGAGAAAGCTCATAATGATGTTGCTGAAGTAGTGGTGAACATGAAGCAAGG 1500
Qy 1501 TTAATGCTCTGGATAATCTTTGGT CAGACTTCTCTACACAGAGCTGCATATTTGGTCAATC 1560
Db 1501 TTAATGCTCTGGATAATCTTTGGT CAGACTTCTCTACACAGAGCTGCATATTTGGTCAATC 1560
Qy 1561 TACAACCTGCCCGCTACTCCTGAGCTATGGGTGATCTCTAACAATTTATATCCCTTCAGG 1620
Db 1561 TACAACCTGCCCGCTACTCCTGAGCTATGGGTGATCTCTAACAATTTATATCCCTTCAGG 1620
Qy 1621 GCCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGATATCT 1680
Db 1621 GCCTTTACTGCTTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGATATCT 1680
Qy 1681 CATTAGGTAAATTCAGAGGCAAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGCG 1740
Db 1681 CATTAGGTAAATTCAGAGGCAAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGCG 1740
Qy 1741 AAATGTAATAAAAACTGTGTACTGTTCCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1800
Db 1741 AAATGTAATAAAAACTGTGTACTGTTCCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1800
Qy 1801 AGTCTACACCACTTCATTTTTCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGC 1860
Db 1801 AGTCTACACCACTTCATTTTTCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGC 1860
Qy 1861 TACAGCATGGAGCTGATGTCATCTAAAGATAAAGAGGCTTGTACCTTTGCACAATG 1920
Db 1861 TACAGCATGGAGCTGATGTCATCTAAAGATAAAGAGGCTTGTACCTTTGCACAATG 1920
Qy 1921 CATGTTCTTATGACATTAATGAAGTTGCAGAACTTCTTGTGTTAAACATGGAGCAGTAGTTA 1980
Db 1921 CATGTTCTTATGACATTAATGAAGTTGCAGAACTTCTTGTGTTAAACATGGAGCAGTAGTTA 1980
Qy 1981 ATGTAGCTGATTTATGAAATTTTACACTTTTACATGAAGCAGACGCAAAAGGAAATATG 2040
Db 1981 ATGTAGCTGATTTATGAAATTTTACACTTTTACATGAAGCAGACGCAAAAGGAAATATG 2040
Qy 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGA 2100
Db 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGA 2100
Qy 2101 ATACTCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2160
Db 2101 ATACTCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2160
Qy 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTT 2220
Db 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTT 2220
Qy 2221 CTCTCTGATAATGTAATTTGCGCGATACCCCAAGGACAGATTTCAACACCTTTACATTTAG 2280
Db 2221 CTCTCTGATAATGTAATTTGCGCGATACCCCAAGGACAGATTTCAACACCTTTACATTTAG 2280
Qy 2281 CAGCTGTTATTAATTTTAAAGTTGACAGATATTTGTTTACACACGAGGCTGATGTA 2340
Db 2281 CAGCTGTTATTAATTTTAAAGTTGACAGATATTTGTTTACACACGAGGCTGATGTA 2340
Qy 2341 ATGCCCAAGCAAAAGGAGGACTTATCTCTTTTACATAATGAGCATCTTACGGGCATGTAG 2400
Db 2341 ATGCCCAAGCAAAAGGAGGACTTATCTCTTTTACATAATGAGCATCTTACGGGCATGTAG 2400
Qy 2401 ATGTAGCAGCTCTACTAATAAAGTATTAATGATGTGTAATGCCACGGAATAATGGGCTT 2460
Db 2401 ATGTAGCAGCTCTACTAATAAAGTATTAATGATGTGTAATGCCACGGAATAATGGGCTT 2460

QY 361 CTGAGAGGTGAACAGCGCGGACACGGGGGCGAGAAATCCACCCCGTGCACCTTCGCCG 420
DB 361 CTGAGAGAGGTGAACAGCGCGGACACGGGGGCGAGAAATCCACCCCGTGCACCTTCGCCG 420
QY 421 CAGGTTTTGGGCGGAAAGACCTAGTTGAATATTTGCTTCAGAATGGTGCAAAATGTCCTCAAG 480
DB 421 CAGGTTTTGGGCGGAAAGACCTAGTTGAATATTTGCTTCAGAATGGTGCAAAATGTCCTCAAG 480
QY 481 CACGTGATGATGGGGGCTTTATTCCTCTTTCATAAATGCAATGCTCTTTGGTCAATGCTGAAG 540
DB 481 CACGTGATGATGGGGGCTTTATTCCTCTTTCATAAATGCAATGCTCTTTGGTCAATGCTGAAG 540
QY 541 TAGTCAATCTCTTTTGGGACATGGTGAGACCCCAATGCTTCGAGATAATTTGGAATTTATA 600
DB 541 TAGTCAATCTCTTTTGGGACATGGTGAGACCCCAATGCTTCGAGATAATTTGGAATTTATA 600
QY 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATTTTGCATTTGCTGTTCACAGC 660
DB 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATTTTGCATTTGCTGTTCACAGC 660
QY 661 ATGGAGCTGAGCCCAACCATCCGAATAACAGATGGAAGGACAGCAATGGATTTAGCAGATC 720
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RESULT 3
US-09-972-115A-5
; Sequence 5, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4275
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(3781)
; OTHER INFORMATION:
US-09-972-115A-5

Query Match 99.4%; Score 3791.4; DB 3; Length 4275;
Best Local Similarity 99.8%; Pred No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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61 TGGGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
121 TGGGCGCGCG - CCATGGGAGCTCGCGCGGATCGCGGAGGAGGAGGAGGAGGAGGAGGAG 179
121 CCCTCAGCGCGCTTCTCTCGGCGCGCGCTCGCGCTCTCTGCTCGCGGCGCGCGCGCTCTCTG 180
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181 TCCGCTGCTGCGCGCTGTTGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
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241 GCG 300
300 GCG 359
301 GAGAGCTGTTGAGGCGCTGCG 360
360 GAGAGCTGTTGAGGCGCTGCG 419
361 CTGAGAAGGTGAACAGCG 420

Db 420 CTGAGAGGTGAA CAGCGCGACACGGGGGCGAGGAAATCCACCCGCTGCACCTTCGCG 479
Qy 421 CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCGAAG 480
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Qy 2521 CCCATGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAAACCTTTAGATTAGTTT 2580
Db 2580 CCCATGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAAACCTTTAGATTAGTTT 2639

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Qy	2641	GTTTACAAGCCCTCAAGTGCCTCAATGGTGTGAGAAAGCCAGGAGCCACTGACAGATGCTCTCT	2700
Db	2700	GTTTACAAGCCCTCAAGTGCCTCAATGGTGTGAGAAAGCCAGGAGCCACTGACAGATGCTCTCT	2759
Qy	2701	CTTCAGGTCCATCTAGGCCCATCAAGCCCTTTCTGCAGCCAGCAGTCTTTGACAACTTATCTG	2760
Db	2760	CTTCAGGTCCATCTAGGCCCATCAAGCCCTTTCTGCAGCCAGCAGTCTTTGACAACTTATCTG	2819
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Db	2820	GGAGTTTTTCAGAACTGTCTTCAGTAGTGTAGTTTCAAGTGGAAACAGAGGTGCTTCCAGTT	2879
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Db	2940	GACTTTGAGCACCTAATGGATATATTTTCAGAGAGAAACAGATCACTTTTGGATGTATTAGTTG	2999
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Qy	3001	TAATTAAGAGGTCGAGAGCTTATCTCCGGACAACAGGTCCTTACCCTATTTTAACTT	3060
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Qy	3121	AGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTCTGAGAGCAACAGAGATGGAGGTCATGCAG	3180
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Qy	3181	GTGGAACTCTCAACAGATACAATATTTCTCAAGATTCAAGAGTTCTGTAACAAGAACTAT	3240
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Qy	3301	AACGAATGCTATTTTCATGGGTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATG	3360
Db	3360	AACGAATGCTATTTTCATGGGTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATG	3419
Qy	3361	AAAGGCATGGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACCTCTT	3420
Db	3420	AAAGGCATGGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACCTCTT	3479
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Db	3480	CCAAAAGCAATCAATATGTATATGGAATTTGGAGGAGTACTGGGTGTCCAGTTTCAACAAG	3539
Qy	3481	ACAGATCTTGTTACATTTGGCCACAGGAGCTGCTCTTTTCCGGGTAAACCTTGGGAAAGT	3540
Db	3540	ACAGATCTTGTTACATTTGGCCACAGGAGCTGCTCTTTTCCGGGTAAACCTTGGGAAAGT	3599
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Qy	3601	CTGGTAGGCCAGTGTAATGGCCCTAGCATTTAGCTGGAATATGTTTATTTTACAGAGGAGAAC	3660
Db	3660	CTGGTAGGCCAGTGTAATGGCCCTAGCATTTAGCTGGAATATGTTTATTTTACAGAGGAGAAC	3719
Qy	3661	AGGCTTATCTCTGAGTATTTAAATTAATCTTACCAGATTTATGAGGCCCTGGAAGTATGGTCGATG	3720

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Db      3720  AGGCTTATCTGAGTATTTAATTACTTACAGATTTATGAGCCCTGAAGGTATGTCGATG 3779
Qy      3721  GATAAAATAGTATTATTAAAGAAACTAAATTCACACTGAACCTAAAATCATCAAGACGACGATG 3780
Db      3780  GATAAAATAGTATTATTAAAGAAACTAAATTCACACTGAACCTAAAATCATCAAGACGACGATG 3839
Qy      3781  GCCTCTACGTTTACTCTCTTTCGTGAAAAAAA 3813
Db      3840  GCCTCTACGTTTACTCTCTTTCGTGAAAAAAA 3872

RESULT 4
US-09-849-602-11
; Sequence 11, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseung
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 6018
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-602-11

Query Match      99.3%; Score 3788.4; DB 3; Length 6018;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3803; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Query Match 99.3%; Score 3788.4; DB 3; Length 6018;

Qy	544	TCATCTCCTTTTGGGACATGGTCGAGACCCCAATGCTCGAGATAATTGGNAATTATATCTC	603
Ds	540	TCAATCTCCTTTTGGGACATGGTCGAGACCCCAATGCTCGAGATAATTGGNAATTATATCTC	599
Qy	604	CTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTTGTCATTGTGCTGTACAGCATG	663
Ds	600	CTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTTGTCATTGTGCTGTACAGCATG	659
Qy	664	GAGCTGAGCCAAACATCCGAAATAACAGATGAAGGACAGCATTTGGATTTAGCAGATCCAT	723
Ds	660	GAGCTGAGCCAAACATCCGAAATAACAGATGAAGGACAGCATTTGGATTTAGCAGATCCAT	719
Qy	724	CTGCCAAGCAGTCTTACTGGTCAATATAGAAAGATGAACCTTTAGAAAGTCCAGGA	783
Ds	720	CTGCCAAGCAGTCTTACTGGTCAATATAGAAAGATGAACCTTTAGAAAGTCCAGGA	779
Qy	784	GTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATGTCAACTGCCACGCCAA	843
Ds	780	GTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATGTCAACTGCCACGCCAA	839
Qy	844	GTGATGGCAGAAAGTCAACTCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGATTG	903
Ds	840	GTGATGGCAGAAAGTCAACTCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGATTG	899
Qy	904	TACAGCTGTACTGCCAATGAGCTGATGCTCCATGCTTAAGATTAAGGTGATCTGGTAC	963
Ds	900	TACAGCTGTACTGCCAATGAGCTGATGCTCCATGCTTAAGATTAAGGTGATCTGGTAC	959
Qy	964	CATTACCAATGCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAGCATG	1023
Ds	960	CATTACCAATGCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAGCATG	1019
Qy	1024	GTGCTGTGTAATGCAATGGAATGTTGGCAATTCATCTCTTTTCATGAGCAGCTTCTA	1083
Ds	1020	GTGCTGTGTAATGCAATGGAATGTTGGCAATTCATCTCTTTTCATGAGCAGCTTCTA	1079
Qy	1084	AGAACGGTTGAAGTATGTTCTTCTCTTAAAGTTATGGTGACAGCCCAACATGCTCA	1143
Ds	1080	AGAACGGTTGAAGTATGTTCTTCTCTTAAAGTTATGGTGACAGCCCAACATGCTCA	1139
Qy	1144	ATTGTCACAATAAAGTGCTATAGACTTTGGCTCCCAACACAGTTAAAGAAAGATTAG	1203
Ds	1140	ATTGTCACAATAAAGTGCTATAGACTTTGGCTCCCAACACAGTTAAAGAAAGATTAG	1199
Qy	1204	CATATGAATTTAAAGGCCACTGTTGTGTCGAAGCTGCAACAGAAAGTGAATTTACTGAA	1263
Ds	1200	CATATGAATTTAAAGGCCACTGTTGTGTCGAAGCTGCAACAGAAAGTGAATTTACTGAA	1259
Qy	1264	TCAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCTCTCAACACATGAAACAG	1323
Ds	1260	TCAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCTCTCAACACATGAAACAG	1319
Qy	1324	CATTGCAATTTGCTGCTGCATCTCCATATCCAAAAAGCAAAATATGTGAATCTGTC	1383
Ds	1320	CATTGCAATTTGCTGCTGCATCTCCATATCCAAAAAGCAAAATATGTGAATCTGTC	1379
Qy	1384	TAAGAAAGGAGCAAAACATCAATGAAAGACTAAAGAAATTTTGAATCTGCACTGG	1443
Ds	1380	TAAGAAAGGAGCAAAACATCAATGAAAGACTAAAGAAATTTTGAATCTGCACTGG	1439
Qy	1444	CATCTGAGAAAGCTCATATGATCTGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1503
Ds	1440	CATCTGAGAAAGCTCATATGATCTGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1499
Qy	1504	ATGCTCTGGATAATCTTGGGTGAGACTTCTCTACACAGAGCTGCAATTTGGTGCATCTAC	1563
Ds	1500	ATGCTCTGGATAATCTTGGGTGAGACTTCTCTACACAGAGCTGCAATTTGGTGCATCTAC	1559
Qy	1564	AAACCTCGCCCTACTCTCTGAGCTATGGGTGATCCTTAACATTTATCTCCCTTCAGGGCT	1623
Ds	1560	AAACCTCGCCCTACTCTCTGAGCTATGGGTGATCCTTAACATTTATCTCCCTTCAGGGCT	1619
Qy	1624	TTACTGCTTTTACAGATGGGAATGAAATGTAACAGCACTCTCTCAAGAGGGTATCTCAT	1683

Ds	1620	TTACTGCTTTTACAGATGGGAATGAAATGTACAGCACTCTCTCAAGAGGGTATCTCAT	1679
Qy	1684	TAGGTAAATTCAGAGGACAGACAATTTGCTGGAAGCTGCAAGGGCTGGAGATGTGAAA	1743
Ds	1680	TAGGTAAATTCAGAGGACAGACAATTTGCTGGAAGCTGCAAGGGCTGGAGATGTGAAA	1739
Qy	1744	CTGTAAAAAACTGTGTACTGTTTCAGAGTCTCAACTGCAGAGACATTTGAAGGGGCTCAGT	1803
Ds	1740	CTGTAAAAAACTGTGTACTGTTTCAGAGTCTCAACTGCAGAGACATTTGAAGGGGCTCAGT	1799
Qy	1804	CTACACCACCTTCAATTTTGACAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCTAC	1863
Ds	1800	CTACACCACCTTCAATTTTGACAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCTAC	1859
Qy	1864	AGCATGGAGCTGATGTCATGCTTAAAGATAAAGAGAGCCCTTGTACCTTTGCACAATGCAT	1923
Ds	1860	AGCATGGAGCTGATGTCATGCTTAAAGATAAAGAGAGCCCTTGTACCTTTGCACAATGCAT	1919
Qy	1924	GTTCTTATGACACATTAAGATTGCAAGTCTTCTTGTAAACATGGAGCAGTATGTTAATG	1983
Ds	1920	GTTCTTATGACACATTAAGATTGCAAGTCTTCTTGTAAACATGGAGCAGTATGTTAATG	1979
Qy	1984	TAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATATGAAA	2043
Ds	1980	TAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATATGAAA	2039
Qy	2044	TTTGCAAAACCTTCTGCCAGCATGGTGACAGCCCTACCAAAAAAAGAGGATGGAATA	2103
Ds	2040	TTTGCAAAACCTTCTGCCAGCATGGTGACAGCCCTACCAAAAAAAGAGGATGGAATA	2099
Qy	2104	CTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTCTTAGGGGAGATG	2163
Ds	2100	CTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTCTTAGGGGAGATG	2159
Qy	2164	CAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAAGTTGTTCTC	2223
Ds	2160	CAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAAGTTGTTCTC	2219
Qy	2224	CTGATAAATGTAATTCGCCGATACCCAGGACAGACATCAACACCTTTACATTTAGCAG	2283
Ds	2220	CTGATAAATGTAATTCGCCGATACCCAGGACAGACATCAACACCTTTACATTTAGCAG	2279
Qy	2284	CTGGTTATATTAATTTAGAAAGTTGCAAGTATTTGTTTACCAACAGGAGCTGATGTAATG	2343
Ds	2280	CTGGTTATATTAATTTAGAAAGTTGCAAGTATTTGTTTACCAACAGGAGCTGATGTAATG	2339
Qy	2344	CCCAAGACAAAAGGAGGACTTTATTCCTTTTACATTAATGCAGCATCTTACGGGCATGTAGATG	2403
Ds	2340	CCCAAGACAAAAGGAGGACTTTATTCCTTTTACATTAATGCAGCATCTTACGGGCATGTAGATG	2399
Qy	2404	TAGCAGCTCTCTAATAAAGTATAATGTCATGTGTCATGTCACGGACAAATGGGCTTTCA	2463
Ds	2400	TAGCAGCTCTCTAATAAAGTATAATGTCATGTGTCATGTCACGGACAAATGGGCTTTCA	2459
Qy	2464	CACCTTTGACGAGCAGCCCAAGGAGCAACACAGCTTTTGTGCTTAGCCCC	2523
Ds	2460	CACCTTTGACGAGCAGCCCAAGGAGCAACACAGCTTTTGTGCTTAGCCCC	2519
Qy	2524	ATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAAACCTTTAGATTTAGTTTTCAG	2583
Ds	2520	ATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAAACCTTTAGATTTAGTTTTCAG	2579
Qy	2584	CGGATGATGTACGGCTCTTCTGACAGCAGCATGCCCCCATCTGCTCGCCCTCTTGT	2643
Ds	2580	CAGATGATGTACGGCTCTTCTGACAGCAGCATGCCCCCATCTGCTCGCCCTCTTGT	2639
Qy	2644	ACAAGCCTCAAGTCTCAATGTTGAGAGCCAGGAGCCACTGCGAGATGCTCTCTCT	2703
Ds	2640	ACAAGCCTCAAGTCTCAATGTTGAGAGCCAGGAGCCACTGCGAGATGCTCTCTCT	2699
Qy	2704	CAGTCTCATCTAGCCCCATCAAGCCTTTCTGACGCGCAGCAGTCTTGACAACCTTATCTGGGA	2763

Db 2700 CAGGTCCATCTAGCCCATCAAGCCCTTTCTGCAGCCAGCAGCTTTCACAACTTATCTCGGA 2759
 Qy 2764 GTTTTTCAGAACTGCTCTTCAGTAGTTAGTTCAGGTGGAACAGAGGCTTCTCCAGTTGG 2823
 Db 2760 GTTTTTCAGAACTGCTCTTCAGTAGTTAGTTCAGGTGGAACAGAGGCTTCTCCAGTTGG 2819
 Qy 2824 AGAAAAAGGAGGTTCCAGGAGTAGATTTTTCAGTAACTCAATTCGTAAAGGAATCTTGGAC 2883
 Db 2820 AGAAAAAGGAGGTTCCAGGAGTAGATTTTTCAGTAACTCAATTCGTAAAGGAATCTTGGAC 2879
 Qy 2884 TTGAGCCTAATAGATATATTTAGAGAGAACAGATCACTTTGATGTATTTAGTTGAGA 2943
 Db 2880 TTGAGCCTAATAGATATATTTAGAGAGAACAGATCACTTTGATGTATTTAGTTGAGA 2939
 Qy 2944 TGGGGCACAAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAACTAA 3003
 Db 2940 TGGGGCACAAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAACTAA 2999
 Qy 3004 TTAAGGAGTCGAGAGACTTATCTCCGGACAAAGAGTCTTAACCCATATTTAACTTTGA 3063
 Db 3000 TTAAGGAGTCGAGAGACTTATCTCCGGACAAAGAGTCTTAACCCATATTTAACTTTGA 3059
 Qy 3064 ACACCTCTGTTAGTGAACAAATCTTATAGATCTGCTCTCTGATGATTAAGAGTTTCAGT 3123
 Db 3060 ACACCTCTGTTAGTGAACAAATCTTATAGATCTGCTCTCTGATGATTAAGAGTTTCAGT 3119
 Qy 3124 CTGTGGAGAGAGATGCAAGTAGTCAAGTTTCGAGACACAGAGATGGAGTCAATGCAAGTG 3183
 Db 3120 CTGTGGAGAGAGATGCAAGTAGTCAAGTTTCGAGACACAGAGATGGAGTCAATGCAAGTG 3179
 Qy 3184 GAATCTTCAACAGATACAAATTTCTCAAGATTTCAGAGTTTGTAAAGAACTATATGGG 3243
 Db 3180 GAATCTTCAACAGATACAAATTTCTCAAGATTTCAGAGTTTGTAAAGAACTATATGGG 3239
 Qy 3244 AAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAACACAAACATGCAATGAAC 3303
 Db 3240 AAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAACACAAACATGCAATGAAC 3299
 Qy 3304 GAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTCATGAAA 3363
 Db 3300 GAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTCATGAAA 3359
 Qy 3364 GGCATGCTACATAGTGGTATGTTTGGAGTGGCAATTTATTTGCTGAAACCTTCTCCA 3423
 Db 3360 GGCATGCTACATAGTGGTATGTTTGGAGTGGCAATTTATTTGCTGAAACCTTCTCCA 3419
 Qy 3424 AAAGCAATCAATATGATATGGAATTTGAGAGAGTACTGGGTGTCAGTTTCAAAAGACA 3483
 Db 3420 AAAGCAATCAATATGATATGGAATTTGAGAGAGTACTGGGTGTCAGTTTCAAAAGACA 3479
 Qy 3484 GATCTTTGTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTCTT 3543
 Db 3480 GATCTTTGTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTCTT 3539
 Qy 3544 TCCTGCACTCAGTGCATTAAGAAATGGCAATTTCTCTCCAGGTCACTCACTCAGTCACTG 3603
 Db 3540 TCCTGCACTCAGTGCATTAAGAAATGGCAATTTCTCTCCAGGTCACTCACTCAGTCACTG 3599
 Qy 3604 GTAGCCCAAGTGAATGGCCTAGCAATTTAGCTGAATATGTTATTTACAGAGAGAACAGG 3663
 Db 3600 GTAGCCCAAGTGAATGGCCTAGCAATTTAGCTGAATATGTTATTTACAGAGAGAACAGG 3659
 Qy 3664 CTTATCTCTAGTATTTATTTATTTACAGATTTATGAGGCTTGAAGTATGCTCGATGAT 3723
 Db 3660 CTTATCTCTAGTATTTATTTATTTATTTACAGATTTATGAGGCTTGAAGTATGCTCGATGAT 3719
 Qy 3724 AAATAGTTATTTTAAAGAACTAAATTTCCACTGAACCTTAAATCATCAAGAGCAGTGGCC 3783
 Db 3720 AAATAGTTATTTTAAAGAACTAAATTTCCACTGAACCTTAAATCATCAAGAGCAGTGGCC 3779
 Qy 3784 TCTAGTTTTTACTCTCTTTGCTGAAAAAAA 3813
 Db 3780 TCTAGTTTTTACTCTCTTTGCTGAAAAAAA 3809

RESULT 5
 US-09-799-451-556
 ; Sequence 556, Application US/09799451
 ; Patent No. 6783969
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Asundl, Vinod
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Ma, Yundong
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 803
 ; CURRENT APPLICATION NUMBER: US/09/799,451
 ; CURRENT FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 948
 ; SOFTWARE: pt FL_genes Version 2.0
 ; SEQ ID NO 556
 ; LENGTH: 5075
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (253)..(3750)
 US-09-799-451-556

Query Match 98.8%; Score 3770.8; DB 3; Length 5075;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 3800; Conservative 0; Mismatches 12; Indels 2; Gaps 2;
 Qy 1 CGCGCTCTCG 60
 Db 29 CGCGCTCTCTCG 88
 Qy 61 TGGGCG 120
 Db 89 TGGGCG 147
 Qy 121 CCCTGAGCGCGCTCTTCTCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 179
 Db 148 CCCTGAGCGCGCTCTTCTCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 207
 Qy 180 CTCCGGTTGCTGGCGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239
 Db 208 CTCCGGTTGCTGGCGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 267
 Qy 240 TGGCG 299
 Db 268 TGGCG 327
 Qy 300 CGAGAGCTGTTTCGAGGCGTCCGCAACCGGAGCGTGGAAACGAGTCAAGAGGCTGCTGACG 359
 Db 328 CGAGAGCTGTTTCGAGGCGTCCGCAACCGGAGCGTGGAAACGAGTCAAGAGGCTGCTGACG 387
 Qy 360 CCTGAGAGGTTGAACAGCGCGGACACCGCGCGGAGGAAATCCACCCGCTGCACCTTCGCC 419
 Db 388 CCTGAGAGGTTGAACAGCGCGGACACCGCGCGGAGGAAATCCACCCGCTGCACCTTCGCC 447

QY 420 GCAGGTTTGGCGGGAAGAGCTAGTTGAAATATTTGCTTTCAGATGCTGCAATGTCCAA 479
DB 448 GCAGGTTTGGCGGGAAGAGCTAGTTGAAATATTTGCTTTCAGATGCTGCAATGTCCAA 507
QY 480 GCAGGTTGATGATGGGGCTTATTTCTCTTTCATATGATGCTCTTTTGGTGCATGCTGAA 539
DB 508 GCACTGATGATGGGGCTTATTTCTCTTTCATATGATGCTCTTTTGGTGCATGCTGAA 567
QY 540 GTAGTCAATCTCTTTTGGCGCATGGTGCAGACCCCAATGCTCGAGATAATTTGAAATTAT 599
DB 568 GTAGTCAATCTCTTTTGGCGACATGGTGCAGACCCCAATGCTCGAGATAATTTGAAATTAT 627
QY 600 ACTCTCTCCATGAAGCTGCATTAATAAGGAAGATTGATGTTTGCATGCTGCTTTACAG 659
DB 628 ACTCTCTCCATGAAGCTGCATTAATAAGGAAGATTGATGTTTGCATGCTGCTTTACAG 687
QY 660 CATGAGCTGAGCCAAACATCCGAAATACAGATGGAAGGACAGCATTTGGATTATAGCAGAT 719
DB 688 CATGAGCTGAGCCAAACATCCGAAATACAGATGGAAGGACAGCATTTGGATTATAGCAGAT 747
QY 720 CCATCTGCCAAGCAGTCTTTACTGGTGAATATTAAGAAAGATGAACCTTTAGAAAGTGCC 779
DB 748 CCATCTGCCAAGCAGTCTTTACTGGTGAATATTAAGAAAGATGAACCTTTAGAAAGTGCC 807
QY 780 AGGAGTGCATGAAGAAATGATGGCTTACTCTACACCATTTAAATGTCAACTGCCAC 839
DB 808 AGGAGTGCATGAAGAAATGATGGCTTACTCTACACCATTTAAATGTCAACTGCCAC 867
QY 840 GCAAGTGAAGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAG 899
DB 868 GCAAGTGAAGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAG 927
QY 900 ATTGTACAGCTGTTTACTGCAACATGAGAGCTGATGCTCAATGCTTAAAGATAAAGTGATCTG 959
DB 928 ATTGTACAGCTGTTTACTGCAACATGAGAGCTGATGCTCAATGCTTAAAGATAAAGTGATCTG 987
QY 960 GTACCATTTACATGATGCTGTTCTTATGGTCATTTATGAAATGAACCTTTTGGTCAAG 1019
DB 988 GTACCATTTACATGATGCTGTTCTTATGGTCATTTATGAAATGAACCTTTTGGTCAAG 1047
QY 1020 CATGGTGCTGTGTAATGCAATGGAGCTTGTGGCAATTCACCTCTTCATGAGGCAGCT 1079
DB 1048 CATGGTGCTGTGTAATGCAATGGAGCTTGTGGCAATTCACCTCTTCATGAGGCAGCT 1107
QY 1080 TCTAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAAGTATGCTGAGACCCCAACTG 1139
DB 1108 TCTAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAAGTATGCTGAGACCCCAACTG 1167
QY 1140 CTCAATTTGCATTAAGTGTCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGA 1199
DB 1168 CTCAATTTGCATTAAGTGTCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGA 1227
QY 1200 TTAGCATATGAATTTAAAGGCCATCTGTTGCTGCAAGCTGCAAGAGAGCTGATGTTACT 1259
DB 1228 TTAGCATATGAATTTAAAGGCCATCTGTTGCTGCAAGCTGCAAGAGAGCTGATGTTACT 1287
QY 1260 CGAATCAAAAAACATCTCTCTCTGGAATGTTGAATTTCAAGCATCTCTCAAAACATGAA 1319
DB 1288 CGAATCAAAAAACATCTCTCTCTGGAATGTTGAATTTCAAGCATCTCTCAAAACATGAA 1347
QY 1320 ACAGCATTTGCTGCTGCTGCTATCCATATCCCAAGAAAGCAATATGTTGAAGTCTG 1379
DB 1348 ACAGCATTTGCTGCTGCTGCTATCCATATCCCAAGAAAGCAATATGTTGAAGTCTG 1407
QY 1380 TTGCTTAAGAAAGAGGACAAACATCAATGAAGAAAGCTTAAAGAAATTTCTGACTCTCTGCAC 1439
DB 1408 TTGCTTAAGAAAGAGGACAAACATCAATGAAGAAAGCTTAAAGAAATTTCTGACTCTCTGCAC 1467
QY 1440 GTGGCATCTGAGAAAGCTCATATGATGTTGTTGAAAGTATGTTGTTGAAAGCAAG 1499
DB 1468 GTGGCATCTGAGAAAGCTCATATGATGTTGTTGAAAGTATGTTGTTGAAAGCAAG 1527
QY 1500 GTTAATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGTCATATTTGGTGCAT 1559

DB 1528 GTTAATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGTCATATTTGGTGCAT 1587
QY 1560 CTACAAACCTGCCCGCTACTCTCTGAGCTATGGGTGATCCTTAACATATATCCCTTCAAG 1619
DB 1588 CTACAAACCTGCCCGCTACTCTCTGAGCTATGGGTGATCCTTAACATATATCCCTTCAAG 1647
QY 1620 GGCTTTACTGCTTTTACAGATGGGAATGAAATGTACAGCAATCTCTCCCAAGAGGGTATC 1679
DB 1648 GGCTTTACTGCTTTTACAGATGGGAATGAAATGTACAGCAATCTCTCCCAAGAGGGTATC 1707
QY 1680 TCATTAGTAAATTTACAGAGGACAGACAAATGCTGGAAGCTGCAAAAGGCTGGAGATGTC 1739
DB 1708 TCATTAGTAAATTTACAGAGGACAGACAAATGCTGGAAGCTGCAAAAGGCTGGAGATGTC 1767
QY 1740 GAAACTGTAAAAAACTGTCTACTGTTTACAGAGTGTCAACTGACAGAGACATTTGAAAGGCGT 1799
DB 1768 GAAACTGTAAAAAACTGTCTACTGTTTACAGAGTGTCAACTGACAGAGACATTTGAAAGGCGT 1827
QY 1800 CAGTCTACACCATTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGATATCTG 1859
DB 1828 CAGTCTACACCATTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGATATCTG 1887
QY 1860 CTACAGCATGAGCTGATGTCATGCTTAAAGATAAAGAGGCGCTTGTACCTTTGCACAAT 1919
DB 1888 CTACAGCATGAGCTGATGTCATGCTTAAAGATAAAGAGGCGCTTGTACCTTTGCACAAT 1947
QY 1920 GCATGTTCTTTATGGACATTAATGAAGTTGCAAGACTTCTTCTTAAACATGAGCAGTAGTT 1979
DB 1948 GCATGTTCTTTATGGACATTAATGAAGTTGCAAGACTTCTTCTTAAACATGAGCAGTAGTT 2007
QY 1980 AATGTAGCTGATTTATGGAATTTACACTTTTACATGAAGCAGCAGCAAAAGGAAATAT 2039
DB 2008 AATGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATAT 2067
QY 2040 GAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAAGCAGGATGGA 2099
DB 2068 GAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAAGCAGGATGGA 2127
QY 2100 AATACTCTTTTGGATCTTTTAAAGATGGAAGATACAGATATTCAAGATCTGCTTAGGGGA 2159
DB 2128 AATACTCTTTTGGATCTTTTAAAGATGGAAGATACAGATATTCAAGATCTGCTTAGGGGA 2187
QY 2160 GATGACGCTTTTGTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAGAGCTGTGCT 2219
DB 2188 GATGACGCTTTTGTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAGAGAGTGTGCT 2247
QY 2220 TCTCCTGATTAATGTAAATTTGCCGATACCAGGACAGACATTCACACCTTTTACATTTA 2279
DB 2248 TCTCCTGATTAATGTAAATTTGCCGATACCAGGACAGACATTCACACCTTTTACATTTA 2307
QY 2280 GCAGCTGGTTTATTAATTTTGAAGTTGCAAGATTTGTTTAAACACGAGCTGATGCTG 2339
DB 2308 GCAGCTGGTTTATTAATTTTGAAGTTGCAAGATTTGTTTAAACACGAGCTGATGCTG 2367
QY 2340 AATGCCCAAGACAAAGAGGACCTTATTCCTTTACATAATGACAGCATCTTACGGGCATGTA 2399
DB 2368 AATGCCCAAGACAAAGAGGAGCTTATTCCTTTACATAATGACAGCATCTTACGGGCATGTA 2427
QY 2400 GATGTAGCAGCTCTACTTAATAAAGTATAATGTCATGTCTCAATGCCAGGACAAATGGGCT 2459
DB 2428 GATGTAGCAGCTCTACTTAATAAAGTATAATGTCATGTCTCAATGCCAGGACAAATGGGCT 2487
QY 2460 TTCAACCTTTTGCAGAGAGGCCCAAAAGGGAGCAACACAGCTTTGTGCTTTGTTGCTA 2519
DB 2488 TTCAACCTTTTGCAGAGAGGCCCAAAAGGGAGCAACACAGCTTTGTGCTTTGTTGCTA 2547
QY 2520 GCCCATGGAGCTGACCCGACTCTTAAATAACAGAAAGGACAAACACCTTTAGATTTAGTT 2579
DB 2548 GCCCATGGAGCTGACCCGACTCTTAAATAACAGAAAGGACAAACACCTTTAGATTTAGTT 2607
QY 2580 TCAGCGGATGATGTACGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCT 2639

2608	TCAGCGATGATGTCAGGGCTCTCTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCT	2666
2640	TGTTACAAGCCTCAAGTGCTCAATGSGTGTGAGAGCCCCAGGAGCCACTGAGATGCTCTC	2699
2668	TGTTACAAGCCTCAAGTGCTCAATGSGTGTGAGAGCCCCAGGAGCCACTGAGATGCTCTC	2727
2700	TCCTCAGGTCCATCTAGCCCATCAAGCCCTTCTGCAGCCAGCAGTCTTGACAACCTTAATCT	2759
2728	TCCTCAGGTCCATCTAGCCCATCAAGCCCTTCTGCAGCCAGCAGTCTTGACAACCTTAATCT	2787
2760	GGGAGTTTTTTTCAGAACTGCTCTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTGCTTCCAGT	2819
2788	GGGAGTTTTTTTCAGAACTGCTCTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTGCTTCCAGT	2847
2820	TTGAGAAAAAGGAGGTTCCAGGAGTAGATTTTATAGCAATACTCAATTCGTAAGGAATCTTT	2879
2848	TTGAGAAAAAGGAGGTTCCAGGAGTAGATTTTATAGCAATACTCAATTCGTAAGGAATCTTT	2907
2880	GGACTTGAGCACCTAATGGATATATTTTGAGAGAGAACAGATCACTTTGGATGATATTAAGTT	2939
2908	GGACTTGAGCACCTAATGGATATATTTTGAGAGAGAACAGATCACTTTGGATGATATTAAGTT	2967
2940	GAGATGGGACACAAGGAGCTGAGGAGATTGGAACTAATGCTTATGACATAGGCACAAA	2999
2968	GAGATGGGACACAAGGAGCTGAGGAGATTGGAACTAATGCTTATGACATAGGCACAAA	3027
3000	CTAATTTAAGGAGTCGAGAGACTTATCTCCGGACAAACAAGGCTTTAAACCCATATTTAACT	3059
3028	CTAATTTAAGGAGTCGAGAGACTTATCTCCGGACAAACAAGGCTTTAAACCCATATTTAACT	3087
3060	TTGAACAACCTCTGGTAGTGGAACAATTTCTTTATAGATCTGTCTCTGATGATATAAGGTTT	3119
3088	TTGAACAACCTCTGGTAGTGGAACAATTTCTTTATAGATCTGTCTCTGATGATATAAGGTTT	3147
3120	CAGTCTGTGGAGGAGAGATGCAAAATGACAGTTTCGAGAGCACAGAGATGAGGTCATGCA	3179
3148	CAGTCTGTGGAGGAGAGATGCAAAATGACAGTTTCGAGAGCACAGAGATGAGGTCATGCA	3207
3180	GGTGGAACTCTTCAACAGATACAATATTTCTCAAGATTCAAGAGTTTCTTAAACAAGAACTA	3239
3208	GGTGGAACTCTTCAACAGATACAATATTTCTCAAGATTCAAGAGTTTCTTAAACAAGAACTA	3267
3240	TGGGAAAGATACACTCAACCGAGAAAAAGATTTCTGAAGAAAAACCAACCCATGCCAAT	3299
3268	TGGGAAAGATACACTCAACCGAGAAAAAGATTTCTGAAGAAAAACCAACCCATGCCAAT	3327
3300	GAACGAATGCTATTTTCATGGGTCTCCTTTTGTGAAATGCAATATTCACAAAGGCTTTGAT	3359
3328	GAACGAATGCTATTTTCATGGGTCTCCTTTTGTGAAATGCAATATTCACAAAGGCTTTGAT	3387
3360	GAAGGCAATGCGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCT	3419
3388	GAAGGCAATGCGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCT	3447
3420	TCCAAAAAGCAATCAATATGTATATGTAATTTGGAGGAGGTACTGGGTCTCCAGTTCAAAA	3479
3448	TCCAAAAAGCAATCAATATGTATATGTAATTTGGAGGAGGTACTGGGTCTCCAGTTCAAAA	3507
3480	GACAGATCTTGTTACATTTTGCCACAGCAGCTGCTCTTTTCCGGGTAAACCTTGGGAAAG	3539
3508	GACAGATCTTGTTACATTTTGCCACAGCAGCTGCTCTTTTCCGGGTAAACCTTGGGAAAG	3567
3540	TCTTTCTCGAGTTTCAGTGCAATGAAAAATGGCAATTTCTCTCCAGGTCACTCACTGATC	3599
3568	TCTTTCTCGAGTTTCAGTGCAATGAAAAATGGCAATTTCTCTCCAGGTCACTCACTGATC	3627
3600	ACTGGTAGGCCAGGTGTAATGGCCTTAGCAATAGCTGAATATGTTATTTTACAGAGGAGAA	3659
3628	ACTGGTAGGCCAGGTGTAATGGCCTTAGCAATAGCTGAATATGTTATTTTACAGAGGAGAA	3687
3660	CAGGCTTATCTCGATATTTTAATTAATCTTACAGATATAGGCCCTGAAGGTATGGTGCAT	3719
3688	CAGGCTTATCTCGATATTTTAATTAATCTTACAGATATAGGCCCTGAAGGTATGGTGCAT	3747

Qy	3720	GGATAAATAGTATTTTAAAGAACTAATTCACCTGAACCTTAAATCATCAAGCAGCAGT	3775
Db	3748	GGATAAATAGTATTTTAAAGAACTAATTCACCTGAACCTTAAATCATCAAGCAGCAGT	3807
Qy	3780	GGCTCTACGTTTCTTACTCCTTTCGTGAAAAAAA	3813
Db	3808	GGCTCTACGTTTCTTACTCCTTTCGTGAAAAAAA	3841
RESULT 6			
US-09-350-982C-3			
; Sequence 3, Application US/09350982C			
; Patent No. 6453290			
; GENERAL INFORMATION:			
; APPLICANT: Berthelsen, Jens			
; APPLICANT: Toma, Salvatore			
; APPLICANT: Iacchi, Antonella			
; TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Met			
; TITLE OF INVENTION: Same			
; FILE REFERENCE: PHRM-0043			
; CURRENT APPLICATION NUMBER: US/09/350,982C			
; CURRENT FILING DATE: 1999-07-09			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 3			
; LENGTH: 4512			
; TYPE: DNA			
; ORGANISM: Artificial			
; FEATURE:			
; OTHER INFORMATION: PCR Primers			
; NAME/KEY: misc feature			
; LOCATION: (1124)..(1124)			
; OTHER INFORMATION: n is any nucleic acid			
; NAME/KEY: misc feature			
; LOCATION: (2672)..(2672)			
; OTHER INFORMATION: n is any nucleic acid			
US-09-350-982C-3			
Query Match 94.2%; Score 3594.8; DB 3; Length 4512;			
Best Local Similarity 99.7%; Pred. No. 0;			
Matches 3593; Conservative 6; Mismatches 5; Indels 0; Gaps 0;			
Qy	210	GCAGCGCCAGGATCATGTCGGTTCGCGCGCGCGGGGAGCGGCTTCGCGAGC	269
Db	8	GCAGCGCCAGGATCATGTCGGTTCGCGCGCGCGGGGAGCGGCTTCGCGAGC	67
Qy	270	GCAGCGCCAGGCGGTGGAGCGCGCGCGCGCGAGAGCTGTTTCGAGGCGTCCGCAACGGG	329
Db	68	GCAGCGCCAGGCGGTGGAGCGCGCGCGCGCGAGAGCTGTTTCGAGGCGTCCGCAACGGG	127
Qy	330	GAGGTGAAACGAGTCAAGAGCGGTGTGACGCTTGAGAGGTGAACAGCGCGGACACGCGG	389
Db	128	GAGGTGAAACGAGTCAAGAGCGGTGTGACGCTTGAGAGGTGAACAGCGCGGACACGCGG	187
Qy	390	GGCAGGAAATCCACCCCGCTGCATTCGCGCGAGGTTTCGCGGGAAGACGTAGTTGAA	449
Db	188	GGCAGGAAATCCACCCCGCTGCATTCGCGCGAGGTTTCGCGGGAAGACGTAGTTGAA	247
Qy	450	TATTTGCTTCAGAAATGGTGCAATGTCCAGCAACGCTGATGATGGGGCCCTTATTCCTCTT	509
Db	248	TATTTGCTTCAGAAATGGTGCAATGTCCAGCAACGCTGATGATGGGGCCCTTATTCCTCTT	307
Qy	510	CATAATGCATGCTTTTGGTTCATGCTGAGTAGTCAATCTCTTTTGCACATGGTGCA	569
Db	308	CATAATGCATGCTTTTGGTTCATGCTGAGTAGTCAATCTCTTTTGCACATGGTGCA	367
Qy	570	GACCCCAATGCTCGAGATAATCGAAATTAATCTCCTCCATGAAGCTGCAATTAAGGA	629
Db	368	GACCCCAATGCTCGAGATAATCGAAATTAATCTCCTCCATGAAGCTGCAATTAAGGA	427
Qy	630	AAGATGATGTTTGCAATGTGCTGTTACAGCATGGAGCTGAGCCAAACCATCCGAAATACA	689

Db 428 AAGATTGATGTTTGCATTGTGCTGTTTACAGCATGGAGCTGAGCCACCATCCGGAATACA 487
Qy 690 GATGGAAGGACAGCATTTGGATTTTACAGATCCATCTGCCAAAGCAGTCTTACTTGGTGAA 749
Db 488 GATGGAAGGACAGCATTTGGATTTTACAGATCCATCTGCCAAAGCAGTCTTACTTGGTGAA 547
Qy 750 TATAAGAAAGATGAATCTTTAGAAAGTCCAGGAGTGGCAATGAAGAAAAAATGATGGCT 809
Db 548 TATAAGAAAGATGAATCTTTAGAAAGTCCAGGAGTGGCAATGAAGAAAAAATGATGGCT 607
Qy 810 CTACTCACACCATTAATATGCAATGCCAGCAGTGTATGTCAGAAAGTCAACTCCATT 869
Db 608 CTACTCACACCATTAATATGCAATGCCAGTGTATGTCAGAAAGTCAACTCCATT 667
Qy 870 CATTTGGCAGCAGGATATAACAGAGTAAGATTTGACAGCTGTTTACTGCAACATGGAGCT 929
Db 668 CATTTGGCAGCAGGATATAACAGAGTAAGATTTGACAGCTGTTTACTGCAACATGGAGCT 727
Qy 930 GATGTCCATGCTAAGATTAAGATGATCTGTGTACCATTAACAAATGGCTGTTCTTATGGT 989
Db 728 GATGTCCATGCTAAGATTAAGATGATCTGTGTACCATTAACAAATGGCTGTTCTTATGGT 787
Qy 990 CATTATGAAGTAACTGAACCTTTTGTCAAGCATGCTGCTGTGTAATGCAATGCAATG 1049
Db 788 CATTATGAAGTAACTGAACCTTTTGTCAAGCATGCTGCTGTGTAATGCAATGCAATG 847
Qy 1050 TGGCAATTCACCTCTTTCATGAGCGAGCTTCTAAGAACAGGGTTGAAGTATGTTCTCTT 1109
Db 848 TGGCAATTCACCTCTTTCATGAGCGAGCTTCTAAGAACAGGGTTGAAGTATGTTCTCTT 907
Qy 1110 CTCCTTAAGTTATGTCGAGCCCAACACTGCTCAATTTGTCTCAATTAAGTCTATAGAC 1169
Db 908 CTCCTTAAGTTATGTCGAGCCCAACACTGCTCAATTTGTCAATTAAGTCTATAGAC 967
Qy 1170 TTGGCTCCACACACAGTTAAAGAAAGATTAGCATATGAATTTAAAGGCCACTCGTTG 1229
Db 968 TTGGCTCCACACACAGTTAAAGAAAGATTAGCATATGAATTTAAAGGCCACTCGTTG 1027
Qy 1230 CTGCAAGCTGACAGAGCTGATGTTTACTCGAATCAAAAAACATCTCTCTCGAAATG 1289
Db 1028 CTGCAAGCTGACAGAGCTGATGTTTACTCGAATCAAAAAACATCTCTCTCGAAATG 1087
Qy 1290 GTGAATTTCAAGCATCTTCAAAACATGAACAGCATTTGCAATTTGCTGCTGCAATCCCA 1349
Db 1088 GTGAATTTCAAGCATCTTCAAAACATGAACAGCATTTGCAATTTGCTGCTGCAATCCCA 1147
Qy 1350 TATCCCAAGAAAGCAAAATATGTGAATGTTGCTTAAGAAAGGAGCAACATCAATGAA 1409
Db 1148 TATCCCAAGAAAGCAAAATATGTGAATGTTGCTTAAGAAAGGAGCAACATCAATGAA 1207
Qy 1410 AAGACTAAGAAATCTTTGACTCTCTGACAGTGGCATCTGAGAAAGCTCATATGATGTT 1469
Db 1208 AAGACTAAGAAATCTTTGACTCTCTGACAGTGGCATCTGAGAAAGCTCATATGATGTT 1267
Qy 1470 GTTGAAGTAGTGTGAAACATGAAGCAAGGTTAATGCTCTGGATTAATCTTTGTCAGACT 1529
Db 1268 GTTGAAGTAGTGTGAAACATGAAGCAAGGTTAATGCTCTGGATTAATCTTTGTCAGACT 1327
Qy 1530 TCTCTACACAGAGCTGCATATTTGTTGTTTCTCATCAAAACCTGCGCCCTACTCTCAGCTAT 1589
Db 1328 TCTCTACACAGAGCTGCATATTTGTTGTTTCTCATCAAAACCTGCGCCCTACTCTCAGCTAT 1387
Qy 1590 GGGTGTGATCTTAACATTATATCCCTTCAGGGCTTTTACTGCTTTTACAGATGGGAAATGAA 1649
Db 1388 GGGTGTGATCTTAACATTATATCCCTTCAGGGCTTTTACTGCTTTTACAGATGGGAAATGAA 1447
Qy 1650 AATGTACAGCAATCTCTCCAAAGAGGTTATCTCATTTAGTAAATTCAGAGGCGACAGACAA 1709
Db 1448 AATGTACAGCAATCTCTCCAAAGAGGTTATCTCATTTAGTAAATTCAGAGGCGACAGACAA 1507
Qy 1710 TTGCTGGAGCTGCAGAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTTCAG 1769
Db 1508 TTGCTGGAGCTGCAGAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTTCAG 1567

Qy 1770 AGTGTCAACTGCAGAGACATTGAAGGGCGTCAGTCTACACCACTTCAATTTTGCAGCTGGG 1829
Db 1568 AGTGTCAACTGCAGAGACATTGAAGGGCGTCAGTCTACACCACTTCAATTTTGCAGCTGGG 1627
Qy 1830 TATAACAGAGTGTCCGTGGTGGAAATATCTGCTACAGCATGAGCTGATGTGCATGCTAAA 1889
Db 1628 TATAACAGAGTGTCCGTGGTGGAAATATCTGCTACAGCATGAGCTGATGTGCATGCTAAA 1687
Qy 1890 GATAAAGAGGCGCTTGTACCTTTTGCACAAATGCATGTTCTTATGGACATTAATGAAGTTGCA 1949
Db 1688 GATAAAGRRSSCCTTGTACCTTTTGCACAAATGCATGTTCTTATGACATTAATGAAGTTGCA 1747
Qy 1950 GAATCTCTTCTTTAAAATGAGAGCAGTAGTTAATGTAGTCTGATTTATGGAATTTTACACCT 2009
Db 1748 GAATCTCTTCTTTAAAATGAGAGCAGTAGTTAATGTAGTCTGATTTATGGAATTTTACACCT 1807
Qy 2010 TTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCACATGGT 2069
Db 1808 TTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCACATGGT 1867
Qy 2070 GCAGACCTTACCACAAAAACAGGGATGGAATATACCTTTTGGATCTTGTTTAAAGATGGA 2129
Db 1868 GCAGACCTTACAAAAACAGGGATGGAATATACCTTTTGGATCTTGTTTAAAGATGGA 1927
Qy 2130 GATACAGATATTCAAGATCTGCTTTAGGGAGATGACAGCTTGTAGATGCTGCCAAGAG 2189
Db 1928 GATACAGATATTCAAGATCTGCTTTAGGGAGATGACAGCTTGTAGATGCTGCCAAGAG 1987
Qy 2190 GGTGTTTACCGAGTGAAGAGTTGCTCTCTCTGATTAATGTAAATTTGCCGCGATACC 2249
Db 1988 AGTTGTTTACCGAGTGAAGAGTTGCTCTCTCTGATTAATGTAAATTTGCCGCGATACC 2047
Qy 2250 CAAGGCAGACATTCACACCTTTTACATTTAGCAGCTGGTTATATAATTTAGAAAGTTGCA 2309
Db 2048 CAAGGCAGACATTCACACCTTTTACATTTAGCAGCTGGTTATATAATTTAGAAAGTTGCA 2107
Qy 2310 GAGTATTTTGTACACACGGAGCTGATGAAATGCCCAAGCAAAAGGAGGACTTTATCCT 2369
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Db 2168 TTACATAATGCAGCTTTACGGGCATGTAGATGTAGCAGCTCTACTAAATAAGTATAAT 2227
Qy 2430 GCATGTCTCAATGCCAGCAAAATGGGCTTTTACACCTTTTGCACGAAGCAGCCCAAAAG 2489
Db 2228 GCATGTCTCAATGCCAGCAAAATGGGCTTTTACACCTTTTGCACGAAGCAGCCCAAAAG 2287
Qy 2490 GGAAGCAACAGCTTTTGTGCTTTGCTAGCCCATGGAGCTGACCCGACTCTTTAAAAAT 2549
Db 2288 GGAAGCAACAGCTTTTGTGCTTTGCTAGCCCATGGAGCTGACCCGACTCTTTAAAAAT 2347
Qy 2550 CAGGAAGCAACACCTTTTAGATTTTGTAGTTTACGGCATGTAGTCAAGCTCTTTAAAAAT 2609
Db 2348 CAGGAAGCAACACCTTTTAGATTTTGTAGTTTACGGCATGTAGTCAAGCTCTTTAAAAAT 2407
Qy 2610 GCAGCCATGCCCCCATCTGCTCTGCCCCCTTTTGTATCAAGCTCTCAAGTGTCAAATGGTGTG 2669
Db 2408 GCAGCCATGCCCCCATCTGCTCTGCCCCCTTTTGTATCAAGCTCTCAAGTGTCAAATGGTGTG 2467
Qy 2670 AGAAGCCAGAGGCACTGCAGATGCTCTCTCTTCAAGTCCATAGCCCATCAAGCTT 2729
Db 2468 AGAAGCCAGAGGCACTGCAGATGCTCTCTCTTCAAGTCCATAGCCCATCAAGCTT 2527
Qy 2730 TCTGACCCAGAGCTCTGACAACTTATCTGGGAGTTTTTTCAGAACTGTCTTCAAGTAGTT 2789
Db 2528 TCTGACCCAGAGCTCTGACAACTTATCTGGGAGTTTTTTCAGAACTGTCTTCAAGTAGTT 2587
Qy 2790 AGTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAAGGAGGTTTCCAGGAGTAGAT 2849
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2850 TTTAGCATAACTCAATTCGTAGGAATCTTGGACCTTGACCACTAATGGATATATTGAG 2909
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2910 AGAGAACAGATCACTTTGGATGTTATAGTGTAGATGGGGCAAGAGAGCTGAAGGAGATT 2969
2708 AGAGAACAGATCACTTTGGATGTTATAGTGTAGATGGGGCAAGAGAGCTGAAGGAGATT 2767
2970 GGAATCAATGCTTTAGGACATAGGACCAAACTAATTAAGAGAGTGCAGAGACTTATCTCC 3029
2768 GGAATCAATGCTTTAGGACATAGGACCAAACTAATTAAGAGAGTGCAGAGACTTATCTCC 2827
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2828 GGACAAACAGGCTTTAAACCCATATTTAACTTTTGAACACCTCTGTGTAGTGGAACTTCTT 2887
3090 ATAGATCTGTCTCTGATGATTAAGAGTTTCACTCTGTGTGGAGGAAGAGATGCAAGTACA 3149
2888 ATAGATCTGTCTCTGATGATTAAGAGTTTCACTCTGTGTGGAGGAAGAGATGCAAGTACA 2947
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2948 GTTCGAGAGCACAGAGATGGAGTTCATGCAGTGAATCTTCAACAGATACAATATTTCTC 3007
3210 AAGATTCAAGAGTTTGTAAACAGAACTATGCGGAAAGATACACTCACCGGAGAAAAGAA 3269
3008 AAGATTCAAGAGTTTGTAAACAGAACTATGCGGAAAGATACACTCACCGGAGAAAAGAA 3067
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3068 GTTCTGAGAAACCAACAACATGCCAATGAAATGCTATTTCAATGGGTCTCTTTT 3127
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3128 GTGATGCAATTTATCCAAAGGCTTTCATGAAAGGATGCTGATAGTGGTATGTTT 3187
3390 GGAGCTGCAATTTATTTTGTGAAATCTTCCAAAGCAATCAATATGTATATGGAATT 3449
3188 GGAGCTGCAATTTATTTTGTGAAATCTTCCAAAGCAATCAATATGTATATGGAATT 3247
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3810 AAAA 3813
3608 AAAA 3611

RESULT 7
US-09-350-982C-4
; Sequence 4, Application US/09350982C
; Patent No. 6455290

GENERAL INFORMATION:
; APPLICANT: Berthelsen, Jens
; APPLICANT: Tona, Salvatore
; APPLICANT: Isacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Relat
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primers
; NAME/KEY: CDS
; LOCATION: (1)..(3498)
; NAME/KEY: misc feature
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (1102)..(1102)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (2650)..(2650)
; OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-4

Query Match 91.4%; Score 3488.8; DB 3; Length 3498;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3487; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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QY 285 GTGAGCGCGCGCGCGCGAGAGCTGTTGAGCGGTGCGCAACGGGAGCTGGAAAGAGTC 344
DB 61 GTGAGCGCGCGCGCGCGAGAGCTGTTGAGCGGTGCGCAACGGGAGCTGGAAAGAGTC 120
QY 345 AAGAGGCTGTGAGCGCTGGAAGTGAACAGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 404
DB 121 AAGAGGCTGTGAGCGCTGGAAGTGAACAGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 180
QY 405 CCGCTGCACTTGGCGCGAGGTTTGGCGGGAAGACGCTAGTGAATATTTGCTTCAGAA 464
DB 181 CCGCTGCACTTGGCGCGAGGTTTGGCGGGAAGACGCTAGTGAATATTTGCTTCAGAA 240
QY 465 GGTCAAAATGTCCAAAGCAGCTGATGATGGGGCGCTTATTCCTCTTCAATGCAATGCTCT 524
DB 241 GGTCAAAATGTCCAAAGCAGCTGATGATGGGGCGCTTATTCCTCTTCAATGCAATGCTCT 300
QY 525 TTTGGTCATGCTGAAGTAGTCAATCTCTTTTGGACATGCTGAGAGCGCGCGCGCGCGCG 584
DB 301 TTTGGTCATGCTGAAGTAGTCAATCTCTTTTGGACATGCTGAGAGCGCGCGCGCGCGCG 360
QY 585 GATTAATTTGGAATTTATCTCTCTCCATGAAGCTGCAATTTAAAGAAAGATTTGTTTGC 644
DB 361 GATTAATTTGGAATTTATCTCTCTCTCCATGAAGCTGCAATTTAAAGAAAGATTTGTTTGC 420
QY 645 ATTGTGCTGTTTACAGCATGGAGCTGAGCCAACTCCGAATACAGATGGAAGGACAGCA 704
DB 421 ATTGTGCTGTTTACAGCATGGAGCTGAGCCAACTCCGAATACAGATGGAAGGACAGCA 480
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DB 481 TTGATTTAGCAGATCCATCTGCCAAAGCAGTGTCTTACTTGGTGAATATAAGAAAGATGAA 540
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DB 541 CTCTTAGAAAGTGCAGGAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTA 600

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DB 601 AATGTCAACTGCCACGCAAGTGATGGCAGAAAGTCAACTCCATTACATTGTCGACGAGGA 660
QY 885 TATAACAGAGTAAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCTTAA 944
DB 661 TATAACAGAGTAAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCTTAA 720
QY 945 GATAAAGGTGATCTGGTACCAATTACAAATGCCCTGTTCTTTATGTCATATTAGAGTAACT 1004
DB 721 GATAAAGGTGATCTGGTACCAATTACAAATGCCCTGTTCTTTATGTCATATTAGAGTAACT 780
QY 1005 GAACCTTTTGTCAAGCATGGTCCCTGTGTAAATGCAATGCAATGCAATGTCGCAATTCACCTCT 1064
DB 781 GAACCTTTTGTCAAGCATGGTCCCTGTGTAAATGCAATGCAATGTCGCAATTCACCTCT 840
QY 1065 CTTTCATCAGGCAGCTTCTAAGAACAGAGGTTGAAGTATGTTCTCTCTCTTAAAGTTATGGT 1124
DB 841 CTTTCATCAGGCAGCTTCTAAGAACAGAGGTTGAAGTATGTTCTCTCTCTTAAAGTTATGGT 900
QY 1125 GCAGACCCAAACACTGCTCAATTGTGCACAAATAAAAGTCTATAGACTTGGCTCCACACCA 1184
DB 901 GCAGACCCAAACACTGCTCAATTGTGCACAAATAAAAGTCTATAGACTTGGCTCCACACCA 960
QY 1185 CAGTTAAAGAAAGATTAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAAGCA 1244
DB 961 CAGTTAAAGAAAGATTAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAAGCA 1020
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DB 1021 GAAGCTGATGTTACTCGAATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCAT 1080
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DB 1081 CCTCAAAACACATGAACAGCATTTGCTGCTGCTCATCTCCATATCCCAAAAGAAAG 1140
QY 1365 CAATATGTGAATCTGTTGCTTAAGAAAGGAGCAACATCAATGAAAGACTTAAGAAATTC 1424
DB 1141 CAATATGTGAATCTGTTGCTTAAGAAAGGAGCAACATCAATGAAAGACTTAAGAAATTC 1200
QY 1425 TTGACTCTCTGCAAGCTGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTG 1484
DB 1201 TTGACTCTCTGCAAGCTGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTG 1260
QY 1485 AAAATGAAGCAAAAGGTTAATGCTCTGGAATAATCTTGGTCAGACTTCTTACACAGAGCT 1544
DB 1261 AAAATGAAGCAAAAGGTTAATGCTCTGGAATAATCTTGGTCAGACTTCTTACACAGAGCT 1320
QY 1545 GCATATTTGTGGTCAATCTACAAACCTGCGGCTACTCTCTGAGCTATGGGTGATCCTTAAC 1604
DB 1321 GCATATTTGTGGTCAATCTACAAACCTGCGGCTACTCTCTGAGCTATGGGTGATCCTTAAC 1380
QY 1605 ATTATATCCCTTCAGGCTTTTACTGCTTTTACAGATGGAAATGAAATGTACAGCAACTC 1664
DB 1381 ATTATATCCCTTCAGGCTTTTACTGCTTTTACAGATGGAAATGAAATGTACAGCAACTC 1440
QY 1665 CTCCAAGAGGGTATCTCATAGGTAAATTTACAGGCGACAGACAAATTTGCTGGAAGCTGCA 1724
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DB 1501 AAGGCTGGAGATGTGAAACTGTAAAAAACTGTGTACTGTTTACAGATGTCAACTGCGAGA 1560
QY 1785 GACATTGAAGGGCGTCAAGTCTACACCACTTCATTTTGCAGCTGGGTATACAGAGTGTCC 1844
DB 1561 GACATTGAAGGGCGTCAAGTCTACACCACTTCATTTTGCAGCTGGGTATACAGAGTGTCC 1620
QY 1845 GTGTGGAATATCTGTACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCTTT 1904
DB 1621 GTGTGGAATATCTGTACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCTTT 1680
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DB 1681 GTACCTTTGCACATGCAATGTTCTTATGGACATTTATGAAAGTGTGCAGAACTTCTTGTGTTAA 1740
QY 1965 CATGGAGCAGTAGTAAATGCTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCA 2024
DB 1741 CATGGAGCAGTAGTAAATGCTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCA 1800
QY 2025 GCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGTCGTCAGAGCCCTTACCAA 2084
DB 1801 GCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGTCGTCAGAGCCCTTACCAA 1860
QY 2085 AAAAAACAGGGATGGAATACCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAA 2144
DB 1861 AAAAAACAGGGATGGAATACCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAA 1920
QY 2145 GATCTGCTTAGGGGAGATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGA 2204
DB 1921 GATCTGCTTAGGGGAGATGCAGCTTTGCTAGATGCTGCCAAGAGAGTGTGTTAGCCAGA 1980
QY 2205 GTGAAGAGTGTCTTCTCTGATTAATGTHAAATGCGCGATACCCAAAGGCGACATTC 2264
DB 1981 GTGAAGAGTGTCTTCTCTGATTAATGTHAAATGCGCGATACCCAAAGGCGACATTC 2040
QY 2265 ACACCTTTACATTTAGCAGCTGGTTATAATAATTTTGAAGTGTGCAGAGTATTTGTTACAA 2324
DB 2041 ACACCTTTACATTTAGCAGCTGGTTATAATAATTTTGAAGTGTGCAGAGTATTTGTTACAA 2100
QY 2325 CACGGAGCTGATGTGAATGCCAAGACAAAGGAGGACTTATTCCTTTACATAATGTCAGCA 2384
DB 2101 CACGGAGCTGATGTGAATGCCAAGACAAAGGAGGACTTATTCCTTTACATAATGTCAGCA 2160
QY 2385 TCTTACGGGATGTAGATGTAGCAGCTCTACTTAATAAGTATTAATGTCATGTGTCATGTC 2444
DB 2161 TCTTACGGGATGTAGATGTAGCAGCTCTACTTAATAAGTATTAATGTCATGTGTCATGTC 2220
QY 2445 ACCGACAAATATGGCTTTTCAACCTTTTGCAGAAAGCAGCCCAAAAGGAGCGAAACACAGCTT 2504
DB 2221 ACCGACAAATATGGCTTTTCAACCTTTTGCAGAAAGCAGCCCAAAAGGAGCGAAACACAGCTT 2280
QY 2505 TGTGCTTTTGTGTAGCCCCATGGAGCTGACCCGACTTTTAAAAATCAGGAAGGCAAAACA 2564
DB 2281 TGTGCTTTTGTGTAGCCCCATGGAGCTGACCCGACTTTTAAAAATCAGGAAGGCAAAACA 2340
QY 2565 CTTTAGATTTTAGTTTTCAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCA 2624
DB 2341 CTTTAGATTTTAGTTTTCAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCA 2400
QY 2625 TCTGCTCTGCCCTCTTGTTCAAAGCCCTCAAGTGTCTCAATGGTGTGAGAAGCCCAAGGAGCC 2684
DB 2401 TCTGCTCTGCCCTCTTGTTCAAAGCCCTCAAGTGTCTCAATGGTGTGAGAAGCCCAAGGAGCC 2460
QY 2685 ACTGCAGATGCTCTCTCTTCAGGTCCATCTAGCCCCATCAAGCCCTTCTGACGCGAGCT 2744
DB 2461 ACTGCAGATGCTCTCTCTTCAGGTCCATCTAGCCCCATCAAGCCCTTCTGACGCGAGCT 2520
QY 2745 CTTGACAACTTATCTGGGAGTTTTTCAGAACTGTCTTCAGTAGTTAGTTCAAGTGGAAACA 2804
DB 2521 CTTGACAACTTATCTGGGAGTTTTTCAGAACTGTCTTCAGTAGTTAGTTCAAGTGGAAACA 2580
QY 2805 GAGGCTGCTTCCAGTTTGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAA 2864
DB 2581 GAGGCTGCTTCCAGTTTGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAA 2640
QY 2865 TTCGTAAGGAATCTTGACCTTGAGCACCTTAATGGATATATTGAGAGAGAACAGATCACT 2924
DB 2641 TTCGTAAGGAATCTTGAGCACCTTAATGGATATATTGAGAGAGAACAGATCACT 2700
QY 2925 TTGGATGTTATGTTGAGATGGGCGCAAGAGCTGAAGGATTTGGAATCAATGCTTAT 2984
DB 2701 TTGGATGTTATGTTGAGATGGGCGCAAGAGCTGAAGGATTTGGAATCAATGCTTAT 2760
QY 2985 GGCATAGGACACAACTTAATTTAAAGGAGTGCAGAGACTTATCTCCGACAAACAGGCTTT 3044

2761	Db	GGACATAGGCACAAACTAAATTAAAGGAGTCGAGAGACTTATCTCCGGACAAACAGGCTTT	2820
3045	Qy	AAACCATATTTAACTTTTGAACACACCTCTGGTAGTGGAAACAATTTCTTATAGATCTGTCTCCT	3104
2821	Db	AAACCATATTTAACTTTTGAACACCTCTGGTAGTGGAAACAATTTCTTATAGATCTGTCTCCT	2880
3105	Qy	GATGATAAAGAGTTTCAGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGA	3164
2881	Db	GATGATAAAGAGTTTCAGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGA	2940
3165	Qy	GATGGAGTCAATGCAGCTGGAACTCTCAACAGATACAAATTTCTCAAGATTCAGAGGTT	3224
2941	Db	GATGGAGTCAATGCAGCTGGAACTCTCAACAGATACAAATTTCTCAAGATTCAGAGGTT	3000
3225	Qy	TGTAACAAGAAACTATGGGAAGATACACTCACCGGAGAAAAGATTTCTGAAGAAAAC	3284
3001	Db	TGTAACAAGAAACTATGGGAAGATACACTCACCGGAGAAAAGATTTCTGAAGAAAAC	3060
3285	Qy	CACAACCATGCCAATGAACGAATGCTATTTCAATGGGTCTCCTTTTGTAATGCAATTATC	3344
3061	Db	CACAACCATGCCAATGAACGAATGCTATTTCAATGGGTCTCCTTTTGTAATGCAATTATC	3120
3345	Qy	CACAAAGCTTTGATGAAGAGCATGCGTACATAGTGGTATGTTTGAGAGTGGCATTTAT	3404
3121	Db	CACAAAGCTTTGATGAAGAGCATGCGTACATAGTGGTATGTTTGAGAGTGGCATTTAT	3180
3405	Qy	TTTGCTCAAAACTCTTCCAAAAGCAATCAATATGATATGGAATTGGAGAGGTACTGGG	3464
3181	Db	TTTGCTCAAAACTCTTCCAAAAGCAATCAATATGATATGGAATTGGAGAGGTACTGGG	3240
3465	Qy	TGTCAGTTTCCAAAAGACAGATCTTGTTACATTTGCCACAGCAGTGTCTTTTGCCGG	3524
3241	Db	TGTCAGTTTCCAAAAGACAGATCTTGTTACATTTGCCACAGCAGTGTCTTTTGCCGG	3300
3525	Qy	GTAACTTTGGGAAAGTCTTTCTCGAGTTCAGTGCAATGAAAATGGCACATTTCTCTCCA	3584
3301	Db	GTAACTTTGGGAAAGTCTTTCTCGAGTTCAGTGCAATGAAAATGGCACATTTCTCTCCA	3360
3585	Qy	GGTCATCACTCAGTCACTGTGTAGGCCAGGTGAATGGCCCTAGCATTTAGCTGAATGTT	3644
3361	Db	GGTCATCACTCAGTCACTGTGTAGGCCAGGTGAATGGCCCTAGCATTTAGCTGAATGTT	3420
3645	Qy	ATTTACAGAGGAGAAAGGCTTATCTCGAGTATTTAAATTACTTACCAGATTTATGAGGCCT	3704
3421	Db	ATTTACAGAGGAGAAAGGCTTATCTCGAGTATTTAAATTACTTACCAGATTTATGAGGCCT	3480
3705	Qy	GAAGGTATGTCGATGGA	3722
3481	Db	GAAGGTATGTCGATGGA	3498

RESULT 8
US-09-696-668-1
Sequence 1, Application US/09696668
Patent No. 6617102
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Xu, Xiang
APPLICANT: Huang, Betty
APPLICANT: Ossoveskaya, Valeria
TITLE OF INVENTION: TANKYRASE H. COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS
FILE REFERENCE: A-68292-1/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/696,668
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 09/427,154
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 3797
TYPE: DNA
ORGANISM: Homo sapiens

Qy 1442 GGCATCTGAGAAAGCTCATATATGATGTGTGTGAAGTAGTGGTGAACATGAAGCAAAAGGT 1501
Db 1423 GGCATCTGAGAAAGCTCATATATGATGTGTGTGAAGTAGTGGTGAACATGAAGCAAAAGGT 1482
Qy 1502 TAATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCATCT 1561
Db 1483 TAATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCATCT 1542
Qy 1562 ACAAACCTGCGCGCTACTCTCTGAGCTATGGGTGTGATCTTAAACATTAATATATCCCTTCAGGG 1621
Db 1543 ACAAACCTGCGCGCTACTCTCTGAGCTATGGGTGTGATCTTAAACATTAATATATCCCTTCAGGG 1602
Qy 1622 CTTTATCTGCTTTACAGATGGGAATGAAATGTACAGCAATCTCTCCAAGAGGGTATCTC 1681
Db 1603 CTTTATCTGCTTTACAGATGGGAATGAAATGTACAGCAATCTCTCCAAGAGGGTATCTC 1662
Qy 1682 ATTAGGTAAATTCAGAGCAGACAGACATTTGCTGGAGCTGCAAGGCTGGAGATGTGGA 1741
Db 1663 ATTAGGTAAATTCAGAGCAGACAGACATTTGCTGGAGCTGCAAGGCTGGAGATGTGGA 1722
Qy 1742 AACTGTAAAAAACTGTGTACTCTCTGAGTGTCAACTGTCAGAGACATTTGAAGGGCGTCA 1801
Db 1723 AACTGTAAAAAACTGTGTACTCTCTGAGTGTCAACTGTCAGAGACATTTGAAGGGCGTCA 1782
Qy 1802 GTCTACACCACTTCATTTTGCGAGCTGGGTAAACAGAGTGTCCGTGTGGAAATATCTGCT 1861
Db 1783 GTCTACACCACTTCATTTTGCGAGCTGGGTAAACAGAGTGTCCGTGTGGAAATATCTGCT 1842
Qy 1862 ACAGCATGGAGCTGATGTCATGCTTAAGATTAAGGAGGCTTGTACTCTTTGCAATATGC 1921
Db 1843 ACAGCATGGAGCTGATGTCATGCTTAAGATTAAGGAGGCTTGTACTCTTTGCAATATGC 1902
Qy 1922 ATGTTCTTATGCAATATTAAGTTGCGAACTTCTTGTAAACATGAGCAGTAGTTAA 1981
Db 1903 ATGTTCTTATGCAATATTAAGTTGCGAACTTCTTGTAAACATGAGCAGTAGTTAA 1962
Qy 2041 TGTAGCTGATTTATGGAATTTACACCTTTATCAAGAGCAGCAGCAAAAGGAAATATGA 2041
Db 1963 TGTAGCTGATTTATGGAATTTACACCTTTATCAAGAGCAGCAGCAAAAGGAAATATGA 2022
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Db 2082 AATTTGCNAATCTTGTCTCCAGCATGTGTCAGACCTTACCNAAAAAACAGGGATGAAA 2082
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Qy 2221 TGCAGCTTTGCTAGATGTCGCAAGAGGGTGTGTTAGCCAGAGTGAAGATTTGCTTTC 2221
Db 2202 TGCAGCTTTGCTAGATGTCGCAAGAGGGTGTGTTAGCCAGAGTGAAGATTTGCTTTC 2202
Qy 2281 TCCTGATTAATGTAATTTGCCGCGATACCCAGGCGAGACATTCACACCTTTACATTTAGC 2281
Db 2262 TCCTGATTAATGTAATTTGCCGCGATACCCAGGCGAGACATTCACACCTTTACATTTAGC 2262
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Db 2382 TGCCCAAGACAAAGGAGACTTATTCCTTTACATAATGTCAGCATCTTACGCGCATGTAGA 2382
Qy 2461 TGTAGCAGCTCTACTAATAAGTATATGCAATGTCTCAATGCCACGCAAAATGGGCTTT 2461
Db 2442 TGTAGCAGCTCTACTAATAAGTATATGCAATGTCTCAATGCCACGCAAAATGGGCTTT 2442
Qy 2521 CACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACACAGCTTTGTGCTTTGTTGCTAGC 2521
Db 2502 CACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACACAGCTTTGTGCTTTGTTGCTAGC 2502

Qy 2522 CCATGAGAGCTGACCCGACTCTTTAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2581
Db 2503 CCATGAGAGCTGACCCGACTCTTTAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2562
Qy 2582 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTCTGCCCTCTTG 2641
Db 2563 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTCTGCCCTCTTG 2622
Qy 2642 TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAAGCCCAAGAGCCACTGACAGATGCTCTC 2701
Db 2623 TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAAGCCCAAGAGCCACTGACAGATGCTCTC 2682
Qy 2702 TTCAAGTCTCAATAGCCCATCAAGCCTTTCTGACGCGCAGCTTTGACAACTATCTGG 2761
Db 2683 TTCAAGTCTCAATAGCCCATCAAGCCTTTCTGACGCGCAGCTTTGACAACTATCTGG 2742
Qy 2762 GAGTTTTTCAAGAACTGTCTTCAAGTGTAGTTCAAGTGGAAACAGAGGCTGCTCCAGTTT 2821
Db 2743 GAGTTTTTCAAGAACTGTCTTCAAGTGTAGTTCAAGTGGAAACAGAGGCTGCTCCAGTTT 2802
Qy 2822 GGAAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTGG 2881
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Qy 2882 ACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTTATAGTTGA 2941
Db 2863 ACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTTATAGTTGA 2922
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Db 2923 GATGGGSCACAAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAACT 2982
Qy 3002 AATTAAGGAGTCEGAGAGACTTATCTCCGACAAACAAAGGCTTTAAACCAATATTTAACTTT 3061
Db 2983 AATTAAGGAGTCEGAGAGACTTATCTCCGACAAACAAAGGCTTTAAACCAATATTTAACTTT 3042
Qy 3121 GAACACCTCTGGTAGTGGAAACAATTTCTTATAGATCTGTCTCTCTGATGATTAAGAGTTTCA 3121
Db 3102 GAACACCTCTGGTAGTGGAAACAATTTCTTATAGATCTGTCTCTCTGATGATTAAGAGTTTCA 3102
Qy 3182 GTCTGTGGAGAGAGATGCAAAAGTACAGTTCGAGAGCAGAGATGGAGTCAATGAGG 3181
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Qy 3241 TGGAAATCTTCAACAGATACAAATATTTCTCAAGATTCAGAAAGGTTTGTAAACAGAACTATG 3241
Db 3222 TGGAAATCTTCAACAGATACAAATATTTCTCAAGATTCAGAAAGGTTTGTAAACAGAACTATG 3222
Qy 3301 GGAAGATACACTCACCGGAGAAAGAAAGTTTCTGAGAAACCAACCAATGCAATGA 3301
Db 3282 GGAAGATACACTCACCGGAGAAAGAAAGTTTCTGAGAAACCAACCAATGCAATGA 3282
Qy 3361 ACCAAATGCTATTTTCATGGGTCTCTCTTTGTGAAATGCAATTTATCCAAAGGCTTTGATGA 3361
Db 3342 ACCAAATGCTATTTTCATGGGTCTCTCTTTGTGAAATGCAATTTATCCAAAGGCTTTGATGA 3342
Qy 3421 AAGGCATGCTACATAGTGGTATGTTTGGAGCTGGCATTTATTTGCTGAAAACTCTTC 3421
Db 3402 AAGGCATGCTACATAGTGGTATGTTTGGAGCTGGCATTTATTTGCTGAAAACTCTTC 3402
Qy 3481 CAAAAGCATCAATATGATATGGAATTTGGAGGAGTCTGGGTGTCCAGTTTCAAAAGA 3481
Db 3462 CAAAAGCATCAATATGATATGGAATTTGGAGGAGTCTGGGTGTCCAGTTTCAAAAGA 3462
Qy 3541 CAGATCTTGTGTACATTTGCCCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3541
Db 3522 CAGATCTTGTGTACATTTGCCCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3522
Qy 3601 TTTTCTGAGTTCAGTGCAATGAAATGGCACATTTCTCTCCAGGTCATCACTCAGTCAAC 3601
Db 3582 TTTTCTGAGTTCAGTGCAATGAAATGGCACATTTCTCTCCAGGTCATCACTCAGTCAAC 3582
Qy 3661 TGGTAGCCCCAGTGTAAATGGCCTAGCAATTAGCTGAATATGTTATTTACAGAGGAGAAACA 3661

! TYPE: DNA
! ORGANISM: Homo sapiens
US-09-427-154-1

Query Match 88.8%; Score 3387.6; DB 3; Length 3394;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3390; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 423 GGTGTTGGCGGAAAGAGCTAGTCTGAATATTTGCTTCAGAAATGGTGCAAAATGTTCAAGCA 482
DB 1 GGTGTTGGCGGAAAGAGCTAGTCTGAATATTTGCTTCAGAAATGGTGCAAAATGTTCAAGCA 60
QY 483 CGTGATGATGGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGTCACTGCAAGTA 542
DB 61 CGTGATGATGGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGTCACTGCAAGTA 120
QY 543 GTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATGGAATATATCT 602
DB 121 GTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATGGAATATATCT 180
QY 603 CCTCTCCATGAAGCTGCAATTAAGGAAAGATTTGATGTTTGCATTTGCTGTTACAGCAT 662
DB 181 CCTCTCCATGAAGCTGCAATTAAGGAAAGATTTGATGTTTGCATTTGCTGTTACAGCAT 240
QY 663 GGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGCAGACATTTGGAATTTAGCAGATCCA 722
DB 241 GGAGCTGAGCCCAACCATCTAAATACAGATGGAAGCAGACATTTGGAATTTAGCAGATCCA 300
QY 723 TCTGCAAGCAGTCTTACTGTTGTAATTAAGAAAGATGAATCTTTAGAAAGTGCAGG 782
DB 301 TCTGCAAGCAGTCTTACTGTTGTAATTAAGAAAGATGAATCTTTAGAAAGTGCAGG 360
QY 783 AGTGCAATGAAGAAATGATGCTCTACTCACACCATTAATGTCACCTGCCACGCA 842
DB 361 AGTGCAATGAAGAAATGATGCTCTACTCACACCATTAATGTCACCTGCCACGCA 420
QY 843 AGTGATGCGAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATT 902
DB 421 AGTGATGCGAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATT 480
QY 903 GTAAGCTGTTATCTGCAACATGAGCTGATGTCATGCTTAAAGATAAAGTGTATCTGGTA 962
DB 481 GTAAGCTGTTATCTGCAACATGAGCTGATGTCATGCTTAAAGATAAAGTGTATCTGGTA 540
QY 963 CCATTTACCAATGCTGTTCTATGCTCATTTATGAAGTAACTGAACTTTTGGTCAAGCAT 1022
DB 541 CCATTTACCAATGCTGTTCTATGCTCATTTATGAAGTAACTGAACTTTTGGTCAAGCAT 600
QY 1023 GGTGCTGTGTAATGCAATGGACTTTGGGCAATTCACCTCTCTTCATGAGGCACTTCT 1082
DB 601 GGTGCTGTGTAATGCAATGGACTTTGGGCAATTCACCTCTCTTCATGAGGCACTTCT 660
QY 1083 AAGAACAGGGTTGAAGTATGTTCTTCTTCTTAAAGTATGTTAGTGCGAGACCCCAACTGCTC 1142
DB 661 AAGAACAGGGTTGAAGTATGTTCTTCTTCTTAAAGTATGTTAGTGCGAGACCCCAACTGCTC 720
QY 1143 AATTTGTCACATAAAGTCTATAGACTGGCTCCACACCAAGTAAAGAAAGATT 1202
DB 721 AATTTGTCACATAAAGTCTATAGACTGGCTCCACACCAAGTAAAGAAAGATT 780
QY 1203 GCATATGAATTTAAAGGGCACTGCTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCGA 1262
DB 781 GCATATGAATTTAAAGGGCACTGCTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCGA 840
QY 1263 ATCAAAACATCTCTCTCTGGAATGTTGAATTTTCAAGCATCTCTCAAAACAATGAAACA 1322
DB 841 ATCAAAACATCTCTCTCTGGAATGTTGAATTTTCAAGCATCTCTCAAAACAATGAAACA 900
QY 1323 GCATTTGATTTGCTGCTGCTATCTCCATATCCAAAGAAAGCAATATGTAAGTGTG 1382
DB 901 GCATTTGATTTGCTGCTGCTATCTCCATATCCAAAGAAAGCAATATGTAAGTGTG 960
QY 1383 CTAAGAAAAGGACCAACATCAATGAAAAGACTTAAAGAAATTTCTGACTCTCTGCACTG 1442

DB 961 CTAAGAAAAGGACCAACATCAATGAAAAGACTAAAGAAATTTCTGACTCTCTGCACTG 1020
QY 1443 GCATCTGAGAAAGCTCATATGATGTTGTTGAGTAGTGTGTAACATGAGCAAAAGTT 1502
DB 1021 GCATCTGAGAAAGCTCATATGATGTTGTTGAGTAGTGTGTAACATGAGCAAAAGTT 1080
QY 1503 AATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCACTCA 1562
DB 1081 AATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCACTCA 1140
QY 1563 CAAACCTGCGGCTTACTCTCTGAGCTATGGGTGATGCTTAAACATTAATCCCTTCAGGGC 1622
DB 1141 CAAACCTGCGGCTTACTCTCTGAGCTATGGGTGATGCTTAAACATTAATCCCTTCAGGGC 1200
QY 1623 TTTTACTGCTTTTACAGATGGGAAATGAAATGTACAGCAATCTCTCCAAAGGGGTATCTCA 1682
DB 1201 TTTTACTGCTTTTACAGATGGGAAATGAAATGTACAGCAATCTCTCCAAAGGGGTATCTCA 1260
QY 1683 TTAGGTAAATTCAGAGGAGCAGACAGCAATTTGCTGAAAGCTGCAAGGCTGGAGATGTCGAA 1742
DB 1261 TTAGGTAAATTCAGAGGAGCAGACAGCAATTTGCTGGAAGCTGCNAAGGCTGGAGATGTCGAA 1320
QY 1743 ACTGTAAAAAACTGTGTACTGTTTACAGAGTGTCAAATGTCAGAGACATTTGAAGGGGCTCAG 1802
DB 1321 ACTGTAAAAAACTGTGTACTGTTTACAGAGTGTCAAATGTCAGAGACATTTGAAGGGGCTCAG 1380
QY 1803 TCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTTGGTGGAAATATCTGCTA 1862
DB 1381 TCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTTGGTGGAAATATCTGCTA 1440
QY 1863 CAGCATGAGAGCTGATGTCATGCTTAAAGATAAAGAGGCGCTTTGACCTTTTGCACAATGCA 1922
DB 1441 CAGCATGAGAGCTGATGTCATGCTTAAAGATAAAGAGGCGCTTTGACCTTTTGCACAATGCA 1500
QY 1923 TGTTCCTTATGGAATTAAGTTGCAAGACTTCTTCTTTAAACATGAGCAGTATGTTAAT 1982
DB 1501 TGTTCCTTATGGAATTAAGTTGCAAGACTTCTTCTTTAAACATGAGCAGTATGTTAAT 1560
QY 1983 GTAGCTGATTTATGGAATTTTACACCTTTTACATGAGCAGCAGCAAGGAAATATATGAA 2042
DB 1561 GTAGCTGATTTATGGAATTTTACACCTTTTACATGAGCAGCAGCAAGGAAATATATGAA 1620
QY 2043 ATTTGCAAACTTCTGCTCCAGCAGTGGTGAGACCTTACCAAAAGGAGGATGGAAT 2102
DB 1621 ATTTGCAAACTTCTGCTCCAGCAGTGGTGAGACCTTACCAAAAGGAGGATGGAAT 1680
QY 2103 ACTCCTTTTGGATCTTGTAAAGATGGAAGATACAGATATTTCAAGATCTGCTTTAGGGAGAT 2162
DB 1681 ACTCCTTTTGGATCTTGTAAAGATGGAAGATACAGATATTTCAATATCTGCTTTAGGGAGAT 1740
QY 2163 GCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTAGCCAGAGTGGAAGATGCTTCTTCT 2222
DB 1741 GCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTAGCCAGAGTGGAAGATGCTTCTTCT 1800
QY 2223 CCTCATATGTTAAATTTCCGCGCATACCAAGGAGACATTTCAACACCTTTTACATTTAGCA 2282
DB 1801 CCTCATATGTTAAATTTCCGCGCATACCAAGGAGACATTTCAACACCTTTTACATTTAGCA 1860
QY 2283 GCTGGTTATTAATTAATTTAGAAAGTTGCAAGATTTTGTTAACAACGAGCTGATGTTGAAT 2342
DB 1861 GCTGGTTATTAATTAATTTAGAAAGTTGCAAGATTTTGTTAACAACGAGCTGATGTTGAAT 1920
QY 2343 GCCCAAGACAAAGGAGCACTTATCTTTCATATTCAGCATCTTTCAGGCACTGATAGAT 2402
DB 1921 GCCCAAGACAAAGGAGCACTTATCTTTCATATTCAGCATCTTTCAGGCACTGATAGAT 1980
QY 2403 GTAGCAGCTTACTTAATAAAGTATAATGATGTCATGTCATGTCACGCAAAATGGGCTTTC 2462
DB 1981 GTAGCAGCTTACTTAATAAAGTATAATGATGTCATGTCATGTCACGCAAAATGGGCTTTC 2040
QY 2463 ACACCTTTTGCAAGAGCAGCCCAAGGAGCGAAACACAGCTTTGCTGTTGTTGCTAGCC 2522

Db 2041 ACACCTTTGCAGAGCAGCCCAAAAGGAGCAACACAGCTTTTGTGCTTTGTTGCTAGCC 2100
Qy 2523 CATGAGCTGACCCGACTCTTAAATAACAGAAAGGACAAACACCTTTAGATTAGTTTCA 2582
Db 2101 CATGAGCTGACCCGACTCTTAAATAACAGAAAGGACAAACACCTTTAGATTAGTTTCA 2160
Qy 2583 GCGGATGATGTCAGGCTCTTCTGACAGCAGCCATGCCCCATCTGCTCTGCCCTCTTGT 2642
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Qy 2643 TACAAGCCTCAAGTGCTCAATGGTGTGAGAGCCAGGAGCCACTGCGAGATGCTCTCTCT 2702
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Db 2461 CTTGAGCACCTTAATGGATATATTTGAGAGAAACAGATCACTTTGGATGATTAAGTTGAG 2520
Qy 2943 ATGGGACAGAGGAGCTGAGGAGATTTGGATCAATGCTTATGACATAGGCACAACTA 3002
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Qy 3003 ATAAAGAGTCGAGAGACTTATCTCGGACAAACAGTCTTTAACCCATATTTAACTTTG 3062
Db 2581 ATAAAGAGTCGAGAGACTTATCTCGGACAAACAGTCTTTAACCCATATTTAACTTTG 2640
Qy 3063 AACACCTCTGATGTGGAAACAATTTCTATAGATCTGCTCTGATGATAAGAGTTTCAG 3122
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RESULT 11

US-09-972-115A-3
; Sequence 3, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4297
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: CDS
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RESULT 12
US-09-972-115A-1
; Sequence 1, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; TYPE: DNA
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 4067 TTTTACTCTTTTGTGAAAAAAA 4090

RESULT 13
 US-09-196-387-1
 ; Sequence 1, Application US/09196387
 ; Patent No. 627613
 ; GENERAL INFORMATION:
 ; APPLICANT: de Lange, Titia
 ; APPLICANT: Smith, Susan
 ; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
 ; TITLE OF INVENTION: OF USE THEREOF

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/
;
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-09-196-387-1

Query Match 49.4%; Score 1885; DB 3; Length 4134;
Best Local Similarity 72.1%; Pred. No. 0;
Matches 2496; Conservative 0; Mismatches 940; Indels 27; Gaps 2;

Qy 252 GGAGGGCTCGCGAGCGCGCGCGAGCGCGCTGAGCGCGCGCGCGCGAGCTGTC 311
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Qy 507 GGGGAGCAGGACCTGGGACAGGGGTCCCAGCAGTGAAGCGGGCCCTACGGGAAGCTG 566
Db |||||
Qy 312 GAGCGCTGCCCAACGGGAGCTGGAACGAGTCAAGAGGCTGGTGACGCTGAGAGGCTG 371
Db |||||
Qy 567 GAGGCTGTGCAATGGGACGTGTCCGGGTAAGAGGCTGGTGGAGCGGCGAAGCTA 626
Db |||||
Qy 372 AACAGCGCGACACGGCGGGGAGGAATCCACCCGCTGCACCTTCGCGCAGGTTTTGGG 431
Db |||||
Qy 627 AATCAAGGACATGGCGCGCGGAAGTCTTCTCCCTGCACCTTCGCTGCAGGTTTTGGA 686
Db |||||
Qy 432 CGGAAGACGTAGTTGAATATTTCCTCAGAAATGGTGCAGAAATGTCAGACGTGATGAT 491
Db |||||
Qy 687 AGGAAGGATGTTGAGAACACTTACTACAGATGGGTGCTAATGTCCAGCTCGTGATGAT 746
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Qy 492 GGGGCGCTTATCTCTTCAATAATGCAATGCTCTTTTGTCTCATGCTGAAGTAGTCAATCTC 551
Db |||||
Qy 747 GGAGGTCTCATCCCGCTTCAATAGCTCTTTTGTGCGCCATGCTGAGGTTGTGAGTCTG 806
Db |||||
Qy 552 CTTTTGGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAAATTATCTCTCTCCAT 611
Db |||||
Qy 807 TTAATGTCGAAGAGCTGATCCAAATGCCAGGGAATACCTGGAACCTATACACCTCTGCAT 866
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Qy 612 GAAGCTGCAATTAAGGAAGATTGATGTTTGCATTTGCTGTTTACAGCATGGAGCTGAG 671
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Qy 867 GAAGCTGCTATTAAGGAAGATCGATGTGCAATTTGTGCTGCTGCAGCAGGAGCTGAC 926
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Db |||||
Qy 927 CCAACCAATTCGGAACACTGATGGGAATCAGCCCTGGACCTGGCAGATCTTTCAGCAAAA 986
Db |||||
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RESULT 15
US-09-972-115A-7
  ; Sequence 7, Application US/09972115A
  ; Patent No. 6599728
  ; GENERAL INFORMATION:
  ; APPLICANT: Geron Corporation
  ; APPLICANT: Gregg, Morin B.
  ; APPLICANT: Walter, Funk D.
  ; APPLICANT: Mieczyslaw, Piatyszek A.
  ; TITLE OF INVENTION: A Second Mammalian Telomerase
  ; FILE REFERENCE: 080/003C
  ; CURRENT APPLICATION NUMBER: US/09/972,115A
  ; CURRENT FILING DATE: 2001-10-05
  ; PRIOR APPLICATION NUMBER: US 60/128,577
  ; PRIOR FILING DATE: 2000-04-10
  ; PRIOR APPLICATION NUMBER: US 60/129,123
  ; PRIOR FILING DATE: 1999-04-13
  ; NUMBER OF SEQ ID NOS: 64
  ; SOFTWARE: PatentIn version 3.1
  ; SEQ ID NO 7
  ; LENGTH: 4134
  ; TYPE: DNA
  ; ORGANISM: Homo sapiens
US-09-972-115A-7

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Query Match	49.4%	Score 1885;	DB 3;	Length 4134;
Best Local Similarity	72.1%;	Pred. No. 0;		
Matches 2496;	Conservative 0;	Mismatches 940;	Indels 27;	Gaps 2;
QY	252	GGAGCGGCGCTGCGCAGCGCGCGGCGGAGCGTGGAGCGCGGCGCGCGAGAGCTGTTCC	311	
DB	507	GGGGCAGCAGGACCTGGGACAGGGGTCCACGACGTGAGCGGGGCCCTACGGGAACCTGCTG	566	
QY	312	GAGGCGTGGCGCAACGGGGACGTTGGAAACAGTCAAGAGGCTGGTGACGCGCTGAGAAAGGTG	371	
DB	567	GAGGCGTGGCGCAACGGGGACGTTGGAAACAGTCAAGAGGCTGGTGACGCGCGCAACGTA	626	
QY	372	AACAGCGCGGACACGCGGGGCGAGAAATCCA CCCCCTGCACTTCGCGCGCAGGTTTGGG	431	
DB	627	AATGCAAGGACATGCGCGCGCGGAAAGTCTTCTCCCTGCACTTCGCTGCGGTTTGGG	686	
QY	432	CGGAAAGAGCTAGTTCAATATTTGCTTCAGAAATGGTGCAAAATGTCGAACGACGATGAT	491	
DB	687	AGGAAGGATGTTGTAAGAACCTTACTACAGATGGGTGCTAAATGTCACGCTCGTGATGAT	746	
QY	492	GGGGGCGTTATTCCTCTTCATATGCACTGCTCTTTTGGGTCACTGCTCAAGTAGTCAATCTC	551	
DB	747	GGAGGTCTCATCCGCTTCATATGCTGTTCTTTTGGCCATGCTGAGTTGTGAGTCTG	806	
QY	552	CTTTTTCGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTATCTCTCTCCAT	611	
DB	807	TTATTGTGCGCAAGGAGCTGATCCAAATGCCAGGATAA CTGGAACTATACACCTCTGCAT	866	
QY	612	GAGCTGCAATTTAAAGGAAGATGTGATTTGCAATTTGCTGTTTACAGCATGAGCTGAG	671	
DB	867	GAGCTGCTATTTAAAGGGGAAGATCGATGTGTGCAITTTGCTGTGACGACGCGAGCTGAC	926	
QY	672	CCAAACCATCGAAATACAGATGGAAGCAGCAGCATTGGATTTAGCAGATCCATCTGCCTCA	731	
DB	927	CCAAACATTCGGAACACTGATGGGAATCAGCCCTGGA CCTGCGCAATCCTTCAGCAAAA	986	
QY	732	GCAGCTCTTACTGGTGAATATAAGAAAGATGAACCTTTAGAAAGTCCAGGAGTGCAAT	791	
DB	987	GCTGTCTTTACAGGTGAATACAAGAAAGACGAACCTCTAGAACTGCTAGGAGTGGTAAT	1046	
QY	792	GAAGAAAAATGATGCTCTACTCACACCATTTAAATGTCAACTGCCACGCAAGTGATGGC	851	
DB	1047	GAAGAAAAATGATGCTCTACTCACACCATTTAAATGTCAACTGCCACGCAAGTGATGGC	1106	
QY	852	AGAAAGTCAACTCCATTCATTTGGCAGCAGGATATAACAGAGTTAAAGATTGTACAGCTG	911	
DB	1107	CGAAAGTCAACTCCATTCATTTGGCAGCAGGATATAACAGAGTTAAAGATTGTACAGCTG	1166	
QY	912	TTACTGCAACATGGAGCTGATGTCCTTAAGATAAGATAAAAGGTGATCTGGTACCATTACAC	971	
DB	1167	CTTCTTCAGCATGGTCTGATGTTTCAATGCAAAAGACAAAGGTGGATCTGTGCTCTTCAT	1226	
QY	972	AATGCGCTGTTCTTATGGTCAATTAAGAAAGTAACTGAACCTTTTGGTCAAGCATGCTGCTGT	1031	
DB	1227	AATGCAATGTTCAATGGACATTTAAGTCAAGAACTGCTACTTAAAGCATGGAGCTGT	1286	
QY	1032	GTAAATGCAATGCACTTGGCAATTTCACTCTCTTCAATGAGGACGCTTCTAAGAACAGG	1091	
DB	1287	GTAAATGCAATGCACTTGGCAATTTCACTCTCTTCAATGAGGACGCTTCTAAGAACAGG	1346	
QY	1092	GTTGAAAGTATGTTCTCTTCTTAAAGTTATGGTGCAGACCCCACTGCTCAATTTGTCAAC	1151	
DB	1347	GTTGAAAGTATGTTCTCTTCTTAAAGTTATGGTGCAGACCCCACTGCTCAATTTGTCAAC	1406	
QY	1152	AATAAAGTGCTATAGACTTTGGCTCCCAACACAGTTTAAAGAAAGATTAGCATATGAA	1211	
DB	1407	GGCAAAAGTGCTGTGGATATGGCTCCAACTCCGGAGCTTAGGGAGAGATTGACTTTATGAA	1466	
QY	1212	TTTAAAGGCCACTCGTTGCTGCAAGCTGCAAGAGAGCTGATGTTACTCGCAATCAAAAA	1271	
DB	1467	TTTAAAGGCCACTCGTTGCTGCAAGCTGCAAGAGAGCTGATGTTACTCGCAATCAAAAA	1526	
QY	1272	CATCTCTCTCTGGAAATGGTGAAATTTCAAGCATCTCTCAAAACATATGAAACGATTTGCAT	1331	

1527 AACTCGCTCTGGAAATCATTAATTTTAAACCAACCGCAGTCTCATGAAACAGCACTGCAC 1586
1532 TGTGCTGCTGCATCTCCATATCCAAAAGAAAGCAAAATATGTGAACCTGTGTCTTAAGAAAA 1591
1587 TGTGCTGTGGCCCTCTCTGCATCCCAAAACGTAACAAAGTGA CAGAATTTGTACTTTAGAAAA 1646
1392 GGAGCAAACTCAATAGAAAAGACTAAAGAAATTTCTTGACTCTCTGACAGTGGGCATCTGAG 1451
1647 GGAGCAAAATGTAATAGAAAATAAAGATTTCAATGACTCCCTCTGCATTTGTGTGACGCCAA 1706
1452 AAAGCTCATATGATGTGTGTAAGTAGTGTGAACATGAAGCAAAAGTTTAATGCTCTG 1511
1707 AGAGCCCAATAATGATGTCATGGAAAGTTCTGCATAGCATGGCCCAAGATGATGCACTG 1766
1512 GATAATCTTGTGTCAGACTCTCTCTACACAGAGCTGCATATTTGTGGTCACTTACAAACCTGC 1571
1767 GACACCTTGTGTCAGACTGCTTTGTCATAGAGCGCCCTAGCAGGCCACCTGCAGACCTGC 1826
1572 CGCCTACTCTGAGCTATGGGTGTGATCTTAACATTAATATCCCTTACAGGGCTTTACTGCT 1631
1827 CGCCTCTGCTGAGTTACGGCTCTGACCCCTGCATCATCTCTCTACAGGGCTTCACAGCA 1886
1632 TTACAGATGGGAATGAAATGTACAGCAACTCTCTCCAAAGGGGTATCTCATATTAGGTAAT 1691
1887 GCACAGATGGGCATGAAGCAGTGCACAGCATTTCTGAGTGAGAGTACACCTPATACGTACT 1946
1692 TCAGAGGCAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTGCAAACTGTAAAA 1751
1947 TCTGATGTGATTATCACTTTAGAGGCATCTTAAGCTGGAGACTTGGAAACTGTGAAG 2006
1752 AAATGTGTACTTTACAGGTGCAACTGCAGAGACATTGAAGGGCGTCACTTACACCA 1811
2007 CAATTTGCACTCTCAAAATGTGAATTTGTAGAGACTTAGAGGGCGGCATTTCCACGCC 2066
1812 CTTCAATTTGCAGCTGGGTATACAGAGTGTCCGTGTGGAATATCTCTACACAGCATGGA 1871
2067 TTACACTTCGACAGAGCTACACCCGCTGTCTGTGTGAGAGTACCTGCTACACACGGT 2126
1872 GCTGATGTGCATGCTAAAGATAAAGAGGCGCTTGTAACCTTTGCAACATGCATGTTCTTAT 1931
2127 GCGATGTCCATGCCAAGACAGGGTGGCTTGGTGGCCCTTCATATGCTGTTTCATAT 2186
1932 GGACATTATGAAGTTGCAGAACTTTGTTAAACATGAGAGCAGTAGTTAAATGTAGCTGAT 1991
2187 GGACACTATGAGTGGCTGAGCTTTTAGTAAAGCATTGGGGCTTCTGTCAATGTGGCGGAC 2246
1992 TTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAA 2051
2247 TTATGGAAATTTACCCCTCTCCATGAAGCAGCAGCTTAAAGGAAAGTATGAAATCTGCAAG 2306
2052 CTTCTGCTCCAGCATGTCAGACCCCTTACCAAAAAAAGAGGATGGAATACCTCCTTTG 2111
2307 CTTCTTTTAAACATGAGCAGATCCCATTAAGAGACAGAGTGGAAATACACCTTTG 2366
2112 GATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAGATGCACTTTG 2171
2367 GATTTGTTAAGGAAGGAGACACAGATATTCAGGACTTACTGAAGGGGATGCTGCTTTG 2426
2172 CTAGATGTCGCAGAAAGGGTTGTTAGCCAGAGTGAAGAGTGTCTTCTCTGTGATTAAT 2231
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2232 GTAAATTCGCCGATACCCAGGCAGACATTTCAACACCTTTTACATTTAGCAGCTGGTTAT 2291
2487 ATCAACTGCAGAGACACCCAGGCGAGAAATTTCAACCTTCTGCACCTGGCAGCAGGGTAT 2546
2292 AATAATTTAGAAAGTTGCAGAGTATTTGTTACACACGGAGCTGATGTGAATGCCCAAGAC 2351
2547 AATAACCTGGAAGTAGCTGAATATCTCTAGAGCATGGAGCTGATGTAAATGCCCAGGAC 2606
2352 AAAGAGGACCTATTCTTTACATTAATGCAGCATCTTACGGGCATGTATAGTGTAGCAGCT 2411

Db 2607 AAGGGTGGTTAAATCCTCTTCAATAATGCGGCATCTTATGGCATGTGACATAGCGGCT 2666
QY 2412 CTACTAATAAGATATATGCTGTCAATGCGACGACAAATGGGCTTTTCAACACTTTG 2471
Db 2667 TTAATGATAAATAACACAGGTGTAAATGCAAGATAAGTGGCGTTTACTCCCTC 2726
QY 2472 CAGGAAGCGCCCAAAAGGAGCAACACAGCTTTGTCTTTGTAGCCCAATGAGCT 2531
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Db 2787 GACCCCAACCATGAAGAACCAAGGAAGCCAGACCCCTCTGGATCTGCAACAGCTGACGAT 2846
QY 2592 GTCAGCGCTCTCTGACAGCAGCCATGCCCCATCTGCTGCCCCCTTTGTTTACAAGCCT 2651
Db 2847 ATCAGAGCTTTGCTGATGATGCTGCTGCCCCCAGAGCCCTTACCTACCTGTTTAAACCT 2906
QY 2652 CAAGTGTCTCAATGGTGTGAGAAGCCAGGAGCCACTGCGAGATGCTCTCTTTCAGGTCCA 2711
Db 2907 CAGG-----CTACTGTAGTGTGCTCTCTGATCTCACCAGCA 2945
QY 2712 TCTAGGCCATCAAGCCCTTCTGAGCAGCAGAGTCTTTGACAACTTATCTGGAGTTTTC 2771
Db 2946 TCCACCCCTCTCTGCTCTGCTGCGTGCAGCAGCATAGACAACCTCACTGGCCCTTTAGCA 3005
QY 2772 GAACTGTCTTCACTAGTGTAGTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAG 2831
Db 3006 GAGTTGGCGTAGGAGAGCCTCCAATGCAAGGGATGGCGCGGGAACAGAAAGGAAG 3065
QY 2832 -----GAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGGAATCTTGGACTT 2885
Db 3066 GAAGGAGAAAGTTGCTGCTTGTGACATATCAGCCAAATTTCTAATAAGCCTTGGCCTT 3125
QY 2886 GAGCACCTAATGGATATATTTAGAGAGAACAGATCACTTTGGATGTATTTAGTTGAGATG 2945
Db 3126 GAACACCTTTGGGATATCTTTGAAACAGAAACAGATTTACACTAGATGTGTGGCTGATATG 3185
QY 2946 GGGCACAAGGAGCTGAAGCAGATTTGAATCAATGCTTATGGACATAGGCACAAACTAATT 3005
Db 3186 GGTCAAGAGATTGAAGAAATAGGCATCAATGCAATATGGGACCGCCCAAAATTAATC 3245
QY 3006 AAAGGAGTCGAGAGACTTATCTCCGCAACAAAGGTCTTAAACCATATTTAACTTTGAAC 3065
Db 3246 AAAGGAGTAGAAGACTTTAGTGGACAAACAAAGCCACCAATCTTATTTGACTTTTCAC 3305
QY 3066 ACTCTGGTAGTGGAAACAATTTCTTATAGATCTGTCTCTCGATGATGAAGAGTTTCAGTCT 3125
Db 3306 TGTGTTAATCAGGGAACGATTTTGTGGATCTTGTCTCCAGAAAGATAAAGAAATATCAGTCA 3365
QY 3126 GTGGAGGAAGATGCAAAAGTACAGTTCCGAGGACAGAGATGGAGTCTATGCAGGTGGA 3185
Db 3366 GTGGAAGAAGATGCAAAAGTACTATTCAGAAACACAGAGATGGTGTAAATGCTGGCGC 3425
QY 3186 ATCTTCAACAGATACAAATATCTCAAGATTCAGAGGTTTGTAAACAAGAAACTATGGGAA 3245
Db 3426 ATCTTCAACAGATACAAATGCTCATTCGAATTCAAAAGTTGTCAACAAGATTGAGGGAG 3485
QY 3246 AGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACAACATGCCAATGAACGA 3305
Db 3486 CGGTTCTGCCACCGACAGAAGGAAGTGTCTGAGGAGAAATCAACAACATCACAATGAGGCG 3545
QY 3306 ATGCTATTTTCATGGGTCTCTTTTGTGAATGCAATTTATCCACAAGGCTTTGATGAAGG 3365
Db 3546 ATGTTGTTTTCATGGGTCTCTCTTTCATTAATGCCATTTATTAAGGGGTTTGTAGGCGA 3605
QY 3366 CATGCGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAATACTCTTCCAAA 3425
Db 3606 CATGCATACATAGGAGGATGTTTGGGCGGGATTTATTTGCTGAATACTCTTCAAAA 3665
QY 3426 AGCAATCAATATGTATATGGAATTTGAGAGGATCTGGGTGTCCAGTTTCAAAAGACAGA 3485
Db 3666 AGCAACCAATATGTTTATGGAATTTGAGGAGGAACAGGCTGCCCTACACACAAGGACAGG 3725

QY 3486 TCTTGTATTACATTGGCACAGGCGCTGTCTTTTTCGCGGTAACTTTGGAAAAGTCTTTT 3545
Db 3726 TCATGCTATATATGTACACAGACAAATGCTCTTCTGTAGAGTGACCCCTTGGGAATCCTTT 3785
QY 3546 CTGCAAGTTTCAAGTCAATGAAAATGGCAATTTCTCTCCAGGTTCATCACTCACTGCTGT 3605
Db 3786 CTGCAAGTTTAGCACCATGAAAATGGCCACGCGCTCCAGGGCACCACTCACTGCTGTTGT 3845
QY 3606 AGGCCCCAGTGTAAATGGCCTAGCATTTAGCTGAATGTTTATTACAGAGGAGAACAGGCT 3665
Db 3846 AGACCGAGCGTCAATGGGCTGGCATATGCTGAATATGTATCTACAGAGGAGAACAGGCA 3905
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Db 3906 TACCAGAGTATCTTATCATTACCAGATCATGAAGCCAGAAAG 3948

Search completed: December 18, 2006, 16:38:05
Job time : 666.632 secs

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1	3816	100.0	3816	4	AA91488	Tankyrase
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4	3816	100.0	3816	14	ADY97760	Human tan
5	3793	99.4	6019	4	AC85294	Human SPA
6	3791.4	99.4	4275	3	AC66825	Human tan
7	3791.4	99.4	4406	5	AP63930	Human tan
8	3791.4	99.4	4992	5	AP63953	Human tan
9	3791.4	99.4	5002	5	AP63952	Human tan
10	3791.4	99.4	6189	13	ADR14766	Nucleotid
11	3791.4	99.4	6189	13	ADR6604	Human pro
12	3791.4	99.4	6189	13	ADR66262	Human pro
13	3791.4	99.4	6189	14	ADW86202	Human Tan
14	3791.4	99.4	6189	14	ADW82026	DNA sequen
15	3788.4	99.3	6018	10	AD54031	Human col
16	3770.8	98.8	5075	6	AB211674	Human pol
17	3770.8	98.8	5075	12	ADM44192	Novel hum
18	3595.8	94.2	4127	5	AP63926	Human tan

PT or preventing cell cycle associated disorders such as cancer.

XX Claim 13; Fig 2; 63pp; English.

XX This sequence encodes the Tankyrase homologue isotype 2 (TaHo-2) protein of the invention. The invention also relates to the TaHo-1 protein. The TaHo proteins are useful for inducing or preventing cell proliferation in cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also useful for the preparation of TaHo, for generating either transgenic animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents, in gene therapy, as vaccine, and for construction of hybridisation probes for mapping the gene which encodes TaHo and for the genetic analysis of individuals with genetic disorders. The TaHo proteins, and their coding sequences are useful in screening assays

SQ Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;

Query Match	100.08;	Score 3816;	DB 4;	Length 3816;
Best Local Similarity	100.08;	Pred. No. 0;		
Matches 3816;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	CGCGCTGCTCGCGCCCGCGCGGCGAGCCGGGGGCGAGGAGCCGAGCGGGGCGGGCGG	60		
DB 1	CGCGCTGCTCGCGCCCGCGCGGCGAGCCGGGGGCGAGGAGCCGAGCGGGGCGGGCGG	60		
QY 61	TGGGCGCGGCGCATGGGACTCGCGCGGATCCGGTGAACAGAGGAGCCAAAGCGCGCGG	120		
DB 61	TGGGCGCGGCGCATGGGACTCGCGCGGATCCGGTGAACAGAGGAGCCAAAGCGCGCGG	120		
QY 121	CCCTGAGCGCTCTTCGCGGGGCGCTCGCCCTCTGCTCGCGGGCGGGGCTCTGCG	180		
DB 121	CCCTGAGCGCTCTTCGCGGGGCGCTCTGCGCCCTCTGCTCGCGGGCGGGGCTCTGCG	180		
QY 181	TCCGGTGTCTGGCGCTGTGTGGGTGTGGCGGGCCAGGATCATGTCTGGGTCTGGCGCT	240		
DB 181	TCCGGTGTCTGGCGCTGTGTGGGTGTGGCGGGCCAGGATCATGTCTGGGTCTGGCGCT	240		
QY 241	GGCGCGGGGGGAGCGGCTCTCGCGAGCGCGCGCGCGCGCGGCGGCGGCGCGCGCC	300		
DB 241	GGCGCGGGGGGAGCGGCTCTCGCGAGCGCGCGCGCGCGGCGGCGGCGGCGCGCGCC	300		
QY 301	GAGAGCTGTTCGAGCGGTGCGCAACCGGGACGTGGAAACGAGTCAAGAGGCTGTGACGC	360		
DB 301	GAGAGCTGTTCGAGCGGTGCGCAACCGGGACGTGGAAACGAGTCAAGAGGCTGTGACGC	360		
QY 361	CTGAGAGGTGAACAGCGCGACACGCGGGGCGAGGAAATCCACCCCGCTGCACCTTCGCGG	420		
DB 361	CTGAGAGGTGAACAGCGCGACACGCGGGGCGAGGAAATCCACCCCGCTGCACCTTCGCGG	420		
QY 421	CAGGTTTGGCGGGAAGACGTAGTTGAATATTTGCTTCAGAAATGTCGCAATGTCGAG	480		
DB 421	CAGGTTTGGCGGGAAGACGTAGTTGAATATTTGCTTCAGAAATGTCGCAATGTCGAG	480		
QY 481	CACGTGATGATGGGGGCTTATCTCTTCATATGCAATGCTCTTTTGGTCTGATGCTGAAG	540		
DB 481	CACGTGATGATGGGGGCTTATCTCTTCATATGCAATGCTCTTTTGGTCTGATGCTGAAG	540		
QY 541	TAGTCAATCTCTTTTGGGACATGGTGAGACCCCAATGCTCGAGATAAATGGAAATATA	600		
DB 541	TAGTCAATCTCTTTTGGGACATGGTGAGACCCCAATGCTCGAGATAAATGGAAATATA	600		
QY 601	CTCTCTCCATGAAGCTGCAATTAAGGAAGATGATGTTTGGATTGCTGTTACGCG	660		
DB 601	CTCTCTCCATGAAGCTGCAATTAAGGAAGATGATGTTTGGATTGCTGTTACGCG	660		
QY 661	ATGGAGCTGAGCGACCACTCCGAATACAGATGGAAGGACAGCATTTGATTTAGCAGATC	720		
DB 661	ATGGAGCTGAGCGCAACCATCCGAATACAGATGGAAGGACAGCATTTGATTTAGCAGATC	720		

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DB 721	CATCTGCGCAAGCAGTCTCTTA	780	CGTGGTGAATATAAGAAAGATGA	780
QY 781	GGAGTGGCAATGAAGAAAATG	840	ATGATGCTCAACATTAATGCTCA	840
DB 781	GGAGTGGCAATGAAGAAAATG	840	ATGATGCTCAACATTAATGCTCA	840
QY 841	CAAGTGTATGGCAGAAAATG	900	CAATTAATGCTCAACATTAATG	900
DB 841	CAAGTGTATGGCAGAAAATG	900	CAATTAATGCTCAACATTAATG	900
QY 901	TTGTACAGCTGTTACTGCAAC	960	TGATGCTCAACATTAATGCTCA	960
DB 901	TTGTACAGCTGTTACTGCAAC	960	TGATGCTCAACATTAATGCTCA	960
QY 961	TACCATTTACAAATGCTCTTT	1020	TATGATGAAGTAACTGAACCTT	1020
DB 961	TACCATTTACAAATGCTCTTT	1020	TATGATGAAGTAACTGAACCTT	1020
QY 1021	ATGCTGCTGTGTAATGCAAT	1080	TGCTGGCAATTCACCTCTTTCA	1080
DB 1021	ATGCTGCTGTGTAATGCAAT	1080	TGCTGGCAATTCACCTCTTTCA	1080
QY 1081	CTAAGAACAGGTTGAAAGTAT	1140	CTCTCTCTTAAGTTATGCTGCA	1140
DB 1081	CTAAGAACAGGTTGAAAGTAT	1140	CTCTCTCTTAAGTTATGCTGCA	1140
QY 1141	TCRAATCTCAATAAAGTGCT	1200	TATAGCTGGCTCCACACACAGT	1200
DB 1141	TCRAATCTCAATAAAGTGCT	1200	TATAGCTGGCTCCACACACAGT	1200
QY 1201	TAGCATATGAATTTAAAGG	1260	CGCTCGTTCGCAAGAGCTGAT	1260
DB 1201	TAGCATATGAATTTAAAGG	1260	CGCTCGTTCGCAAGAGCTGAT	1260
QY 1261	GAATCAAAAACATCTCTCT	1320	TGGAATGCTGAACATCAATCA	1320
DB 1261	GAATCAAAAACATCTCTCT	1320	TGGAATGCTGAACATCAATCA	1320
QY 1321	CAGCATTTGCAATGCTGCT	1380	CCATATCCAAAAGAAAGCAAT	1380
DB 1321	CAGCATTTGCAATGCTGCT	1380	CCATATCCAAAAGAAAGCAAT	1380
QY 1381	TGCTTAAGAAAGGAGCAAC	1440	ATCAATGAAGAGCTAAAGAA	1440
DB 1381	TGCTTAAGAAAGGAGCAAC	1440	ATCAATGAAGAGCTAAAGAA	1440
QY 1441	TGGCATCTGAGAAAGCTCA	1500	TATGTTGTTGAGTAGTGGTGA	1500
DB 1441	TGGCATCTGAGAAAGCTCA	1500	TATGTTGTTGAGTAGTGGTGA	1500
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DB 1501	TTAATGCTCTGGATAATCT	1560	TGTCACAGAGCTGCAATTTGT	1560
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DB 1561	TACAAACCTCGCGCTACT	1620	CTCTGAGCTATGGGTGTGAT	1620
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RESULT 2
ABQ77067
ID ABQ77067 standard; DNA; 3816 BP.
XX
AC ABQ77067;
XX
DT 08-APR-2003 (first entry)
XX
DE Tankyrase H, isotype 2 TaHo-2 DNA from clone K23.

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Qy ||||| 3241 GGGAAAGATACATCTCAGGAGAAAGAGTTTCTGAAGAAACCAACCATGCCAATG 3300
Db ||||| 3241 GGGAAAGATACATCTCAGGAGAAAGAGTTTCTGAAGAAACCAACCATGCCAATG 3300
Qy ||||| 3301 AACGAATGCTATTTTCATGGGTCCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTTGATG 3360
Db ||||| 3301 AACGAATGCTATTTTCATGGGTCCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTTGATG 3360
Qy ||||| 3361 AAAGCATGGGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAACTCTTT 3420
Db ||||| 3361 AAAGCATGGGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAACTCTTT 3420
Qy ||||| 3421 CCAAAAGCAATCAATATGATATGGAATTTGGAAGAGGTAATGAGTGTCCAGTTCCAAAG 3480
Db ||||| 3421 CCAAAAGCAATCAATATGATATGGAATTTGGAAGAGGTAATGAGTGTCCAGTTCCAAAG 3480
Qy ||||| 3481 ACAGATCTGTATCATTTTGCACAGGAGCTGCTCTTTTCCGGGTAACTTTGGGAAGT 3540
Db ||||| 3481 ACAGATCTGTATCATTTTGCACAGGAGCTGCTCTTTTCCGGGTAACTTTGGGAAGT 3540
Qy ||||| 3541 CTTTCTGCAAGTTCAGTGCATGAAATGGACATTTCTCTCCAGGTCATCACTCAGTCA 3600
Db ||||| 3541 CTTTCTGCAAGTTCAGTGCATGAAATGGACATTTCTCTCCAGGTCATCACTCAGTCA 3600
Qy ||||| 3601 CTGTTAGGCCAGTGTAAATGGCCCTAGCATTTAGTGAATATGTTATTTTACAGAGGAAC 3660
Db ||||| 3601 CTGTTAGGCCAGTGTAAATGGCCCTAGCATTTAGTGAATATGTTATTTTACAGAGGAAC 3660
Qy ||||| 3661 AGGCTTATCTGAGTATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3720

Db 3661 AGGCTTATCTGAGTATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3720
Qy 3721 GATAAATAGTATTTTAAAGAACTAATTCACCTGAACCTAAATCATCAAGCAGCAGTG 3780
Db 3721 GATAAATAGTATTTTAAAGAACTAATTCACCTGAACCTAAATCATCAAGCAGCAGTG 3780
Qy 3781 GCCTCTACGTTTCTACCTCTTCTGCTGAAAAA 3816
Db 3781 GCCTCTACGTTTCTACCTCTTCTGCTGAAAAA 3816
RESULT 5
AAC85294
ID AAC85294 standard; cDNA; 6019 BP.
XX
XX AAC85294;
XX
DT 29-MAR-2001 (first entry)
XX
DE Human SPANK cDNA.
XX
KW SPANK; SAM; sterile alpha motif; PARP; insulin resistance;
KW poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK;
KW ankyrin repeat; cytosol; insulin-responsive aminopeptidase; IRAP; GLUT4;
KW adipocyte; insulin signalling pathway; hyperlipidaemia;
KW glucose intolerance; atherosclerotic disease; atherosclerosis; obesity;
KW cardiac insufficiency; coronary insufficiency; stroke;
KW high blood pressure; non-insulin dependent diabetes; hypertension;
KW hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 252..3735
FT /tag= a
FT /product= "Human SPANK"
FT /transl_except= (pos:768..878,aa:173..209)
FT /transl_except= (pos:1230..1337,aa:327..362)
FT /transl_except= (pos:1374..1445,aa:375..398)
FT /transl_except= (pos:1695..1823,aa:482..524)
FT /transl_except= (pos:2172..2282,aa:641..677)
XX
PN WO200077225-A1.
XX
XX 21-DEC-2000.
PD
XX 09-JUN-2000; 2000WO-US015926.
PF
XX 11-JUN-1999; 99US-0138957P.
PR
XX (WHEE) WHITEHEAD INST BIOMEDICAL RES.
XX (GHEO) GEN HOSPITAL CORP.
PA
XX Chi N, Lodish HF;
PI
XX WPI; 2001-091404/10.
DR P-PSDB; AAB47022.
XX
XX New insulin signaling protein SPANK, useful for reducing body mass,
PT glucose intolerance or insulin resistance and for preventing or treating
PT obesity-related and muscle-related diseases.
XX
PS Claim 3; Fig 4; 65pp; English.
XX
XX This sequence represents the human SPANK cDNA. The SPANK protein
CC comprises 3 domains: (a) a SAM (sterile alpha motif) domain; (b) a PARP
CC (poly adenosine diphosphate-ribose polymerase) catalytic domain; and (c)
CC an ANK domain composed of ankyrin repeats. SPANK is a cytosolic protein
CC which can poly(ADP-ribose)ate itself. SPANK binds insulin-responsive
CC aminopeptidase (IRAP) and modulates translocation of GLUT4 in the
CC perinuclear region of adipocytes. It is an effector in the insulin
CC signalling pathway in eukaryotic cells. SPANK is useful for reducing body
CC mass, reducing glucose intolerance or insulin resistance, for preventing

868	DB	CAAGTGAATGCAGAAAGTCAACTCCATTACATTTGGCAGCAGAGATATACACAGAGTAAAGA	927
901	QY	TTGTACAGCTGTTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAAAGGTGATCTGG	960
928	DB	TTGTACAGCTGTTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAAAGGTGATCTGG	987
961	QY	TACCAATTACCAATGCCGTGTTCTTATGGTCATTTATGAAGTAACTGAACITTTTGGTCAAGC	1020
988	DB	TAGCATTATACAAATGCCGTGTTCTTATGGTCATTTATGAAGTAACTGAACITTTTGGTCAAGC	1047
1021	QY	ATGGTCGCTGTGTAAATGCAATGGACTTGTGGCAAATTCACCTCCTCTTCATGAGGCAGCTT	1080
1048	DB	ATGGTCGCTGTGTAAATGCAATGGACTTGTGGCAAATTCACCTCCTCTTCATGAGGCAGCTT	1107
1081	QY	CTAAGAACAGGGTTGAAGTAGTTCTCTCTCTTTAAAGTTATAGTGCAGACCCCAACACTGC	1140
1108	DB	CTAAGAACAGGGTTGAAGTAGTTCTCTCTCTTTAAAGTTATAGTGCAGACCCCAACACTGC	1167
1141	QY	TCAAATTGTCACAATAAAAGTGTATAGACTTGGCTCCCAACACACAGTTTAAAGAAGAAGAT	1200
1168	DB	TCAAATTGTCACAATAAAAGTGTATAGACTTGGCTCCCAACACACAGTTTAAAGAAGAAGAT	1227
1201	QY	TAGCATATGAATTTTAAAGGCCACTCGTGTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC	1260
1228	DB	TAGCATATGAATTTTAAAGGCCACTCGTGTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC	1287
1261	QY	GAATCAAAAAACATCTCTCTGGAATTTGGTGAATTTTCAAGCATCTCTCAACACATGAAA	1320
1288	DB	GAATCAAAAAACATCTCTCTGGAATTTGGTGAATTTTCAAGCATCTCTCAACACATGAAA	1347
1321	QY	CAGCATTGCAATTGTGCTGCTGCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACCTG	1380
1348	DB	CAGCATTGCAATTGTGCTGCTGCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACCTG	1407
1381	QY	TGCTTAGAAAAGGAGCAACATCAATGAAAGACTTAAAGAAATTTCTTGACCTCTCTGCACG	1440
1408	DB	TGCTTAGAAAAGGAGCAACATCAATGAAAGACTTAAAGAAATTTCTTGACCTCTCTGCACG	1467
1441	QY	TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAAGTAGTGGTGAACATGAAGCAAAAGG	1500
1468	DB	TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAAGTAGTGGTGAACATGAAGCAAAAGG	1527
1501	QY	TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCACT	1560
1528	DB	TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCACT	1587
1561	QY	TACAAACCTGCCCTTACTCTCTGAGCTATGGGTGTGATCCTACATTTATATCCCTTCAGG	1620
1588	DB	TACAAACCTGCCCTTACTCTCTGAGCTATGGGTGTGATCCTACATTTATATCCCTTCAGG	1647
1621	QY	GCCTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT	1680
1648	DB	GCCTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT	1707
1681	QY	CATTAGGTAATTACAGAGGCAGACAGACAATTCGTGGAAGCTGCAAAAGCTGGAGATGTG	1740
1708	DB	CATTAGGTAATTACAGAGGCAGACAGACAATTCGTGGAAGCTGCAAAAGCTGGAGATGTG	1767
1741	QY	AAACTGTAAAAAATCTGTACTTGTTCAGAGTGTCAACTGCACAGACATTTGAAGGGGCTC	1800
1768	DB	AAACTGTAAAAAATCTGTACTTGTTCAGAGTGTCAACTGCACAGACATTTGAAGGGGCTC	1827
1801	QY	AGTCTACACCACTTCATTTTTCAGCTGGGTATAAACAGAGTGTCCGTGGTGGAAATATCTGC	1860
1828	DB	AGTCTACACCACTTCATTTTTCAGCTGGGTATAAACAGAGTGTCCGTGGTGGAAATATCTGC	1887
1861	QY	TACAGCATGGAGCTGATGTGCATGCTCTAAAGATAAAGGAGGCCCTTGTAACCTTTGCCAATG	1920
1888	DB	TACAGCATGGAGCTGATGTGCATGCTCTAAAGATAAAGGAGGCCCTTGTAACCTTTGCCAATG	1947
1921	QY	CATGTTCTTATGACAATTATGAAGTTGCAGAACTCTTGTTTAAACATGGAGCAGTAGTTA	1980
1948	DB	CATGTTCTTATGACAATTATGAAGTTGCAGAACTCTTGTTTAAACATGGAGCAGTAGTTA	2007

QY	1981	ATGTAGCTGATTTATGGAAATTTTACACCTTTATCATGAAGCAGCAGCAAAAGGAAAAATATG	2040
Db	2008	ATGTAGCTGATTTATGGAAATTTTACACCTTTATCATGAAGCAGCAGCAAAAGGAAAAATATG	2067
QY	2041	AAATTTGCAAACTTTGCTCCAGCATGGTGCGAGCCCTACCAAAAAAAAACAGGGATGGAA	2100
Db	2068	AAATTTGCAAACTTTGCTCCAGCATGGTGCGAGCCCTACCAAAAAAAAACAGGGATGGAA	2127
QY	2101	ATACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTCAAAGATCTGCTTTAGGGAG	2160
Db	2128	ATACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTCAAAGATCTGCTTTAGGGAG	2187
QY	2161	ATCAGCTTTGCTAGATGCTGCCAAAGGGTTGTTTAGCCAGAGTGAAGAAGTCTGCTTT	2220
Db	2188	ATCAGCTTTGCTAGATGCTGCCAAAGGGTTGTTTAGCCAGAGTGAAGAAGTCTGCTTT	2247
QY	2221	CTCCTGATTAATGTAATTTGCCGCGATCCCAAGGCAGACATTCACACCTTTTACATTTAG	2280
Db	2248	CTCCTGATTAATGTAATTTGCCGCGATCCCAAGGCAGACATTCACACCTTTTACATTTAG	2307
QY	2281	CAGCTGGTTATATAATTTAGAAAGTTGCAGAGTATTGTTTACAACGCGAGCTGATGTGA	2340
Db	2308	CAGCTGGTTATATAATTTAGAAAGTTGCAGAGTATTGTTTACAACGCGAGCTGATGTGA	2367
QY	2341	ATGCCAAGCAAAAGGAGGACTTATTCCCTTTACATAATGCAGCATCTTACGGGCATGTAG	2400
Db	2368	ATGCCAAGCAAAAGGAGGACTTATTCCCTTTACATAATGCAGCATCTTACGGGCATGTAG	2427
QY	2401	ATGTAGCAGCTCTACTAATAAAGTATAATGTCATGTGTCATATGCCACGGACAATGGGCTT	2460
Db	2428	ATGTAGCAGCTCTACTAATAAAGTATAATGTCATGTGTCATATGCCACCAAATGGGCTT	2487
QY	2461	TCACACCTTTTGCACGAAGCAGCCCAAAAGGGAAGAACACAGCTTTGTGTGCTTTGTCGTAG	2520
Db	2488	TCACACCTTTTGCACGAAGCAGCCCAAAAGGGAAGAACACACAGCTTTGTGTGCTTTGTCGTAG	2547
QY	2521	CCCATGGAGCTGACCCGACTCTTTAAAAACAGAGAGGACAACAACCTTTAGATTTAGTTT	2580
Db	2548	CCCATGGAGCTGACCCGACTCTTTAAAAACAGAGAGGACAACAACCTTTAGATTTAGTTT	2607
QY	2581	CAGCGGATGATGTCAGCGCTCTTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTT	2640
Db	2608	CAGCGGATGATGTCAGCGCTCTTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTT	2667
QY	2641	GTTTAAAGCCTCAAGTGTCTCAATGGTGTGAGAGCCAGGAGCCATGCGAGATGCTCTCT	2700
Db	2668	GTTTAAAGCCTCAAGTGTCTCAATGGTGTGAGAGCCAGGAGCCATGCGAGATGCTCTCT	2727
QY	2701	CTTTCAGTCCATCTAGCCCATCAAGCTTTCTGACGCCAGCAGTCTTTGACAACTTATCTG	2760
Db	2728	CTTTCAGTCCATCTAGCCCATCAAGCTTTCTGACGCCAGCAGTCTTTGACAACTTATCTG	2787
QY	2761	GGAGTTTTTTCAGAACTGTCTTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTGTCTCCAGTT	2820
Db	2788	GGAGTTTTTTCAGAACTGTCTTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTGTCTCCAGTT	2847
QY	2821	TGAGAAAAAGGAGGTTTCAGGAGTATATTTTAGCATTAACCTCAATTCGTAAAGAAATCTTG	2880
Db	2848	TGAGAAAAAGGAGGTTTCAGGAGTATATTTTAGCATTAACCTCAATTCGTAAAGAAATCTTG	2907
QY	2881	GACTTGAGCACCTTAAATGGATATATTTTGGAGAGNACAGATCACTTTTGGATGTTATAGTTG	2940
Db	2908	GACTTGAGCACCTTAAATGGATATATTTTGGAGAGNACAGATCACTTTTGGATGTTATAGTTG	2967
QY	2941	AGATGGGGCAAGGAGCTGAAGGATTTGGAATCAATGCTTATGGACATAGGCACAAAAC	3000
Db	2968	AGATGGGGCAAGGAGCTGAAGGATTTGGAATCAATGCTTATGGACATAGGCACAAAAC	3027
QY	3001	TAAATTAAGGAGTCGAGAGACTTATCTCCGGACAACAAAGTCTTAAACCCATATTTAACTTT	3060
Db	3028	TAAATTAAGGAGTCGAGAGACTTATCTCCGGACAACAAAGTCTTAAACCCATATTTAACTTT	3087

3061	QY	TGAACACCTCTGGTAGTGAAACAATTCTTTATAGATCTGTCTCTCTGTATGATATAAGAGGTTTC	3121
3088	Db	TGAACACCTCTGGTAGTGAAACAATTCTTTATAGATCTGTCTCTGTATGATATAAGAGGTTTC	3147
3121	QY	AGTCTGTGGAGNAGATGCAAGGTACAGTTTCGAGACACAGAGATGGAGGTCATGCAG	3180
3148	Db	AGTCTGTGGAGNAGATGCAAGGTACAGTTTCGAGACACAGAGATGGAGGTCATGCAG	3207
3181	QY	GTGGAAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTCTTAACAAGAAACTAT	3240
3208	Db	GTGGAAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTATCAAGAAACTAT	3267
3241	QY	GGGAAAGATACACTCACCGGAGAAAGAGTTCTTGAAGAAAACCAACACCATGCCAATG	3300
3268	Db	GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAAACCAACACCATGCCAATG	3327
3301	QY	AACGAATGCTATTTCATGGGTCTCCTTTTGTGAATGCAATTATCCACAAGGCTTTTGATG	3360
3328	Db	AACGAATGCTATTTCATGGGTCTCCTTTTGTGAATGCAATTATCCACAAGGCTTTTGATG	3387
3361	QY	AAAGGCATCGGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGAAAACTCTT	3420
3388	Db	AAAGGCATCGGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGAAAACTCTT	3447
3421	QY	CCAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGCCAGTTTCAAAAG	3480
3448	Db	CCAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGCCAGTTTCAAAAG	3507
3481	QY	ACAGATCTTGTTCATTTGCCACAGCAGCTGCTCTTTTGGCCGGGTAACTTGGGAAAGT	3540
3508	Db	ACAGATCTTGTTCATTTGCCACAGCAGCTGCTCTTTTGGCCGGGTAACTTGGGAAAGT	3567
3541	QY	CTTCTCTGCAGTTTCAGTGCACATGAAATGSCACATTTCTCTCCAGGTTCATCTCAGTCA	3600
3568	Db	CTTCTCTGCAGTTTCAGTGCACATGAAATGSCACATTTCTCTCCAGGTTCATCTCAGTCA	3627
3601	QY	CTGTAGGCCAGTGTAAATGGCTAGCATTAAGTGAATATGTTATTTACAGAGGAGAAC	3660
3628	Db	CTGTAGGCCAGTGTAAATGGCTAGCATTAAGTGAATATGTTATTTACAGAGGAGAAC	3687
3661	QY	AGGCTTATCCTGAGTATTTAAATTACACAGATTAAGGCCCTGAAGGTATGGTGCATG	3720
3688	Db	AGGCTTATCCTGAGTATTTAAATTACACAGATTAAGGCCCTGAAGGTATGGTGCATG	3747
3721	QY	GATAAATAGTATTTTAAAGAACTAATTCACCTGGAACCTTAAATCATCAAAGCAGCAGTG	3780
3748	Db	GATAAATAGTATTTTAAAGAACTAATTCACCTGGAACCTTAAATCATCAAAGCAGCAGTG	3807
3781	QY	GCCTCTACGTTTTTACTCTCTTTGCTGAAAAAAA	3813
3808	Db	GCCTCTACGTTTTTACTCTCTTTGCTGAAAAAAA	3840
RESULT 6			
AAC66825			
ID	AAC66825 standard; cDNA; 4275 BP.		
XX	AAC66825;		
XX	27-FEB-2001 (first entry)		
XX	Human tankyrase II coding sequence SEQ ID NO: 5.		
DE	Human; tankyrase II; telomere length; signal transduction; ss.		
XX	Homo sapiens.		
XX	Key		
XX	Location/Qualifiers		
FT	284..3784		
FT	/*tag= a		
FT	/product= "tankyrase II"		
FT	/transl_except= (pos:655..660,aa:TyrThr)		
XX			

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Db 1441 TGGCATCTGAGAAAGCTCATTAATGATGTTGTTGAAGTAGTGGTGAACACATGAAGCAAGG 1500
Db 1506 TGGCATCTGAGAAAGCTCATTAATGATGTTGTTGAAGTAGTGGTGAACACATGAAGCAAGG 1565
Qy 1501 TTAATGCTCTGGATAAATCTTGGTCAGACTCTCTACACAGAGCTGCATATTTGGTCATC 1560
Db 1566 TTAATGCTCTGGATAAATCTTGGTCAGACTCTCTACACAGAGCTGCATATTTGGTCATC 1625
Qy 1561 TACAAACTGCGCGCTACTCTCTGAGCTATGGTGTGATCCTAACTATATATCCCTTCAGG 1620
Db 1626 TACAAACCTGCGCGCTACTCTCTGAGCTATGGTGTGATCCTAACTATATATCCCTTCAGG 1685
Qy 1621 GCTTTACTGCTTTACAGATGGGAATGAAAATGTACAGCAACTCTCCAAAGAGGGTATCT 1680
Db 1686 GCTTTACTGCTTTACAGATGGGAATGAAAATGTACAGCAACTCTCCAAAGAGGGTATCT 1745
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Db 1746 CATTAGGTAAATTCAGAGCAGACAGACAATTTGCTGGAGCTGCAAGGCTGGAGATGTG 1805
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Db 1806 AAACCTGTAAGAAAACCTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1865
Qy 1801 AGTCTACACCACTTCATTTTCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC 1860
Db 1866 AGTCTACACCACTTCATTTTCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC 1925
Qy 1861 TACAGATGGAGCTGTGTGATGCTAAGATAAGAGGCGCTTGTACCTTTGTCACAATG 1920
Db 1926 TACAGATGGAGCTGTGTGATGCTAAGATAAGAGGCGCTTGTACCTTTGTCACAATG 1985
Qy 1921 CATGCTCTTATGGACATTAATGAGTTCAGAACTTCTTGTAAACATGGAGCAGTACTTA 1980
Db 1986 CATGCTCTTATGGACATTAATGAGTTCAGAACTTCTTGTAAACATGGAGCAGTACTTA 2045
Qy 1981 ATGAGCTGATTTATGGAATTTACACCTTTACATGAGCAGCAGCAAGGAAATATG 2040
Db 2046 ATGAGCTGATTTATGGAATTTACACCTTTACATGAGCAGCAGCAAGGAAATATG 2105
Qy 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGAGACCTTACCAAAAAAACHAGGATGGAA 2100
Db 2106 AAATTTGCAAACTTCTGCTCCAGCATGGTGAGACCTTACCAAAAAAACHAGGATGGAA 2165
Qy 2101 ATACTCTTTGGATCTGTTAAAGATGGAGATCAGATATTTCAAGATCTGCTTAGGGGAG 2160
Db 2166 ATACTCTTTGGATCTGTTAAAGATGGAGATCAGATATTTCAAGATCTGCTTAGGGGAG 2225
Qy 2161 ATGAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAAGTTGCTTT 2220
Db 2226 ATGAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAAGTTGCTTT 2285
Qy 2221 CTCTGTATATGTAAATTTGCGCGATACCCAAAGGAGACATTTCAACCTTTACATTTAG 2280
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Db 2346 CAGCTGGTTATATTAATTTAGAACTTCAGAGTATTTGTTACACACGGAGCTCATGTGA 2405
Qy 2341 ATGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGACAGCATCTTACCGGCATGTAG 2400
Db 2406 ATGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGACAGCATCTTACCGGCATGTAG 2465
Qy 2401 ATGTAGCAGCTCTACTAATAAAGTATATGTCATGTGTCAATGCCACGCAAAATGGGCTT 2460
Db 2466 ATGTAGCAGCTCTACTAATAAAGTATATGTCATGTGTCAATGCCACGCAAAATGGGCTT 2525
Qy 2461 TCACACCTTTGCAGAGCAGCCCAAGAGGACGAACACAGCTTTGTGCTTTGCTAG 2520

Db 2526 TCACACCTTTGCAGAGCAGCCCAAAAGGACGAACACACAGCTTTGTGCTTTGTTGCTAG 2585
Qy 2521 CCATATGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAAACACCTTTTAGTTAGTTT 2580
Db 2586 CCATATGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAAACACCTTTTAGTTAGTTT 2645
Qy 2581 CAGCGGATGATGTACGGCTCTTTCTGACAGACGCCATGCCCCCATCTGCTCTGCCCTCTT 2640
Db 2646 CAGCAGATGATGTACGGCTCTTTCTGACAGACGCCATGCCCCCATCTGCTCTGCCCTCTT 2705
Qy 2641 GTTACAGAGCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGCGAGATGCTCTCT 2700
Db 2706 GTTACAGAGCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGCGAGATGCTCTCT 2765
Qy 2701 CTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGACGACGAGCTTTTGACAACCTTATCTG 2760
Db 2766 CTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGACGACGAGCTTTTGACAACCTTATCTG 2825
Qy 2761 GGAGTTTTTCAGAACTGTCTTCAGTAGTTAGTTTCAAGTGAAACAGAGGCTGCTTCCAGTT 2820
Db 2826 GAGTTTTTTTCAGAACTGTCTTCAGTAGTTAGTTTCAAGTGAAACAGAGGCTGCTTCCAGTT 2885
Qy 2821 TGAGAAAAAGGAGGTTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGGAATCTTG 2880
Db 2886 TGAGAAAAAGGAGGTTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGGAATCTTG 2945
Qy 2881 GACTTGAGCACTTAATGGATATATTTTGAGAGAGAAACAGATCACTTTTGGATGTATAGTTG 2940
Db 2946 GACTTGAGCACTTAATGGATATATTTTGAGAGAGAAACAGATCACTTTTGGATGTATAGTTG 3005
Qy 2941 AGATGGGCAACAGGAGCTGAAAGGAGTTGGAATCAATGCTTATGGACATAGGCACAAAC 3000
Db 3006 AGATGGGCAACAGGAGCTGAAAGGAGTTGGAATCAATGCTTATGGACATAGGCACAAAC 3065
Qy 3001 TAATTAAGGAGTGCAGAGACTTATCTCCGACAAACAAAGCTCTTAAACCCATATTTAACTT 3060
Db 3066 TAATTAAGGAGTGCAGAGACTTATCTCCGACAAACAAAGCTCTTAAACCCATATTTAACTT 3125
Qy 3061 TGAACACCTCTGCTAGTGGAACTTCTTATAGATCTGTCTCTGATGATAAAGAGTTTC 3120
Db 3126 TGAACACCTCTGCTAGTGGAACTTCTTATAGATCTGTCTCTGATGATAAAGAGTTTC 3185
Qy 3121 AGTCTGTGGAGGAGAGATGCAAGTACAGTTCGAGAGCAGACAGATGGAGTTCATGAG 3180
Db 3186 AGTCTGTGGAGGAGAGATGCAAGTACAGTTCGAGAGCAGACAGATGGAGTTCATGAG 3245
Qy 3181 GTGGAATCTTCAACAGATACAATATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTAT 3240
Db 3246 GTGGAATCTTCAACAGATACAATATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTAT 3305
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Qy 3301 AAGCAATGCTATTTCAATGGGTCTCTTTTCTGATGCAATTTATCCACAAAGGCTTTGATG 3360
Db 3366 AAGCAATGCTATTTCAATGGGTCTCTTTTCTGATGCAATTTATCCAAAGGCTTTGATG 3425
Qy 3361 AAAGGCAATGCGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAACCTCTT 3420
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Qy 3421 CCAAAAGCAATCAATATGATATGGAATTCGAGAGGATCTGGGTGTCAGTTTCAAAAG 3480
Db 3486 CCAAAAGCAATCAATATGATATGGAATTCGAGAGGATCTGGGTGTCAGTTTCAAAAG 3545
Qy 3481 ACAGATCTGCTTACATTTGCCACAGGAGCTGCTTTTTCGCGGGTAACTTGGGAAAGT 3540
Db 3546 ACAGATCTGCTTACATTTGCCACAGGAGCTGCTTTTTCGCGGGTAACTTGGGAAAGT 3605
Qy 3541 CTTTCTGCAAGTTCAGTGCATGAAAATGGCACATTTCTCTCCAGGTCATCAGTCA 3600
Db 3606 CTTTCTGCAAGTTCAGTGCATGAAAATGGCACATTTCTCTCCAGGTCATCAGTCA 3665

Db 1792 TCAATGTACAAATAAAGTGCTATAGACTTGGCTCCACACCAAGTTAAAGAAAGAT 1851
Qy |||||
Db 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAAAGCTGATGTACTC 1260
Qy |||||
Db 1852 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAAAGCTGATGTACTC 1911
Qy |||||
Db 1261 GAATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCTCAACACATGAAA 1320
Qy |||||
Db 1912 GAATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCTCAACACATGAAA 1971
Qy |||||
Db 1321 CAGCATTCGATTTGCTGCTCATCTCCATATCCAAAGAAAGCAATATGTGAACCTGT 1380
Qy |||||
Db 1972 CAGCATTCGATTTGCTGCTCATCTCCATATCCAAAGAAAGCAATATGTGAACCTGT 2031
Qy |||||
Db 1381 TGCTAAAGAAAGGAGCAACATCAATGAAAGACTTAAAGAAATCTTGACTCTCTGCAAG 1440
Qy |||||
Db 2032 TGCTAAAGAAAGGAGCAACATCAATGAAAGACTTAAAGAAATCTTGACTCTCTGCAAG 2091
Qy |||||
Db 1441 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGG 1500
Qy |||||
Db 2092 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGG 2151
Qy |||||
Db 1501 TTAATGCTCTGATAATCTTCTGCTCAGACTTCTCTACACAGAGCTGCATATTTGTGCTCATC 1560
Qy |||||
Db 2152 TTAATGCTCTGATAATCTTCTGCTCAGACTTCTCTACACAGAGCTGCATATTTGTGCTCATC 2211
Qy |||||
Db 1561 TACAAACCTGCGCCCTACTCTCTGAGCTATGGGTGTGATCTTAACATATATATCTCTCAGG 1620
Qy |||||
Db 2212 TACAAACCTGCGCCCTACTCTCTGAGCTATGGGTGTGATCTTAACATATATATCTCTCAGG 2271
Qy |||||
Db 1621 GCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT 1680
Qy |||||
Db 2272 GCTTTACTGCTTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT 2331
Qy |||||
Db 1681 CATTAGGTAAATTCAGAGCAGACAGCAATTTCTGGAAGCTGCAAGCTGGAGATGTGCG 1740
Qy |||||
Db 2332 CATTAGGTAAATTCAGAGCAGACAGCAATTTCTGGAAGCTGCAAGCTGGAGATGTGCG 2391
Qy |||||
Db 1741 AAACTGTAAAAAAACTGTGTACTGTTCTAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1800
Qy |||||
Db 2392 AAACTGTAAAAAAACTGTGTACTGTTCTAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 2451
Qy |||||
Db 1801 AGTCTACACCACTTCAATTTGCGAGCTGGGTATACAGAGTGTCCGTGGTGAATATCTGC 1860
Qy |||||
Db 2452 AGTCTACACCACTTCAATTTGCGAGCTGGGTATACAGAGTGTCCGTGGTGAATATCTGC 2511
Qy |||||
Db 1861 TACAGCATGGAGCTGATGTGATGCTAAAGATTAAGGAGGCTTGTACCTTTGCACAATG 1920
Qy |||||
Db 2512 TACAGCATGGAGCTGATGTGATGCTAAAGATTAAGGAGGCTTGTACCTTTGCACAATG 2571
Qy |||||
Db 1921 CATGTTCTTATGGACATTTAATGAATGTCAGAACTTCTTTGTTAAACATGGAGCAGTAGTTA 1980
Qy |||||
Db 2572 CATGTTCTTATGGACATTTAATGAATGTCAGAACTTCTTTGTTAAACATGGAGCAGTAGTTA 2631
Qy |||||
Db 1981 ATGTAGCTGATTTATGAAAAATTTACACTTTACATGAAGAGCAGCAAAAGGAAAAATATG 2040
Qy |||||
Db 2632 ATGTAGCTGATTTATGAAAAATTTACACTTTACATGAAGAGCAGCAAAAGGAAAAATATG 2691
Qy |||||
Db 2041 AAAATTTGCAAAATTTCTGCTCCAGCATGTGTGAGACCTTACCACAAAAAAGAGGATGAAA 2100
Qy |||||
Db 2692 AAAATTTGCAAAATTTCTGCTCCAGCATGTGTGAGACCTTACCACAAAAAAGAGGATGAAA 2751
Qy |||||
Db 2101 ATACTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2160
Qy |||||
Db 2752 ATACTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2811
Qy |||||
Db 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTTTAGCCAGAGTGAAGATGTGCTT 2220
Qy |||||
Db 2812 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTTTAGCCAGAGTGAAGAAAGTGTGCTT 2871
Qy |||||
Db 2221 CTCCTGATAATGTAAATTTGCCGATACCCCAAGGCAGACATTTCAACACTTTTACATTTAG 2280
Qy |||||

Db 2872 CTCTCGATATGTAAATTTGCCGCGATACCCAAAGCAGACATTTCAACACCTTTTACATTTAG 2931
Qy |||||
Db 2281 CAGCTGGTTTAAATAATTTAGAAAGTTGCAGAGTATTTGTTTACAAACACGAGAGCTGATGTGA 2340
Qy |||||
Db 2932 CAGCTGGTTTAAATAATTTAGAAAGTTGCAGAGTATTTGTTTACAAACACGAGAGCTGATGTGA 2991
Qy |||||
Db 2341 ATGCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTACGGGCATGTAG 2400
Qy |||||
Db 2992 ATGCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTACGGGCATGTAG 3051
Qy |||||
Db 2401 ATGTAGCAGCTCTACTAATAAAGTATAATGCATGTGTCAATGCCACGACAAAATGGGCTT 2460
Qy |||||
Db 3052 ATGTAGCAGCTCTACTAATAAAGTATAATGCATGTGTCAATGCCACGACAAAATGGGCTT 3111
Qy |||||
Db 2461 TCACACCTTTTGCGACGAAGCAGGCCAAAGGAGCAACACAGCTTTGTGCTTTGTTGCTAG 2520
Qy |||||
Db 3112 TCACACCTTTTGCGACGAAGCAGGCCAAAGGAGCAACACAGCTTTGTGCTTTGTTGCTAG 3171
Qy |||||
Db 2521 CCCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAAACCTTTTATAGATTTAGTTT 2580
Qy |||||
Db 3172 CCCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAAACCTTTTATAGATTTAGTTT 3231
Qy |||||
Db 2581 CAGCGATGATGTGAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTT 2640
Qy |||||
Db 3232 CAGCGATGATGTGAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTT 3291
Qy |||||
Db 2641 GTTACAAGCCTCAAGTGCTCAATGGTGTGAAGGCCCAGAGGCCCATGCGAGATGCTCTCT 2700
Qy |||||
Db 3292 GTTACAAGCCTCAAGTGCTCAATGGTGTGAAGGCCCAGAGGCCCATGCGAGATGCTCTCT 3351
Qy |||||
Db 2701 CTTTCAGTCTCCATCTAGCCCATCAAGCCTTTCTCAGCCAGCAGCTTTTGACAACCTTATCTG 2760
Qy |||||
Db 3352 CTTTCAGTCTCCATCTAGCCCATCAAGCCTTTCTCAGCCAGCAGCTTTTGACAACCTTATCTG 3411
Qy |||||
Db 2761 GGAGTTTTTTCAGAACTGTCTTTCAGTGTAGTTAGTTCAAGTGGAAACAGAGGGTGTCTTCCAGTT 2820
Qy |||||
Db 3412 GGAGTTTTTTCAGAACTGTCTTTCAGTGTAGTTCAAGTGGAAACAGAGGGTGTCTTCCAGTT 3471
Qy |||||
Db 2821 TGGAGAAAAAGGAGGTTTCCAGGAGTAGATTTTACATTAATCTCAATTCGTAAAGNATCTTG 2880
Qy |||||
Db 3472 TGGAGAAAAAGGAGGTTTCCAGGAGTAGATTTTACATTAATCTCAATTCGTAAAGNATCTTG 3531
Qy |||||
Db 2881 GACTTTGAGCACTTAATGCGATATATTTGAGAGAGAAACAGATCAGCTTTTGGATGTATTAGTTG 2940
Qy |||||
Db 3532 GACTTTGAGCACTTAATGCGATATATTTGAGAGAGAAACAGATCAGCTTTTGGATGTATTAGTTG 3591
Qy |||||
Db 2941 AGATGGGCGCAAGAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAAC 3000
Qy |||||
Db 3592 AGATGGGCGCAAGAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAAC 3651
Qy |||||
Db 3001 TAATTTAAGGAGTCGAGAGACTTATCTCCGCGACAAACAGGCTCTTAAACCATATTTAACTT 3060
Qy |||||
Db 3652 TAATTTAAGGAGTCGAGAGACTTATCTCCGCGACAAACAGGCTCTTAAACCATATTTAACTT 3711
Qy |||||
Db 3061 TGAACACCTCTGTTAGTGGAAACAAATCTTATAGATCTGCTCTCTGATGATAAGAGTTTC 3120
Qy |||||
Db 3712 TGAACACCTCTGTTAGTGGAAACAAATCTTATAGATCTGCTCTCTGATGATAAGAGTTTC 3771
Qy |||||
Db 3121 AGTCTGTGGAGGAGAGATGCAAGTACAGTTCGAGAGCAGAGATGGAGGTCATGCAG 3180
Qy |||||
Db 3772 AGTCTGTGGAGGAGAGATGCAAGTACAGTTCGAGAGCAGAGATGGAGGTCATGCAG 3831
Qy |||||
Db 3181 GTGGAATCTTCAACAGATACAAATATTTCTCAAGATTGAGAAGGTTTGTAAACAGAAACTAT 3240
Qy |||||
Db 3832 GTGGAATCTTCAACAGATACAAATATTTCTCAAGATTGAGAAGGTTTGTAAACAGAAACTAT 3891
Qy |||||
Db 3241 GGGAAAGATACACTCACCGGAGAAAGAAAGTTCCTGAAGAAACCAACCAATGCCCAATG 3300
Qy |||||
Db 3892 GGGAAAGATACACTCACCGGAGAAAGAAAGTTCCTGAAGAAACCAACCAATGCCCAATG 3951
Qy |||||
Db 3301 AACGAATGCTATTTTCATGGGTCCTTTTGTGAAATCAATTTATCCACAAAGGCTTTGATG 3360
Qy |||||
Db 3952 AACGAATGCTATTTTCATGGGTCCTTTTGTGAAATCAATTTATCCACAAAGGCTTTGATG 4011
Qy |||||

QY 421 CAGGTTTGGGCGAAGACGTAGTTGAATATTTGCTTCAGNATGGTGCAATGTCCAAG 480
DB 576 CAGGTTTGGGCGAAGACGTAGTTGAATATTTGCTTCAGNATGGTGCAATGTCCAAG 635
QY 481 CACGTGATGATGGGGGCTTATTCCTCTTTCATAATGCATGCTCTTTTGGTTCATGCTGAAG 540
DB 636 CACGTGATGATGGGGGCTTATTCCTCTTTCATAATGCATGCTCTTTTGGTTCATGCTGAAG 695
QY 541 TAGTCAATCTCCTTTTGGCATGGTGCAGACCCCAATGCTCGAGATAATTTGGAAATTA 600
DB 696 TAGTCAATCTCCTTTTGGCATGGTGCAGACCCCAATGCTCGAGATAATTTGGAAATTA 755
QY 601 CTCCTCTCCATGAGCTGCAATTAAGGAAAGATTGATTTTGCAATTTGCTGTTACAGC 660
DB 756 CTCCTCTCCATGAGCTGCAATTAAGGAAAGATTGATTTTGCAATTTGCTGTTACAGC 815
QY 661 ATGGAGCTGAGCCCAACATCCGAATACAGATGGAAGCAGACATTCGATTTAGCAGATC 720
DB 816 ATGGAGCTGAGCCCAACATCCGAATACAGATGGAAGCAGACATTCGATTTAGCAGATC 875
QY 721 CATCTGCCAAAGCAGTGTCTACTCGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 780
DB 876 CATCTGCCAAAGCAGTGTCTACTCGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 935
QY 781 GGAGTGGCAATGAAGAAAAAATGATGCTCTACTCAACCAATTAATGTCNACTGCCACG 840
DB 936 GGAGTGGCAATGAAGAAAAAATGATGCTCTACTCAACCAATTAATGTCNACTGCCACG 995
QY 841 CAAAGTGAGGAGAAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAGA 900
DB 996 CAAAGTGAGGAGAAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAGAGTAAGA 1055
QY 901 TTGTACAGCTGTTACTGCAACATGGAGCTGATGCCATGCTTAAAGATAAAGGTGATCTGG 960
DB 1056 TTGTACAGCTGTTACTGCAACATGGAGCTGATGCCATGCTTAAAGATAAAGGTGATCTGG 1115
QY 961 TACCATTAACAATGCCCTGTTCTTATGGTCATTATGAAGTAACTGAACCTTTGGTCAAGC 1020
DB 1116 TACCATTAACAATGCCCTGTTCTTATGGTCATTATGAAGTAACTGAACCTTTGGTCAAGC 1175
QY 1021 ATGGTGCTGTGTAATGSCAATGACTTTGGCAATTCACCTCCTTCATGAGGACGCTT 1080
DB 1176 ATGGTGCTGTGTAATGSCAATGACTTTGGCAATTCACCTCCTTCATGAGGACGCTT 1235
QY 1081 CTAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAAGTTATGGTGCAGACCCACACTGC 1140
DB 1236 CTAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAAGTTATGGTGCAGACCCACACTGC 1295
QY 1141 TCAATTTGTCACAATAAAGTGTATAGACTTGGCTCCACACACAGTTAAAGAAAGAT 1200
DB 1296 TCAATTTGTCACAATAAAGTGTATAGACTTGGCTCCACACACAGTTAAAGAAAGAT 1355
QY 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC 1260
DB 1356 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC 1415
QY 1261 GAATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCCTCAACACATGAAA 1320
DB 1416 GAATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCCTCAACACATGAAA 1475
QY 1321 CAGCATTTGCATTTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTTGAATGT 1380
DB 1476 CAGCATTTGCATTTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTTGAATGT 1535
QY 1381 TGCTTAAGAAAAGGAGCAAAACATCAATGAAGAAGCTTAAAGAAATTCCTGACTCCTCTGCAAG 1440
DB 1536 TGCTTAAGAAAAGGAGCAAAACATCAATGAAGAAGCTTAAAGAAATTCCTGACTCCTCTGCAAG 1595
QY 1441 TGGCATCTGAAGAAAGCTCATTAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGG 1500
DB 1596 TGGCATCTGAAGAAAGCTCATTAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGG 1655
QY 1501 TTAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTTGTCATC 1560

DB 1656 TTAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTTGTCATC 1715
QY 1561 TACAAAACCTGCCGCCCTACTCCTCAGCTATGGGTGTGATCCTAAATATATATATCCCTTCAGG 1620
DB 1716 TACAAAACCTGCCGCCCTACTCCTCAGCTATGGGTGTGATCCTAAATATATATATCCCTTCAGG 1775
QY 1621 GCCTTACTGCTTTTACAGATGGGAAATGAANAATGTACAGCAACTCCTCCAGAGGGTATCT 1680
DB 1776 GCCTTACTGCTTTTACAGATGGGAAATGAANAATGTACAGCAACTCCTCCAGAGGGTATCT 1835
QY 1681 CATTTAGTAAATTCAGAGGACAGACACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTG 1740
DB 1836 CATTTAGTAAATTCAGAGGACAGACACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTG 1895
QY 1741 AAACTGTAAAAAAACTGTGTACTGTTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1800
DB 1896 AAACTGTAAAAAAACTGTGTACTGTTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1955
QY 1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGNATATCTGC 1860
DB 1956 AGTCTACACCACTTCATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGNATATCTGC 2015
QY 1861 TACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCTTGTACCTTTTGCACAATG 1920
DB 2016 TACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCTTGTACCTTTTGCACAATG 2075
QY 1921 CATGTTCTTATGGACATTAATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTA 1980
DB 2076 CATGTTCTTATGGACATTAATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTA 2135
QY 1981 ATGTAGCTGATTTTATGGAAATTTACACCTTTTACATGAGCAGCAGCAAAAGGAAATATG 2040
DB 2136 ATGTAGCTGATTTTATGGAAATTTACACCTTTTACATGAGCAGCAGCAAAAGGAAATATG 2195
QY 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACAAAAAACAAGGATCGAA 2100
DB 2196 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACAAAAAACAAGGATCGAA 2255
QY 2101 ATACTCCTTTGGATCTTTGTTTAAAGATGGAATACAGATATTCAGATCTGCTTAGGGGAG 2160
DB 2256 ATACTCCTTTGGATCTTTGTTTAAAGATGGAATACAGATATTCAGATCTGCTTAGGGGAG 2315
QY 2161 ATGAGCTTTGCTAGATGCTGCCAAGNAGGTTGTTTAGCCAGAGTGAAGNAGTTGCTTT 2220
DB 2316 ATGAGCTTTGCTAGATGCTGCCAAGNAGGTTGTTTAGCCAGAGTGAAGNAGTTGCTTT 2375
QY 2221 CTCTGTATAATGTAATAATTTGCCGCGATACCAAGCGACACATTCACACCTTTTACATTTAG 2280
DB 2376 CTCTGTATAATGTAATAATTTGCCGCGATACCAAGCGACACATTCACACCTTTTACATTTAG 2435
QY 2281 CAGCTGGTTATAATAATTTAGAAAGTTGCAGAGTATTTGTTTACACACGAGAGCTGATGTA 2340
DB 2436 CAGCTGGTTATAATAATTTAGAAAGTTGCAGAGTATTTGTTTACACACGAGAGCTGATGTA 2495
QY 2341 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTACGGGATGTAG 2400
DB 2496 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTACGGGATGTAG 2555
QY 2401 ATGTAGCAGCTCTACTAATAAAGTATTAATCATGTGTCAAATGCCACGACAAAATGGGGCTT 2460
DB 2556 ATGTAGCAGCTCTACTAATAAAGTATTAATCATGTGTCAAATGCCACGACAAAATGGGGCTT 2615
QY 2461 TCACACCTTTTGCAGAGACAGCCCAAAAGGAGGAGAACACAGCTTTTGTGCTGTAG 2520
DB 2616 TCACACCTTTTGCAGAGACAGCCCAAAAGGAGGAGAACACAGCTTTTGTGCTGTAG 2675
QY 2521 CCNATGAGCTGACCCGACTCTTAAAAATCAGNAGGACAAAACACCTTTAGATTTAGTTT 2580
DB 2676 CCNATGAGCTGACCCGACTCTTAAAAATCAGNAGGACAAAACACCTTTAGATTTAGTTT 2735
QY 2581 CAGCGAGTATGTACGGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTT 2640

Db 2736 CAGCAGATGATGTCAGCGCTCTCTCTGACAGAGCCATGCCCCCTCTGCTCTGCTGCTCTT 2795
 Qy 2641 GTTCAAGCCTCAAGTGTCTCAATGCTGTGAGAGCCAGAGGACCACTGACAGTCTCTCT 2700
 Db 2796 GTTCAAGCCTCAAGTGTCTCAATGCTGTGAGAGCCAGAGGACCACTGACAGTCTCTCT 2855
 Qy 2701 CTTCAAGTGTCTCAAGTGTCTCAATGCTGTGAGAGCCAGAGGACCACTGACAGTCTCTCT 2760
 Db 2856 CTTCAAGTGTCTCAAGTGTCTCAATGCTGTGAGAGCCAGAGGACCACTGACAGTCTCTCT 2915
 Qy 2761 GGAGTTTTCAGAACTGCTTTCAGTAGTGTGAGAGCCAGAGGACCACTGACAGTCTCTCT 2820
 Db 2916 GGAGTTTTCAGAACTGCTTTCAGTAGTGTGAGAGCCAGAGGACCACTGACAGTCTCTCT 2975
 Qy 2821 TGGAGAAAGAGAGGCTTCCAGAGTGTGAGAGCCAGAGGACCACTGACAGTCTCTCT 2880
 Db 2976 TGGAGAAAGAGAGGCTTCCAGAGTGTGAGAGCCAGAGGACCACTGACAGTCTCTCT 3035
 Qy 2881 GACTTGGACCTCAATGATATATTTGAGAGAGCAAGATCACTTGGATGTATTTAGTTG 2940
 Db 3036 GACTTGGACCTCAATGATATATTTGAGAGAGCAAGATCACTTGGATGTATTTAGTTG 3095
 Qy 2941 AGATGGGGCAAGAGAGCTGAAGAGATTTGAGAGCCAGAGGACCACTGACAGTCTCTCT 3000
 Db 3096 AGATGGGGCAAGAGAGCTGAAGAGATTTGAGAGCCAGAGGACCACTGACAGTCTCTCT 3155
 Qy 3001 TAAATTAAGAGTCCAGAGATTTATCTCCGACACAGAGGCTTAAACCATATTTAACTT 3060
 Db 3156 TAAATTAAGAGTCCAGAGATTTATCTCCGACACAGAGGCTTAAACCATATTTAACTT 3215
 Qy 3061 TGAACACCTCTGTTAGTGGAAATTTCTTATAGATCTCTCTCTGATGATAAAGATTTTC 3120
 Db 3216 TGAACACCTCTGTTAGTGGAAATTTCTTATAGATCTCTCTCTGATGATAAAGATTTTC 3275
 Qy 3121 AGTCTGTGAGAGAGAGATGCAAGTACAGTTTCGAGAGCAAGAGATGGAGGTCAATGAG 3180
 Db 3276 AGTCTGTGAGAGAGAGATGCAAGTACAGTTTCGAGAGCAAGAGATGGAGGTCAATGAG 3335
 Qy 3181 GTGGAATCTTCAACAGATACAAATTTCTCAAGATTTCAAGGTTTGTAAAGAACTAT 3240
 Db 3336 GTGGAATCTTCAACAGATACAAATTTCTCAAGATTTCAAGGTTTGTAAAGAACTAT 3395
 Qy 3241 GGGAAAGATACACTCACCGGAGAAAGATTTCTGAAAGAAACCAACCATGCCCAATG 3300
 Db 3396 GGGAAAGATACACTCACCGGAGAAAGATTTCTGAAAGAAACCAACCATGCCCAATG 3455
 Qy 3301 AACGAATCTATTTCAATGGGTCTCTCTTTGTAATGCAATTTATCCAAAGAGGCTTTGATG 3360
 Db 3456 AACGAATCTATTTCAATGGGTCTCTCTTTGTAATGCAATTTATCCAAAGAGGCTTTGATG 3515
 Qy 3361 AAAGCATGCTACATAGTGGTATGTTGGAGCTGGCAATTTATTTGCTGAAACCTCTT 3420
 Db 3516 AAAGCATGCTACATAGTGGTATGTTGGAGCTGGCAATTTATTTGCTGAAACCTCTT 3575
 Qy 3421 CCAAGAGCAATCAATATGATATGAAATGAGAGAGGTTCTGGGTGCTCCAGTTCAACAAG 3480
 Db 3576 CCAAGAGCAATCAATATGATATGAAATGAGAGAGGTTCTGGGTGCTCCAGTTCAACAAG 3635
 Qy 3481 ACAGATCTTGTACATTTGCCACAGGAGCTCTCTTTTGGCGGTAACTTGGGAAAGT 3540
 Db 3636 ACAGATCTTGTACATTTGCCACAGGAGCTCTCTTTTGGCGGTAACTTGGGAAAGT 3695
 Qy 3541 CTTTCTCTGAGTTCAGTCAATGAAATGGCAATTTCTCTCCAGGTCATCACTCACTGCA 3600
 Db 3696 CTTTCTCTGAGTTCAGTCAATGAAATGGCAATTTCTCTCCAGGTCATCACTCACTGCA 3755
 Qy 3601 CTGTGTAGCCCAAGTGTAAATGGCTAGCATTTAGCTGAATGTTATTTACAGAGAGAAC 3660
 Db 3756 CTGTGTAGCCCAAGTGTAAATGGCTAGCATTTAGCTGAATGTTATTTACAGAGAGAAC 3815
 Qy 3661 AGGCTTATCTCTGAGTATTTAAATTTACTTACAGATTTATGAGGCTTGGTGGATG 3720
 Db 3816 AGGCTTATCTCTGAGTATTTAAATTTACTTACAGATTTATGAGGCTTGGTGGATG 3875

Qy 3721 GATAAATAGTATTTTAAAGAACTAAATTCACCTGAACCTAAATCATCAAGCAGCAGTG 3780
 Db 3876 GATAAATAGTATTTTAAAGAACTAAATTCACCTGAACCTAAATCATCAAGCAGCAGTG 3935
 Qy 3781 GCCTCTACGTTTACTCTCTTTGCTGAAAAAAA 3813
 Db 3936 GCCTCTACGTTTACTCTCTTTGCTGAAAAAAA 3968

RESULT 11
 ADR66604
 ID ADR66604 standard; DNA; 6189 BP.
 XX AC ADR66604;
 XX DT 02-DEC-2004 (first entry)
 XX DE Human prostatic carcinoma derived DNA SEQ ID 116 #3.
 XX KW human; cytostatic; diagnosis; prostatic cancer;
 XX KW differential expression analysis; ds.
 XX OS Homo sapiens.
 XX PN WO2004076614-A2.
 XX PD 10-SEP-2004.
 XX PF 22-FEB-2004; 2004WO-DE000433.
 XX PR 27-FEB-2003; 2003DE-01009985.
 XX PR 14-MAY-2003; 2003DE-01022134.
 XX PA (HINZ/) HINZMANN B.
 XX PA (DAHL/) DAHL E.
 XX PA (ROSE/) ROSENTHAL A.
 XX PA (HERM/) HERMANN K.
 XX PA (PILA/) PILARSKY C.
 XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
 PI Xinzhang L, Staub E;
 XX WPI; 2004-653386/63.
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 useful for diagnosis, treatment and in screening for specific binding
 agents.
 Claim 1; Page 976-978; 1607pp; German.
 This invention describes novel cytostatic polynucleotide and polypeptide
 sequences which can be used in a method for diagnosing prostatic cancer
 or the risk of developing prostatic cancer. Diagnosis is based on
 determining over transcription or over expression of the sequences in
 prostatic tissue. Screening for inhibitors of the sequences or detection
 substances involves a binding assay, any compounds that bind are
 selected, optionally after deconvolution of mixtures. Detection of a
 predetermined minimum level of the reporter indicates the presence of
 tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 short-interfering RNA or ribozymes; an organic molecule of molecular
 weight below 5000, preferably 300, that binds to the polypeptide; an
 aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 polypeptide, preferably humanised or human; an anti-idiotypic, non-human
 (monoclonal) antibody directed against Ab or any of the above derivatised
 with a reporter group, cell toxin, immunostimulatory molecules and/or
 radioisotope. The polynucleotides are identified in human prostatic
 cancer by differential expression analysis, using DNA microarrays,
 between normal and tumorous tissues, with (over)expression being detected
 by quantitative PCR. Analysis of prostatic cancer samples showed that
 CD24 was upregulated in many of them. Sections of tissue, isolated from
 prostatic cancer patients, or subjects at risk, were incubated

sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, lymph node metastases were also stained. ADR65805-ADR65954 represented polynucleotide and polypeptide sequences used in the method of the invention.

Sequence 6189 BP; 1772 A; 1233 C; 1386 G; 1798 T; 0 U; 0 Other;

Query Match 99.4%; Score 3791.4; DB 13; Length 6189;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

1 CGGCTGCTCCGCCCGCGGGGAGCCGGGGGACGGAGCCAGCGAGGGGCGCG 60

b : 157 CGCGCTGCCTCCGCCGCCCGCGGGGCAGCCGGGGGCAGGGAGCCAGCCAGGGGCGCGG 216

61 TGGCGCGCGGCCCATGGGACTGGCGCCGGATCCGGTGACAGCAGGAGGCCAAGCGGCCCGGG 120

[illegible]

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

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336 TCCGGTTCCTGGCGCTGTTCCTGGCTGGCTGGCAATCATGTCGGGTCGCCGC

241 GCGCCGGCGGGGAGCGGCCCTGCGCGAGCGCCGCGGCGGAGCCGGCCGCC 300

b 396 GCGCCGGCGGGAGCGGCCTGCGCGAGCGCCGCGGCCGAGCCGTTGGAGCCGGCCGCC 455

301 GAGAGCTGTTCTGAGGGCGTGCCGCAACGGGGACGTGGAACGAGTCAAGAGGCTGGTGACGC 360

b 456 GAGAGCTTTCGAGGCGTGCCGCAACGGGACGTGGACGAGTCAAGAGGCTGGTGACGC 515

361 CTGAGAGGTGAACAGCCGCGACACGGCGGCAGGAATCCACCCGCTGCACCTTCGCCG 420

b 516 CTGAGAGGTGAACAGCCGCGACACGGCGGGCAGGAATCCACCCCGCTGCATTGCGCG 575

421 CAGGTTTGGCGGAAAGACGTAGTTGAATATTGCTTCAGAAATGGTGCAATGTCCAAG 480

576 CACCTTTTCCCCCAACACCTTACCTTCAATATTTTCCTTCACATTCCTCCACATCTCTCCACAC 635

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696 TAGTC AATCTCCCTTTTGGGACATGGGTGCAGAGCCCCCAATGCTCGAGAGTAAATGGGAATATA 755

601 CTCCTCCTCAAGAAGCTGCAATTAAAGGAAGATGATGTTGCATTTGTGCTGTACAGC 660

b 756 CTCCTCTCCATGAAGCTGCAATTAAAGGAAGATTGATGTTTGCAATTGTGCTGTTACAGC 815

561 ATGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGACAGCATTGGATTAGCAGATC 720

b 816 ATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATC 875

721 CATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACCTCTTAGAAAGTGCCA 780

876 CATCTGCCAAAGCAGTGCCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCA 935

781 CCGCTGCGAATGCAACAAATCTGCTGCACTGCTGCGC 840

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Db	996		CAAGTGA	GGCAGAAAGT	CAACTCC	AATTACATTTT	GCAGCAGGATAT	AACAGAGTAA	GA	1056		
Qy	901	TTGTCA	CAGCTGTTT	ACTGCAAC	CATGGAGCTG	ATGTCCATGCT	ATAAGATAAA	AGGTGATCT	CG	960		
Db	1056	TTGTCA	CAGCTGTTT	ACTGCAAC	CATGGAGCTG	ATGTCCATGCT	ATAAGATAAA	AGGTGATCT	CG	1115		
Qy	961	TACCAT	TACACATG	CCTGTTCTT	TATGGTCAT	TATGAAGT	TAACTGAAC	CTTTTGGTCA	AGC	1020		
Db	1116	TACCAT	TACACAAT	GCGCTGTTCTT	TATGGTCAT	TATGAAGT	TAACTGAAC	CTTTTGGTCA	AGC	1175		
Qy	1021	ATGGTGC	CTGTGTAAAT	TGCAATGG	CAATTGTGGCA	ATTCACTCCTCTT	CATGAGCCAG	CTT	1080			
Db	1176	ATGGTGC	CTGTGTAAAT	TGCAATGG	CAATTGTGGCA	ATTCACTCCTCTT	CATGAGCCAG	CTT	1235			
Qy	1081	CTAAGA	ACAGGGTTGA	AGTATGTTCTTCT	CTTTAAGTTAT	TGTCGACAG	CCCAACACTGC		1140			
Db	1236	CTAAGA	ACAGGGTTGA	AGTATGTTCTTCT	CTTTAAGTTAT	TGTCGACAG	CCCAACACTGC		1295			
Qy	1141	TCAATT	TGTCACATA	AAAAAGTCTATAG	ACTTGGCTCC	CACACCA	CACAGTTAAAA	AGAAAGAT	1200			
Db	1296	TCAATT	TGTCACAT	ATAAAGTCTATAG	ACTTGGCTCC	CACACCA	CACAGTTAAAA	AGAAAGAT	1355			
Qy	1201	TAGCAT	TATGAATTAA	AGGCCACTCGT	TGTCGCAAGCTG	CAAGTGCAC	GAGAGCTGATGTT	ACTC	1260			
Db	1356	TAGCAT	TATGAATTAA	AGGCCACTCGT	TGTCGCAAGCTG	CAAGTGCAC	GAGAGCTGATGTT	ACTC	1415			
Qy	1261	GAATCA	AAAAACATCTCT	CTCGGAATGGT	GAATTTCAAGCAT	CTCTCAACACAT	GATGAAA	1320				
Db	1416	GAATCA	AAAAACATCTCT	CTCGGAATGGT	GAATTTCAAGCAT	CTCTCAACACAT	GATGAAA	1475				
Qy	1321	CAGCAT	TGCAATTGCTG	CTGTGCACTCC	ATATCCCAAA	AGAAAGCAAA	TATGTGA	ACTGT	1380			
Db	1476	CAGCAT	TGCAATTGCTG	CTGTGCACTCC	ATATCCCAAA	AGAAAGCAAA	TATGTGA	ACTGT	1535			
Qy	1381	TGCTAGA	AAAGGAGCA	AAACATCAAT	GAAAGACT	ATAAGAA	TTCTTGACTCT	CTGCACG	1440			
Db	1536	TGCTAGA	AAAGGAGCA	AAACATCAAT	GAAAGACT	ATAAGAA	TTCTTGACTCT	CTGCACG	1595			
Qy	1441	TGCACT	CTGAGAAGCT	CATAATGAT	TGTTTCAAGT	TAGTGGT	GAAACATGA	AGCAAGG	1500			
Db	1596	TGCACT	CTGAGAAGCT	CATAATGAT	TGTTTCAAGT	TAGTGGT	GAAACATGA	AGCAAGG	1655			
Qy	1501	TTAATG	CTCTGG	AATCTT	TGGTCAGACT	TTCTTACAGAG	CTGCANAT	TTGTGGTCA	TC	1560		
Db	1656	TTAATG	CTCTGG	AATCTT	TGGTCAGACT	TTCTTACAGAG	CTGCANAT	TTGTGGTCA	TC	1715		
Qy	1561	TACAA	ACCTGCC	CTACTCTC	GAGCTATG	GGGTGATCCT	TAACATTTAT	ATCCCTC	CAGG	1620		
Db	1716	TACAA	ACCTGCC	CTACTCTC	GAGCTATG	GGGTGATCCT	TAACATTTAT	ATCCCTC	CAGG	1775		
Qy	1621	GCTTTA	CTGTTTAC	AGATGGG	AAATGAA	AAATGTA	CAGCAACTCT	CTCCAA	AGGGTATCT	1680		
Db	1776	GCTTTA	CTGTTTAC	AGATGGG	AAATGAA	AAATGTA	CAGCAACTCT	CTCCAA	AGGGTATCT	1835		
Qy	1681	CATTAG	GTAA	TTACAG	GGCAGACAG	ACAA	TTGCTGG	AAAGCTG	CAGAGATG	TCG	1740	
Db	1836	CATTAG	GTAA	TTACAG	GGCAGACAG	ACAA	TTGCTGG	AAAGCTG	CAGAGATG	TCG	1895	
Qy	1741	AAACTG	TTAAAAA	AACTGTGT	ACTGTTT	CAGAGTGT	CAACTC	CAGAGAC	CA	1800		
Db	1896	AAACTG	TTAAAAA	AACTGTGT	ACTGTTT	CAGAGTGT	CAACTC	CAGAGAC	CA	1955		
Qy	1801	AGTCTA	CA	CACTTCA	TTTTG	CAGCTGGG	TATAAC	CAGAGTGT	CCGTGGT	GGAATATCTCG	1860	
Db	1956	AGTCTA	CA	CACTTCA	TTTTG	CAGCTGGG	TATAAC	CAGAGTGT	CCGTGGT	GGAATATCTCG	2015	
Qy	1861	TACAG	CA	TGGAGCTG	ATGTCATG	CTCTAA	AGATAA	AGGAGG	CCCTTG	TACCTTTG	CACAATG	1920
Db	2016	TACAG	CA	TGGAGCTG	ATGTCATG	CTCTAA	AGATAA	AGGAGG	CCCTTG	TACCTTTG	CACAATG	2075
Qy	1921	CATG	TTCTTTAT	GACATAT	TGAAGTT	GCAGAACTT	CTTGT	TTAAAC	ATG	GAGCAGT	AGTATTA	1980

Db 2076 CATGTTCTTATGCAATATGAAGTTGCAGAACTTCTTGTTAAACATGAGCAGTAGTTA 2135
 Qy 1981 ATGTAGCTGATTTATGGAATTTTACACCTTTTACATGACACGACCAAAAGGAAATATG 2040
 Db 2136 ATGTAGCTGATTTATGGAATTTTACACCTTTTACATGAGCAGCAGCAAAAGGAAATATG 2195
 Qy 2041 AAATTTGCAAACTTCTGCTCCAGCATGTCAGACCTTACCAAAAAAAGGAGTGGAA 2100
 Db 2196 AAATTTGCAAACTTCTGCTCCAGCATGTCAGACCTTACCAAAAAAAGGAGTGGAA 2255
 Qy 2101 ATACTCTTTTGGATCTTGTAAAGATGAGAGATACAGATTTCAAGATCTGCTTAGGGAG 2160
 Db 2256 ATACTCTTTTGGATCTTGTAAAGATGAGAGATACAGATTTCAAGATCTGCTTAGGGAG 2315
 Qy 2161 ATGACGCTTTGCTAGATGCTGCCAAGAGGTTGTTTACCCAGAGTGGAAGATTTGCTT 2220
 Db 2316 ATGACGCTTTGCTAGATGCTGCCAAGAGGTTGTTTACCCAGAGTGGAAGATTTGCTT 2375
 Qy 2221 CTCTCTGATAATGTAAATTTGCCCGCATACCAAGGCAGACATTTCAACACCTTTTACATTTAG 2280
 Db 2376 CTCTCTGATAATGTAAATTTGCCCGCATACCAAGGCAGACATTTCAACACCTTTTACATTTAG 2435
 Qy 2281 CAGCTGGTTATATTAATTTAGAAAGTTGAGATTTTGTGTAACAACGAGCTGATGTGA 2340
 Db 2436 CAGCTGGTTATATTAATTTAGAAAGTTGAGATTTTGTGTAACAACGAGCTGATGTGA 2495
 Qy 2341 ATGCCCAAGACAAAGGAGCTTATTCCTTTTACATAATGCGACATCTTACGGGCATGTAG 2400
 Db 2496 ATGCCCAAGACAAAGGAGCTTATTCCTTTTACATAATGCGACATCTTACGGGCATGTAG 2555
 Qy 2401 ATGTAGCAGCTCTACTAATAAAGTATAATGCAATGTCCTCAATGCCAGGACAAATGGGCTT 2460
 Db 2556 ATGTAGCAGCTCTACTAATAAAGTATAATGCAATGTCCTCAATGCCAGGACAAATGGGCTT 2615
 Qy 2461 TCACACCTTTGCAAGAGCAGCCCAAAAGGAGCGAACACAGCTTTGTGCTTTGCTAG 2520
 Db 2616 TCACACCTTTGCAAGAGCAGCCCAAAAGGAGCGAACACAGCTTTGTGCTTTGCTAG 2675
 Qy 2521 CCATGGAGCTGACCGGCTCTTAAATATCAGAGGACAAACACCTTTAGATTTAGTTT 2580
 Db 2676 CCATGGAGCTGACCGGCTCTTAAATATCAGAGGACAAACACCTTTAGATTTAGTTT 2735
 Qy 2581 CAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCATGCCCATCTGCTGCTCCCTCTT 2640
 Db 2736 CAGCAGATGATGTCAGCGCTCTTCTGACAGCAGCATGCCCATCTGCTGCTCCCTCTT 2795
 Qy 2641 GTTACAAGCCTCAAGTGCTCAATGTGTGAGAGCCAGGAGCCACTGCAAGATGCTCTCT 2700
 Db 2796 GTTACAAGCCTCAAGTGCTCAATGTGTGAGAGCCAGGAGCCACTGCAAGATGCTCTCT 2855
 Qy 2701 CTTCAAGTCCATCTAGCCCATCAAGCCTTTCTGACGCGCAGCTGTCACACTTTATCTG 2760
 Db 2856 CTTCAAGTCCATCTAGCCCATCAAGCCTTTCTGACGCGCAGCTGTCACACTTTATCTG 2915
 Qy 2761 GGAGTTTTTTCAGAACTGCTCTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTGCTCCAGTT 2820
 Db 2916 GGAGTTTTTTCAGAACTGCTCTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTGCTCCAGTT 2975
 Qy 2821 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTATGACATACTCAATTCGTAAGAAATCTTTG 2880
 Db 2976 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTATGACATACTCAATTCGTAAGAAATCTTTG 3035
 Qy 2881 GACTTGAGCACTTAATGGATATATTTGAGAGGACAGATCACTTTGGATGTTAGTTG 2940
 Db 3036 GACTTGAGCACTTAATGGATATATTTGAGAGGACAGATCACTTTGGATGTTAGTTG 3095
 Qy 2941 AGATGGGCAACAGGAGCTGAAGGAGATTGGAAATCAATGCTTATGACATAGGCACAAAC 3000
 Db 3096 AGATGGGCAACAGGAGCTGAAGGAGATTGGAAATCAATGCTTATGACATAGGCACAAAC 3155
 Qy 3001 TAATTAAGGAGTCGAGAGACTTATCTCCGGACAAAGGCTCTTAACCCATATTTAACTT 3060
 Db 3156 TAATTAAGGAGTCGAGAGACTTATCTCCGGACAAAGGCTCTTAACCCATATTTAACTT 3215

Qy 3061 TGAACACCTCTGGTAGTGGAACTTCTTATAGATCTGCTCTCTGATGATTAAGAGTTTC 3120
 Db 3216 TGAACACCTCTGGTAGTGGAACTTCTTATAGATCTGCTCTCTGATGATTAAGAGTTTC 3275
 Qy 3121 AGTCTGCGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGACACAGAGATGGAGGTCATGCA 3180
 Db 3276 AGTCTGCGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGACACAGAGATGGAGGTCATGCA 3335
 Qy 3181 GTGGATCTTCAACAGATACAAATTTCTCAAGATTTCAAGGTTTGTAAACAGAAACTAT 3240
 Db 3336 GTGGATCTTCAACAGATACAAATTTCTCAAGATTTCAAGGTTTGTAAACAGAAACTAT 3395
 Qy 3241 GGGAAAGATACACTCACCGGAGAAAGAAAGTTTCTGAAAGAAACCAACCATGCAATG 3300
 Db 3396 GGGAAAGATACACTCACCGGAGAAAGAAAGTTTCTGAAAGAAACCAACCATGCAATG 3455
 Qy 3301 AACGAATGCTATTTCAATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAAGGCTTTGATG 3360
 Db 3456 AACGAATGCTATTTCAATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAAGGCTTTGATG 3515
 Qy 3361 AAAGCATGCGTACATAGTGTATGTTGGAGCTGGCATTTATTTGCTGAAACTCTT 3420
 Db 3516 AAAGCATGCGTACATAGTGTATGTTGGAGCTGGCATTTATTTGCTGAAACTCTT 3575
 Qy 3421 CCMAAGCAATCAATATGATATGAAATTTGAGAGGAGTACTGGGTGTCCAGTTTCAAAAG 3480
 Db 3576 CCMAAGCAATCAATATGATATGAAATTTGAGAGGAGTACTGGGTGTCCAGTTTCAAAAG 3635
 Qy 3481 ACAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACCTTTGGGAAAGT 3540
 Db 3636 ACAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACCTTTGGGAAAGT 3695
 Qy 3541 CTTTCTCAGTTCAGTGCATGAAATGGAATGGACATTTCTCTCCAGGTCACTCACTCAGTCA 3600
 Db 3696 CTTTCTCAGTTCAGTGCATGAAATGGAATGGACATTTCTCTCCAGGTCACTCACTCAGTCA 3755
 Qy 3601 CTGTGAGCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGGAGAAC 3660
 Db 3756 CTGTGAGCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGGAGAAC 3815
 Qy 3661 AGGCTTATCTGAGTATTTAATTTACTTACCAGATTTATGAGGCTGAAGGTATGGTCATG 3720
 Db 3816 AGGCTTATCTGAGTATTTAATTTACTTACCAGATTTATGAGGCTGAAGGTATGGTCATG 3875
 Qy 3721 GATAAATAGTATTTTAAAGAACTTAATTTCCACTGAACTTAAATCATCAAAAGCAGCAGT 3780
 Db 3876 GATAAATAGTATTTTAAAGAACTTAATTTCCACTGAACTTAAATCATCAAAAGCAGCAGT 3935
 Qy 3781 GCCTCTAGCTTTTACTCCTTTGCTGAAAAAAA 3813
 Db 3936 GCCTCTAGCTTTTACTCCTTTGCTGAAAAAAA 3968

RESULT 12
 ADR66262
 ID ADR66262 standard; DNA; 6189 BP.
 XX
 AC ADR66262;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human prostatic carcinoma derived DNA SEQ ID 116 #2.
 XX
 KW human; cytostatic; diagnosis; prostatic cancer;
 XX differential expression analysis; ds.
 OS Homo sapiens.
 XX
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 XX

Db 1116 TACCAATTACAAATGCCCTGTTCTTATGTGTCATTATGAAGTAACCTGAACTTTTGGTCAAGC 1175
Qy 1021 ATGGTCCTGTGTAAATGCAATGGACTTTGTGGCAATTCACCTCTTTCATGAGCGAGCTT 1080
Db 1176 ATGGTGCCTGTGTAAATGCAATGGACTTTGTGGCAATTCACCTCTTTCATGAGCGAGCTT 1235
Qy 1081 CTAAGAACAGGGGTTGAAGTATGTTCTCTCTTAAAGTTATGGTGCAGACCCCAACACTGC 1140
Db 1236 CTAAGAACAGGGGTTGAAGTATGTTCTCTCTTAAAGTTATGGTGCAGACCCCAACACTGC 1295
Qy 1141 TCAATTGTCACAATAAAGTGTCTATAGACTTTGGCTCCCAACACAGCTTAAAGAAAGAT 1200
Db 1296 TCAATTGTCACAATAAAGTGTCTATAGACTTTGGCTCCCAACACAGCTTAAAGAAAGAT 1355
Qy 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGACTGATGTTACTC 1260
Db 1356 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGACTGATGTTACTC 1415
Qy 1261 GAATCAAAAAACATCTCTCTCGGAAATGGTGAATTTCAAGCATCTCAAAACACATGAAA 1320
Db 1416 GAATCAAAAAACATCTCTCTCGGAAATGGTGAATTTCAAGCATCTCAAAACACATGAAA 1475
Qy 1321 CAGCAATGCAATGCTGCTGCATCTCCATATCCAAAAAGAAACAAATATGTGAACCTGT 1380
Db 1476 CAGCAATGCAATGCTGCTGCATCTCCATATCCAAAAAGAAACAAATATGTGAACCTGT 1535
Qy 1381 TGCTAAGAAAAGGAGCAACATCAATGAAGACTTAAAGAAATCTTGACTCTCTGACAG 1440
Db 1536 TGCTAAGAAAAGGAGCAACATCAATGAAGACTTAAAGAAATCTTGACTCTCTGACAG 1595
Qy 1441 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAGG 1500
Db 1596 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAGG 1655
Qy 1501 TTAATGCTCTGGATAATCTTGCTCAGACTCTCTACACAGAGCTGCATATGTGCTCATC 1560
Db 1656 TTAATGCTCTGGATAATCTTGCTCAGACTCTCTACACAGAGCTGCATATGTGCTCATC 1715
Qy 1561 TACAACCTCGCCCTACTCTCGAGCTATGGGTGTGATCCTAACTATATATCCCTTCAGG 1620
Db 1716 TACAACCTCGCCCTACTCTCGAGCTATGGGTGTGATCCTAACTATATATCCCTTCAGG 1775
Qy 1621 GCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCCAAAGAGGTATCT 1680
Db 1776 GCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCCAAAGAGGTATCT 1835
Qy 1681 CATTAGGTAAATTCAGAGGCAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCG 1740
Db 1836 CATTAGGTAAATTCAGAGGCAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCG 1895
Qy 1741 AAACGTGTAAGAAAACGTGTACTGTTACAGAGTGTCAACTGCAGAGACATTTGAAGGGGTC 1800
Db 1896 AAACGTGTAAGAAAACGTGTACTGTTACAGAGTGTCAACTGCAGAGACATTTGAAGGGGTC 1955
Qy 1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGC 1860
Db 1956 AGTCTACACCACTTCATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGC 2015
Qy 1861 TACAGCATGGAGCTGATGTCATGCTAAAGATTAAGAGGAGGCTTGATCTTTGCACAATG 1920
Db 2016 TACAGCATGGAGCTGATGTCATGCTAAAGATTAAGAGGAGGCTTGATCTTTGCACAATG 2075
Qy 1921 CATGTTCTTATGGACATTAATGAAGTTGAGAACTTCTTGTGTTAAACATGGAGCAGTAGTTA 1980
Db 2076 CATGTTCTTATGGACATTAATGAAGTTGAGAACTTCTTGTGTTAAACATGGAGCAGTAGTTA 2135
Qy 1981 ATGTAGCTGATTTATGGAATTTACCTTTACATGAAGCAGCAGCAAAAGGAATATG 2040
Db 2136 ATGTAGCTGATTTATGGAATTTACCTTTACATGAAGCAGCAGCAAAAGGAATATG 2195
Qy 2041 AAAATTTGCAAACTCTGCTCCAGCATGGTGCAGACCTTACCAGCAAAAAACAGGATGAAA 2100

Db 2196 AAAATTTGCAAACTCTGCTCCAGCATGGTGCAGACCTTACAAAAAACAAGGATGAAA 2255
Qy 2101 ATACTCCTTTTGGATCTTTGTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2160
Db 2256 ATACTCCTTTTGGATCTTTGTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2315
Qy 2161 ATGCAAGCTTTGCTAGATGCTGCGCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTTGCTTT 2220
Db 2316 ATGCAAGCTTTGCTAGATGCTGCGCAAGAGGGTGTGTTAGCCAGAGTGAAGAGTTGCTTT 2375
Qy 2221 CTCTGATATATGTAATTTGCGCGCATACCCNAGGACAGATTTCAACACCTTTACATTTAG 2280
Db 2376 CTCTGATATATGTAATTTGCGCGCATACCCNAGGACAGATTTCAACACCTTTACATTTAG 2435
Qy 2281 CAGCTGGTTATTAATTTTGAAGTTGCAGAGTATTTGTTTACAACACGGAGCTCATGTGA 2340
Db 2436 CAGCTGGTTATTAATTTTGAAGTTGCAGAGTATTTGTTTACAACACGGAGCTCATGTGA 2495
Qy 2341 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGACGATCTTTACGGGATGTAG 2400
Db 2496 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGACGATCTTTACGGGATGTAG 2555
Qy 2401 ATGTAGCAGCTCTACTAATAAAGTATATGATGTGTCAATGTCACCGACAAATGGGCTT 2460
Db 2556 ATGTAGCAGCTCTACTAATAAAGTATATGATGTGTCAATGTCACCGACAAATGGGCTT 2615
Qy 2461 TCACACCTTTGCGAAGACAGCCCAAAAGGAGGACCAACACAGCTTTGTGCTTTGTGCTAG 2520
Db 2616 TCACACCTTTGCGAAGACAGCCCAAAAGGAGGACCAACACAGCTTTGTGCTTTGTGCTAG 2675
Qy 2521 CCCATGGAGCTGACCCGAGCTCTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTT 2580
Db 2676 CCCATGGAGCTGACCCGAGCTCTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTT 2735
Qy 2581 CAGCGATGATGTGAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTT 2640
Db 2736 CAGCAGATGATGTGAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTT 2795
Qy 2641 GTTACAAGCCTCAAGTGTCAATGCTGTGAGAGCCAGGAGGACCACTGCAGATGCTCTCT 2700
Db 2796 GTTACAAGCCTCAAGTGTCAATGCTGTGAGAGCCAGGAGGACCACTGCAGATGCTCTCT 2855
Qy 2701 CTTCAGGTCCATCTAGCCCATCAAGCCCTTTCTGACAGCCAGCAGCTTTTGACAACTTATCTG 2760
Db 2856 CTTCAGGTCCATCTAGCCCATCAAGCCCTTTCTGACAGCCAGCAGCTTTTGACAACTTATCTG 2915
Qy 2761 GGAGTTTTTCAGAACTGTCTTCACTAGTTAGTTCAAGTGGAAACAGAGGGTCTTCCAGTT 2820
Db 2916 GGAGTTTTTCAGAACTGTCTTCACTAGTTAGTTCAAGTGGAAACAGAGGGTCTTCCAGTT 2975
Qy 2821 TGGAGAAAAGGAGGTTCCAGGAGTAGATTTTACGATAAATCAATTCGTAAGGATCTTG 2880
Db 2976 TGGAGAAAAGGAGGTTCCAGGAGTAGATTTTACGATAAATCAATTCGTAAGGATCTTG 3035
Qy 2881 GACTTTGAGCAGCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTG 2940
Db 3036 GACTTTGAGCAGCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTG 3095
Qy 2941 AGATGGGCGCAAGGAGCTGAAGAGATTGGAATCAATGCTTATGACATAGGACAAAC 3000
Db 3096 AGATGGGCGCAAGGAGCTGAAGAGATTGGAATCAATGCTTATGACATAGGACAAAC 3155
Qy 3001 TAAATTAAGGAGTGCAGAGACTTATCTCCGACAAACAGGCTTTAAACCATTTTAACTT 3060
Db 3156 TAAATTAAGGAGTGCAGAGACTTATCTCCGACAAACAGGCTTTAAACCATTTTAACTT 3215
Qy 3061 TGAACACCTCTGGTAGTGGAAACAAATTTTATAGATCTGTCTCTGATGATTAAGAGTTT 3120
Db 3216 TGAACACCTCTGGTAGTGGAAACAAATTTTATAGATCTGTCTCTGATGATTAAGAGTTT 3275
Qy 3121 AGTCTGTGGAGGAAAGAGATGCAAAAGTACAGTTCCAGAGCACAGAGATGGAGGTCATGCAG 3180
Db 3276 AGTCTGTGGAGGAAAGAGATGCAAAAGTACAGTTCCAGAGCACAGAGATGGAGGTCATGCAG 3335

Db	756	CTCTCTCCCATGAAGCTGCAATTTAAAGGAAGATTTGATGTTTGCATTTGCTGTGTACAGC	815
Qy	661	ATGAGCTGAGCCAAACCATCCGAATAACAGATGGAAGCAGACAGATTTGGATTTAGCAGATC	720
Db	816	ATGGAGCTGAGCCAAACCATCCGAATAACAGATGGAAGCAGCAGATTTGGATTTAGCAGATC	875
Qy	721	CATCTGCCAAGCAGTGCTTTACTGGTGAAATATAAGAAAGATGAACCTCTTATAGAAAGTGCCCA	780
Db	876	CATCTGCCAAGCAGTGCTTTACTGGTGAAATATAAGAAAGATGAACCTTATAGAAAGTGCCCA	935
Qy	781	GGAGTGGCAATGAAGAAAATGATGCTCTACTCACCACTTAAATGATCAACTGCGCACG	840
Db	936	GGAGTGGCAATGAAGAAAATGATGCTCTACTCACCACTTAAATGATCAACTGCGCACG	995
Qy	841	CAAGTGATGGCAGAAAGTCAACTCCATTAACATTTGGCAGCAGGATATAACAGAGTAAAGA	900
Db	996	CAAGTGATGGCAGAAAGTCAACTCCATTAACATTTGGCAGCAGGATATAACAGAGTAAAGA	1055
Qy	901	TTGTACAGCTGTTACTGGAACATGGAGCTGATGTCATGCTATAAGATAAAGGTGATCTGG	960
Db	1056	TTGTACAGCTGTTACTGGAACATGGAGCTGATGTCATGCTATAAGATAAAGGTGATCTGG	1115
Qy	961	TACCAATTACCAATGCCCTGTTCTTATGGTCATTAATGAAGTAACTGAACCTTTTGGTCAAGC	1020
Db	1116	TACCAATTACCAATGCCCTGTTCTTATGGTCATTAATGAAGTAACTGAACCTTTTGGTCAAGC	1175
Qy	1021	ATGGTGCTGTGTAATAGCAATGGACCTGTGGCAATTCACCTCTCTTCATGAGCGACGTT	1080
Db	1176	ATGGTGCTGTGTAATAGCAATGGACCTGTGGCAATTCACCTCTCTTCATGAGCGACGTT	1235
Qy	1081	CTAAGAACACGGGTTGAAGTAGTTCTCTCTCTTTAAGTTATGGTGCAGACCCCAACACTGC	1140
Db	1236	CTAAGAACACGGGTTGAAGTAGTTCTCTCTCTTTAAGTTATGGTGCAGACCCCAACACTGC	1295
Qy	1141	TCAATTGTGCACATAAAAGTGCTATAGACTTTGGCTCCCAACACACAGTTTAAAGAAAGAT	1200
Db	1296	TCAATTGTGCACATAAAAGTGCTATAGACTTTGGCTCCCAACACACAGTTTAAAGAAAGAT	1355
Qy	1201	TAGCATATGAATTTAAAGGGCCACTCGTTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC	1260
Db	1356	TAGCATATGAATTTAAAGGGCCACTCGTTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC	1415
Qy	1261	GAATCAAAAACATCTCTCTCTCGAAATGGTGAATTTCAAGCATCTCTCAAAACACATGAAA	1320
Db	1416	GAATCAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCTCAAAACACATGAAA	1475
Qy	1321	CAGCATTTGCATTTGTGCTGCTGCATCTCCATATCCCAAAAGAAAGCAATATGTGAACGTG	1380
Db	1476	CAGCATTTGCATTTGTGCTGCTGCATCTCCATATCCCAAAAGAAAGCAATATGTGAACGTG	1535
Qy	1381	TGCTAAGAAAGGAGCAAAACATCAATGAAAGACTTAAAGAAATTTCTTGACCTCTGCAAG	1440
Db	1536	TGCTAAGAAAGGAGCAAAACATCAATGAAAGACTTAAAGAAATTTCTTGACCTCTGCAAG	1595
Qy	1441	TGGCATCTGAGAAAGCTCATAATGATGTGTTGTAAGTAGTGGTGAACATGAAAGCAAGG	1500
Db	1596	TGGCATCTGAGAAAGCTCATAATGATGTGTTGTAAGTAGTGGTGAACATGAAAGCAAGG	1655
Qy	1501	TTAAATGCTCTGGATAAATCTTGGTGCAGACTCTCTACACAGAGCTGCATATTTGGTGCATC	1560
Db	1656	TTAAATGCTCTGGATAAATCTTGGTGCAGACTCTCTACACAGAGCTGCATATTTGGTGCATC	1715
Qy	1561	TACAAACCTGCGGCTACTCTGAGCTATGGGTGTGATCCTTAACATTTATATCCCTTCAGG	1620
Db	1716	TACAAACCTGCGGCTACTCTGAGCTATGGGTGTGATCCTTAACATTTATATCCCTTCAGG	1775
Qy	1621	GCTTTACTGCTTTACAGATGGAAATGAAAATGTGACGAACCTCTCCAGAGGGGTATCT	1680
Db	1776	GCTTTACTGCTTTACAGATGGAAATGAAAATGTGACGAACCTCTCCAGAGGGGTATCT	1835
Qy	1681	CATTAGGTAAATTCAGAGGCAGACAGACAAATGCTGTGGAAGCTGCAAGAGCTGGAGATGTGCG	1740
Db	1836	CATTAGGTAAATTCAGAGGCAGACAGACAAATGCTGTGGAAGCTGCAAGAGCTGGAGATGTGCG	1895

Qy	2821	2881	TGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAGGAATCTTG	2888
Db	2976	3035	TGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAGGAATCTTG	3035
Qy	2881	2940	GACTTGAGCACCTAAATGSGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTG	2940
Db	3036	3095	GACTTGAGCACCTAAATGSGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTG	3095
Qy	2941	3000	AGATGGGGCAAGGAGCTGAAGGAGATTGGAATCAATGCTTTATGGCATAGGCACAAAC	3000
Db	3096	3155	AGATGGGGCAAGGAGCTGAAGGAGATTGGAATCAATGCTTTATGGCATAGGCACAAAC	3155
Qy	3001	3060	TAATTTAAAGAGTCGAGAGACTTATCTCCGGACAAACAGGCTCTTAACCCATATTTAACTT	3060
Db	3156	3215	TAATTTAAAGAGTCGAGAGACTTATCTCCGGACAAACAGGCTCTTAACCCATATTTAACTT	3215
Qy	3061	3120	TGAACACCTCTGGTAGTGGAAACAATCTTATAGATCTGTCTCTCGATGATAAAGAGTTTC	3120
Db	3216	3275	TGAACACCTCTGGTAGTGGAAACAATCTTATAGATCTGTCTCTCGATGATAAAGAGTTTC	3275
Qy	3121	3180	AGTCTGTGGAGGAAGAGATCAAAAGTACAGTTCGAGAGCAACAGAGATGGAGGTCATGCAG	3180
Db	3276	3335	AGTCTGTGGAGGAAGAGATCAAAAGTACAGTTCGAGAGCAACAGAGATGGAGGTCATGCAG	3335
Qy	3181	3240	GTGGATCTTCAACAGATACAATTTCTCAAGATTCAGAGGTTGTGTAAACAAGAAACTAT	3240
Db	3336	3395	GTGGATCTTCAACAGATACAATTTCTCAAGATTCAGAGGTTGTGTAAACAAGAAACTAT	3395
Qy	3241	3300	GGGAAAGATACACTCACCGGAGAAAAGATTCTTGAAGAAAAACCAACCATGCCCAATG	3300
Db	3396	3455	GGGAAAGATACACTCACCGGAGAAAAGATTCTTGAAGAAAAACCAACCATGCCCAATG	3455
Qy	3301	3360	AACGAATGCTATTTTCATGGGTCTCTTTGTGAATGCAATTTATCCAAAGGCTTTGATG	3360
Db	3456	3515	AACGAATGCTATTTTCATGGGTCTCTTTGTGAATGCAATTTATCCAAAGGCTTTGATG	3515
Qy	3361	3420	AAAGGCATGGTACATAGSGTGGTATGTTTCGAGCTGCAATTTATTTTGTGAAAACCTCTT	3420
Db	3516	3575	AAAGGCATGGTACATAGSGTGGTATGTTTCGAGCTGCAATTTATTTTGTGAAAACCTCTT	3575
Qy	3421	3480	CCAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCCAGTTCACAAAG	3480
Db	3576	3635	CCAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCCAGTTCACAAAG	3635
Qy	3481	3540	ACAGATCTTGTTACATTTGGCCACAGGACGTGCTCTTTTGGCGGGTAACTCTTGGAAAAGT	3540
Db	3636	3695	ACAGATCTTGTTACATTTGGCCACAGGACGTGCTCTTTTGGCGGGTAACTCTTGGAAAAGT	3695
Qy	3541	3600	CTTTCTCGCAGTTTCAGTGCATGAAAATGGCAATCTCTCTCCAGGTCATCACTCAGTCA	3600
Db	3696	3755	CTTTCTCGCAGTTTCAGTGCATGAAAATGGCAATCTCTCTCCAGGTCATCACTCAGTCA	3755
Qy	3601	3660	CTGGTAGGCCAGGTGTAATGGGCTAGCATTAGCTGAAATATGTTATTTTACAGAGGAGAAC	3660
Db	3756	3815	CTGGTAGGCCAGGTGTAATGGGCTAGCATTAGCTGAAATATGTTATTTTACAGAGGAGAAC	3815
Qy	3661	3720	AGGCTTATCTGAGTATTTTAAATTTACTTTACAGATTATGAGGCTTGAGGTTATGGTCGATG	3720
Db	3816	3875	AGGCTTATCTGAGTATTTTAAATTTACTTTACAGATTATGAGGCTTGAGGTTATGGTCGATG	3875
Qy	3721	3780	GATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACTTAAAAATCAATCAAGAGCAGAGTG	3780
Db	3876	3935	GATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACTTAAAAATCAATCAAGAGCAGAGTG	3935
Qy	3781	3813	GCCTCTACGTTTACTCCTTTTGTGAAAAAAA	3813
Db	3936	3968	GCCTCTACGTTTACTCCTTTTGTGAAAAAAA	3968

RESULT 15
AAD54031
ID AAD54031 standard; DNA; 6018 BP.
XX

AC	AA054031;
XX	
DT	17-JUN-2003 (first entry)
XX	
DE	Human colon cancer-associated polypeptide gene, TNKL (BC-203).
XX	
KW	Human; colon cancer-associated polypeptide; immune response; therapy;
KW	colon cancer; gene; ds.
XX	
OS	Homo sapiens.
XX	
PH	Location/Qualifiers
PH	33..3283
FT	/tag= a
FT	/product= "Human colon cancer-associated polypeptide"
FT	/transl_except= (pos:84..87, aa:Ser)
FT	/transl_except= (pos:262..265, aa:Asp)
FT	/note= "CDS does not include start and stop codon"
FT	/partial
XX	
XX	WO200290986-A1.
PN	
XX	
XX	14-NOV-2002.
PD	
XX	
XX	02-MAY-2002; 2002WO-US013994.
PF	
XX	
XX	04-MAY-2001; 2001US-00849602.
PR	
XX	(LUDW-) LUDWIG INST CANCER RES.
PA	(CORR) CORNELL RES FOUND INC.
PA	
XX	
XX	Chen Y, Old LJ, Scanlan MJ, Stockert E;
PI	
XX	WPI; 2003-112003/10.
XX	P-PSDB; AAE35352.
DR	
DR	
DR	
XX	
PT	Diagnosing colon cancer in a subject comprises identifying colon cancer-
PT	associated polypeptides as antigens that elicit immune response in colon
PT	cancer.
XX	
XX	Claim 1; Page 85-89; 122pp; English.
PS	
PS	
XX	
CC	The invention relates to a method for diagnosing colon cancer in a
CC	subject which comprises identifying colon cancer-associated polypeptides
CC	as antigens that elicit immune response in colon cancer. The method is
CC	useful for diagnosing, determining onset, progression, or regression of
CC	colon cancer in a subject, or for selecting a course of treatment of a
CC	subject having or suspected of having colon cancer. The colon cancer-
CC	associated polypeptides are useful as markers for diagnosing colon
CC	cancer, and for following the course of treatment of colon cancer. The
CC	present sequence is human colon cancer-associated polypeptide gene
XX	
SQ	Sequence 6018 BP; 1741 A; 1171 C; 1328 G; 1778 T; 0 U; 0 Other;

	Query Match	99.3%	Score 3788.4	DB 10	Length 6018	
	. Best Local Similarity 99.8%	Pred. No. 0				
	Matches 3803	Conservative 0	Mismatches 6	Indels 1	Gaps 1	
Qy	4	GCTGCTCCGCCCGCGGGGACCGGGGGGAGGGAGCCACAGCGAGGGCGCGCGCTGG	63			
Db	1	GTGCTCTCCGCCCGCGGGGACCGCGGGGGAGGGAGCCACAGCGAGGGCGCGCGCTGG	60			
Qy	64	GC CGCGGCCATGGAGTGC GCCCGATCCGTGACAGCAGGAGGCCAAGCGGCCCGCGGCC	123			
Db	61	GC GCGG -CCATGGGACTGCGCCGATCCGTGACAGCAGGAGGCCAAGCGGCCCGCGGCC	119			
Qy	124	TGAGCGGCTCTCTCGGGGGGCGTGCCTCTCTGCTCGGGGCGCGGGCTCTCTGCTCC	183			
Db	120	TGAGCGGCTCTCTCGGGGGGCGTGCCTCTCTGCTCGGGGCGCGGGCTCTCTGCTCC	179			
Qy	184	GATTGCTGGCGCTGTGCTGGCTGTGGCGCGGCCAGGATCATGTGCGGTGCGCGCTGCG	243			
Db	180	GATTGCTGGCGCTGTGCTGGCTGTGGCGCGGCCAGGATCATGTGCGGTGCGCGCTGCG	239			

Db 2400 TAGCAGCTCTACTAATAAAGTATTAATCATGTGTCAATGCCAGGACAAATGGGCTTTCA 2459
Qy 2464 CACCTTTGCAAGAGCAGCCAAAGGAGGAGAAACACAGCTTTTGTGCTTTTGTGCTAGCCC 2523
Db 2460 CACCTTTGCAAGAGCAGCCAAAGGAGGAGGACACACAGCTTTTGTGCTTTTGTGCTAGCCC 2519
Qy 2524 ATGAGCTGACCCCGACTCTCTTAAAAATCAGGAAGGACAAACACCTTTTATAGATTAGTTTCAG 2583
Db 2520 ATGAGCTGACCCCGACTCTCTTAAAAATCAGGAAGGACAAACACCTTTTATAGATTAGTTTCAG 2579
Qy 2584 CGGATGATGTGACGGCTCTCTGACACAGCCATGCCCCCATCTGCTCTGCCCTCTTGT 2643
Db 2580 CAGATGATGTGACGGCTCTCTGACACAGCCATGCCCCCATCTGCTCTGCCCTCTTGT 2639
Qy 2644 ACAAGCCTCAAGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGACAGATGCTCTCTCTT 2703
Db 2640 ACAAGCCTCAAGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGACAGATGCTCTCTCTT 2699
Qy 2704 CAGGTCCATCTAGCCCATCAAGCCCTTTCTGACGCCAGCAGCTTTGACAACTTATCTGGGA 2763
Db 2700 CAGGTCCATCTAGCCCATCAAGCCCTTTCTGACGCCAGCAGCTTTGACAACTTATCTGGGA 2759
Qy 2764 GTTTTTCAGAACCTGCTCTCAGTAGTTAGTTCAAGTGGAACAGAGGGTCTTCCAGTTTGG 2823
Db 2760 GTTTTTCAGAACCTGCTCTCAGTAGTTAGTTCAAGTGGAACAGAGGGTCTTCCAGTTTGG 2819
Qy 2824 AGAAAAGGAGGTTCCAGGAGTAGATTTTATAGCATAACTCAATTCGTAAAGGAATCTTGGAC 2883
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Qy 2884 TTGAGCACTTAATGGAATATTTTGAGAGAGAAACAGATCACTTTGGATGATTTAGTTGAGA 2943
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Qy 2944 TGGGCAACAGGAGCTCAAGGAGATTTGGAATCAATGCTTATGGACATAGGACACAAACTAA 3003
Db 2940 TGGGCAACAGGAGCTCAAGGAGATTTGGAATCAATGCTTATGGACATAGGACACAAACTAA 2999
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Db 3000 TTAAGGAGTCGAGAGACTTATCTCCGACAAACAGGTCTTAAACCATATTTAACTTTGA 3059
Qy 3064 ACACCTCTGCTAGTGGAACTTCTTATAGATCTGCTCTCTGATGATAAAGAGTTTCAGT 3123
Db 3060 ACACCTCTGCTAGTGGAACTTCTTATAGATCTGCTCTCTGATGATAAAGAGTTTCAGT 3119
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Qy 3244 AAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAAACCAACCATGCCAATGAAC 3303
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Qy 3304 GAATGCTTATTTCAAGGCTCTCTTGTGATGCAATTTATCCAAAGGGCTTTGATGAAA 3363
Db 3300 GAATGCTTATTTCAAGGCTCTCTTGTGATGCAATTTATCCAAAGGGCTTTGATGAAA 3359
Qy 3364 GGCAATGCTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAAACCTTTCCA 3423
Db 3360 GGCAATGCTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAAACCTTTCCA 3419
Qy 3424 AAAGCAATCAATATGATATGGAATTTGGAGAGGATCTGGGTGTCCAGTTTCAAAAGACA 3483
Db 3420 AAAGCAATCAATATGATATGGAATTTGGAGAGGATCTGGGTGTCCAGTTTCAAAAGACA 3479
Qy 3484 GATCTTCTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTGGGAAAGTCTT 3543

Db 3480 GATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTGGGAAAGTCTT 3539
Qy 3544 TCCTGCAGTTTCAGTGCATGAAATGGCAATTTCTCTCCTCAGGTCACTCATCAGTCACTG 3603
Db 3540 TCCTGCAGTTTCAGTGCATGAAATGGCAATTTCTCTCCTCAGGTCACTCATCAGTCACTG 3599
Qy 3604 GTAGGCCAGGTAAATGGCCTAGCATTTAGCTGAATATGTTATTTACAGAGGAGAACAGG 3663
Db 3600 GTAGGCCAGGTAAATGGCCTAGCATTTAGCTGAATATGTTATTTACAGAGGAGAACAGG 3659
Qy 3664 CTTATCTGTAGTATTTAAATTTACTTTACAGATTATGAGGCCCTGAAGGTATGTTCCATGGAT 3723
Db 3660 CTTATCTGTAGTATTTAAATTTACTTTACAGATTATGAGGCCCTGAAGGTATGTTCCATGGAT 3719
Qy 3724 AAATAGTATTTTAAAGAACTAATTTCCACTGAACCTTAAATCATCAAAAGCAGCAGTGGCC 3783
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Db 3780 TCTACGTTTTTACTCTCTTTGCTGAAAAAAA 3809

Search completed: December 18, 2006, 13:14:45
Job time : 2074.14 secs

Result No.	Score	Query		Length	DB	ID	Description
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2	3816	100.0	3816	2	AR653624	AR653624	Sequence
3	3793	99.4	6028	5	AF309033	Homo sapi	AF309033
4	3793	99.4	6123	4	AX057579	Sequence	AX057579
5	3791.4	99.4	4275	2	AR361486	Sequence	AR361486
6	3791.4	99.4	4406	2	AX062247	Sequence	AX062247
7	3791.4	99.4	4992	2	AX062275	Sequence	AX062275
8	3791.4	99.4	5002	2	AX062273	Sequence	AX062273
9	3791.4	99.4	6189	2	Q0896544	Sequence	Q0896544
10	3791.4	99.4	6189	2	CS019687	Sequence	CS019687
11	3791.4	99.4	6189	2	CS023798	Sequence	CS023798
12	3791.4	99.4	6189	5	AF438201	Homo sapi	AF438201
13	3788.4	99.3	6018	2	AR584137	Sequence	AR584137
14	3770.8	98.8	5075	2	AR578380	Sequence	AR578380
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16	3724.8	97.6	3815	5	AF329696	Homo sapi	AF329696
17	3595.8	94.2	4137	2	AX062241	Sequence	AX062241
18	3594.8	94.2	4512	2	AR232161	Sequence	AR232161

Qy	241	CGCGCGCGGGGAGCGGCTTGGCGAGCGCGCGGCGCGAGCGCGCGCGCC	300
Db	241	CGCGCGCGGGGAGCGGCTTGGCGAGCGCGCGGCGCGAGCGCGCGCGCC	300
Qy	301	GAGAGCTGTTCGAGCGTGGCGCAACGCGGACGTGGACAGTCAAGAGGCTGTGACGC	360
Db	301	GAGAGCTGTTCGAGCGTGGCGCAACGCGGACGTGGACAGTCAAGAGGCTGTGACGC	360
Qy	361	CTGAGAGGTGAACAGCGCGCACGCGCGGCGAGGAAATCCACCCGCTGCATTCGCGG	420
Db	361	CTGAGAGGTGAACAGCGCGCACGCGCGGCGAGGAAATCCACCCGCTGCATTCGCGG	420
Qy	421	CAGGTTTTGGCGGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCGAAG	480
Db	421	CAGGTTTTGGCGGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCGAAG	480
Qy	481	CACGTGATGATGGGGGCTTATTCCTCTTCAATATGCAATGCTCTTTTGGTCAATGCTGAAG	540
Db	481	CACGTGATGATGGGGGCTTATTCCTCTTCAATATGCAATGCTCTTTTGGTCAATGCTGAAG	540
Qy	541	TAGTCAATCTCTTTTGGCAATGGTGAGACCCCAATGCTCGAGATAAATGGAAATATA	600
Db	541	TAGTCAATCTCTTTTGGCAATGGTGAGACCCCAATGCTCGAGATAAATGGAAATATA	600
Qy	601	CTCCTCTCCATGAAGCTGCAATTAAGAAAGATTGATGTTTGGCATTTGCTGTTACAGC	660
Db	601	CTCCTCTCCATGAAGCTGCAATTAAGAAAGATTGATGTTTGGCATTTGCTGTTACAGC	660
Qy	661	ATGAGCTGAGCCACCAATCCGAATACAGATGGAAGACAGCATTCGATTTTACAGATC	720
Db	661	ATGAGCTGAGCCACCAATCCGAATACAGATGGAAGACAGCATTCGATTTTACAGATC	720
Qy	721	CATCTGCCAAAGCAGTGTCTTCTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA	780
Db	721	CATCTGCCAAAGCAGTGTCTTCTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA	780
Qy	781	GGAGTGGCAATGAAGAAAAATGATGGCTCTACTCACCAATTAATGTCAACTGCGCAGC	840
Db	781	GGAGTGGCAATGAAGAAAAATGATGGCTCTACTCACCAATTAATGTCAACTGCGCAGC	840
Qy	841	CAAGTATGAGCAAGGCAACTCCATTCATTTGGCAGCAGGATATAACAGAGTAAAGA	900
Db	841	CAAGTATGAGCAAGGCAACTCCATTCATTTGGCAGCAGGATATAACAGAGTAAAGA	900
Qy	901	TTGTACAGCTGTACTGCAACATGAGAGCTGATGCCATGCTTAAAGATAAAGGTGATCTGG	960
Db	901	TTGTACAGCTGTACTGCAACATGAGAGCTGATGCCATGCTTAAAGATAAAGGTGATCTGG	960
Qy	961	TACCATTAACAATGCGCTGTTCTTATGTCATTTATGAAGTAACTTTTGGTCAAGC	1020
Db	961	TACCATTAACAATGCGCTGTTCTTATGTCATTTATGAAGTAACTTTTGGTCAAGC	1020
Qy	1021	ATGTTGCTGTGTAATGCAATGGAATGCTGGCAATTCACCTCTTTCATGAGCAGCTT	1080
Db	1021	ATGTTGCTGTGTAATGCAATGGAATGCTGGCAATTCACCTCTTTCATGAGCAGCTT	1080
Qy	1081	CTAAGAAACAGGGTTGAAGTATGTTCTTCTTCTTAAAGTTATGGTGCAACCACTGTC	1140
Db	1081	CTAAGAAACAGGGTTGAAGTATGTTCTTCTTCTTAAAGTTATGGTGCAACCACTGTC	1140
Qy	1141	TCAATTTGCAATAAAGGTGATAGACTTTGGCTGCCACACCAAGTAAAGAAAGAT	1200
Db	1141	TCAATTTGCAATAAAGGTGATAGACTTTGGCTGCCACACCAAGTAAAGAAAGAT	1200
Qy	1201	TAGCATATGAATTTAAGGCCCATCTGTTGCTGCAAGCTGCAAGAGCTCATGTTACTC	1260
Db	1201	TAGCATATGAATTTAAGGCCCATCTGTTGCTGCAAGCTGCAAGAGCTCATGTTACTC	1260
Qy	1261	GAATCAAAAAACATCTCTCTCTGGAATATGGTGAATTTTCAAGCATCTTCAACACATGAAA	1320
Db	1261	GAATCAAAAAACATCTCTCTCTGGAATATGGTGAATTTTCAAGCATCTTCAACACATGAAA	1320

Qy	1321	CAGCATTCGATTCGTGCTGCATCTCCATATCCCAAAAGAAAGCAATATGTGAACCTGT	1380
Db	1321	CAGCATTCGATTCGTGCTGCATCTCCATATCCCAAAAGAAAGCAATATGTGAACCTGT	1380
Qy	1381	TGCTAAGAAAAAGAGCAAAACATCAATGAAAAAGACTAAAGAAATCTTGTGACTCTCTCTGACAG	1440
Db	1381	TGCTAAGAAAAAGAGCAAAACATCAATGAAAAAGACTAAAGAAATCTTGTGACTCTCTCTGACAG	1440
Qy	1441	TGGCATCTGAGAAAGCTCAATAATGATGTTGTTGAAGTAGTGGTGAACATGAACAAAGG	1500
Db	1441	TGGCATCTGAGAAAGCTCAATAATGATGTTGTTGAAGTAGTGGTGAACATGAACAAAGG	1500
Qy	1501	TTAATGCTCTGGGTAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCAATC	1560
Db	1501	TTAATGCTCTGGGTAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCAATC	1560
Qy	1561	TACAAAACCTCCGCGCTACTCTCTGAGCTATGGGTGATGATCTCTTAACATTTATATCTCCCTTCAGG	1620
Db	1561	TACAAAACCTCCGCGCTACTCTCTGAGCTATGGGTGATGATCTCTTAACATTTATATCTCCCTTCAGG	1620
Qy	1621	GCTTTACTGCTTTACAGATGGGAAATGAAAATGTAACAGCAACTCTCTCAAGAGGGTATCT	1680
Db	1621	GCTTTACTGCTTTACAGATGGGAAATGAAAATGTAACAGCAACTCTCTCAAGAGGGTATCT	1680
Qy	1681	CATTAGGTAAATTCAGAGCGCAGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCTG	1740
Db	1681	CATTAGGTAAATTCAGAGCGCAGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCTG	1740
Qy	1741	AAACTGTAAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAAGGGGCTC	1800
Db	1741	AAACTGTAAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAAGGGGCTC	1800
Qy	1801	AGTCTACACCACTTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC	1860
Db	1801	AGTCTACACCACTTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC	1860
Qy	1861	TACAGCATGAGCTGATGTCATGCTAAAGATAAGAGGCTTGTACCTTTTGACCAATG	1920
Db	1861	TACAGCATGAGCTGATGTCATGCTAAAGATAAGAGGCTTGTACCTTTTGACCAATG	1920
Qy	1921	CATGTTCTTATGGAACATTTATGAAGTTGCAGAACTTCTTTGTAAACATGGAGCAGTAGTTA	1980
Db	1921	CATGTTCTTATGGAACATTTATGAAGTTGCAGAACTTCTTTGTAAACATGGAGCAGTAGTTA	1980
Qy	1981	ATGTAGCTGATTTATGGAATTTACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG	2040
Db	1981	ATGTAGCTGATTTATGGAATTTTACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG	2040
Qy	2041	AAATTTGCAAACTTCTCTCCAGCATGGTGAGACCTTACCACAAAAAACAAGGATGGAA	2100
Db	2041	AAATTTGCAAACTTCTCTCCAGCATGGTGAGACCTTACCACAAAAAACAAGGATGGAA	2100
Qy	2101	ATATCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAG	2160
Db	2101	ATATCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAG	2160
Qy	2161	ATGAGCTTTGCTAGATGCTGCGCAAGAGGGTGTGTTAGCCAGAGTGAAGATGTGCTT	2220
Db	2161	ATGAGCTTTGCTAGATGCTGCGCAAGAGGGTGTGTTAGCCAGAGTGAAGATGTGCTT	2220
Qy	2221	CTCCTGATAATGTAATTTGCCGGATACCAAGGCAGACATTTCAACCTTTTACATTTAG	2280
Db	2221	CTCCTGATAATGTAATTTGCCGGATACCAAGGCAGACATTTCAACCTTTTACATTTAG	2280
Qy	2281	CAGCTGTTATTAATAATTTAGAGTTTCAGAGTATTTGTTTACAAACACGAGCTGATGTGA	2340
Db	2281	CAGCTGTTATTAATAATTTAGAGTTTCAGAGTATTTGTTTACAAACACGAGCTGATGTGA	2340
Qy	2341	ATGCCAAGCAAAAGGAGGACTTATTCCTTTTACATATGAGCATCTTACGGGATGTAG	2400
Db	2341	ATGCCAAGCAAAAGGAGGACTTATTCCTTTTACATATGAGCATCTTACGGGATGTAG	2400
Qy	2401	ATGTAGCAGCTCTACTATAAAGTATAATGTCATGTGTCAATGCCACGCAAAATGGGCTT	2460

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Qy 2521 CCCATGGAGCTGACCCGAGCTCTTAAAAATCAGGAAGGCAAAACACCTTTAGATTTAGTTT 2580
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Db 2581 CAGCGGATGATGTACGGCTCTTCTGACAGAGCCCAATGCCCACTGCTCTGCGCTCTTT 2640
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Db 2641 GTTACAAGCCTCAAGTGTCAATGCTGAGAGGCCAGGACCACTGCAGATGCTCTCT 2700
Qy 2701 CTTCAGGTCCTATAGCCCATCAAGCCTTTCTGCAGCAGCAGTCTTGACAACTTATCTG 2760
Db 2701 CTTCAGGTCCTATAGCCCATCAAGCCTTTCTGCAGCAGCAGTCTTGACAACTTATCTG 2760
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Db 2761 GGAGTTTTCAGAACTGTCTTCAGTATGTTTCAAGTGGAAACAGAGGCTGCTTCCAGTT 2820
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RESULT 2
LOCUS AR653624 3816 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 2 from patent US 6887675.
ACCESSION AR653624
VERSION AR653624.1 GI:67584113
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3816)
AUTHORS Luo, Y., Chan, E., Xu, X., Huang, B. and Ossovskaya, V.
TITLE Tankyrase H, compositions involved in the cell cycle and methods of use
JOURNAL Patent: US 6887675-A 2 03-MAY-2005;
Rigel Pharmaceuticals, Inc.; South San Francisco, CA
FEATURES
source location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 3816; DB 2; Length 3816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CGCGCTGCTCCGCCCGCCGCGGGGCGAGCCGGGGGCGAGGAGCCCGAGGGGGCGCGG 60
Qy 61 TGGCGCGCGCCCATGGGACTGCGCGGATCCGGTGACACGAGGGAGCCAAAGCGCCGCGG 120
Db 61 TGGCGCGCGCCCATGGGACTGCGCGGATCCGGTGACACGAGGGAGCCAAAGCGCCGCGG 120
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DEFINITION Homo sapiens tankyrase-2 (TNKS-2) mRNA, complete cds.
ACCESSION AF309033
VERSION AF309033.1 GI:15042551
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Chi, N.-W. and Lodish, H. F.
TITLE A novel homolog of Tankyrase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6028)
AUTHORS Chi, N.-W. and Lodish, H. F.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2000) Whitehead Institute for Biomedical Research, 9 Cambridge Center, Cambridge, MA 02142, USA

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VERSION	AX057579.1	GI:12310301			
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ORGANISM	ORGANISM	Homo sapiens			
REFERENCE	1	Chi,N.W. and Lodish,H.F.			
AUTHORS	TITLE	A novel insulin signaling molecule			
JOURNAL	TITLE	Patent: WO 0077225-A 21-DEC-2000;			
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ACCESSION AR361486
VERSION AR361486.1 GI:33769334
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4275)
AUTHORS Morin,G.B., Funk,W.D. and Piatyszek,M.A.
TITLE Second mammalian tankyrase
JOURNAL Patent: US 6599728-A 5 29-JUL-2003;
Geron Corporation; Menlo Park, CA
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Db	240	TCCGGTTGCTGGCGCTGTTCCTGCTGTGGGGGGCCAGGATCATGTCTGGGTGCGCGCT	299
Qy	241	CGCGCGGGGGGAGCGGCTCTCGCGAGCGCGGGGCGGAGCGCGCGCGCC	300
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Db	480	CAGGTTTTGGCGGAAAGACGCTAGTTGAATATTTGCTTCAGAACTGGTCAAAATGTCGAAG	539
Qy	481	CAGTGATGATGGGGGCTTATTCCTCTTCATTAATGCAATGCTCTTTGGTCAATGCTGAAG	540
Db	540	CAGTGATGATGGGGGCTTATTCCTCTTCATTAATGCAATGCTCTTTGGTCAATGCTGAAG	599
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Db	660	CTCCTCTCCATGAAGCTCAATTAAGGAAAGATTTGATTTGCAATGTGCTGTTACAGC	719
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Db	1440	TGCTAAGAAAGGAGCAACATCAATGAAGAAAGCTAAGAAATTTCTTACCTCTCGACG	1499
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Db	1500	TGGCATCTGAGAAAGCTCAATAATGATTTGTTGAAGTAGTGGTGAACATGAACAAAGG	1559
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ACCESSION AX062247
VERSION AX062247.1 GI:12540148
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Christenson, E., Demaggio, A. J., Goldman, P. S. and Mcelligott, D. L.
TITLE Tankyrase2 materials and methods
JOURNAL Patent: WO 0100849-A 106 04-JAN-2001;
ICOS CORPORATION (US)
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ORIGIN

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 REFERENCE
 1 Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.
 Authors
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ORGANISM	Homo sapiens							
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REFERENCE	1. Christenson, E., Denaggio, A.J., Goldman, P.S. and Mcelligott, D.L.							
AUTHORS	Tankyrase2 materials and methods							
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Qy	1201	TAGCATATGAATTTAAAGGCCACTCGTTGTGCAAGCTGCAAGAGAGCTGATGTTACTC	1260		
Db	1862	TAGCATATGAATTTAAAGGCCACTCGTTGTGCAAGCTGCAAGAGAGCTGATGTTACTC	1921		
Qy	1261	GAATCAAAAAACATCTCTCTCTGGAATGTTGAAATTTCAAGCATCTCTCAACACATGAA	1320		
Db	1922	GAATCAAAAAACATCTCTCTCTGGAATGTTGAAATTTCAAGCATCTCTCAACACATGAA	1981		
Qy	1321	CAGCATTTGCTGCTGCTGCTCATATCCAAAAAGAAAGCAAAATATGTGAACCTGT	1380		

Db 1982 CAGCAATTGCTGTGCTCATCTCCATATATCCAAAAGAAAGCAAAATATGTGAACCTGT 2041
Qy 1381 TGCTAAGAAAAGGAGCAACATCAATGAAGAAAGACATAAAGAAATCTTGTGACTCCTCTGACAG 1440
Db 2042 TGCTAAGAAAAGGAGCAACATCAATGAAGAAAGACATAAAGAAATCTTGTGACTCCTCTGACAG 2101
Qy 1441 TGGCACTCTGAGAAAGCTCATATATGATGTGTGTAAGTAGTGTGTAAGCAATGAAGCAAAAG 1500
Db 2102 TGGCACTCTGAGAAAGCTCATATATGATGTGTGTAAGTAGTGTGTAAGCAATGAAGCAAAAG 2161
Qy 1501 TTAATGCTCTGGATTAATCTTGTGTGACACTTCTCTACACAGAGCTGCATATTTGTGTGATC 1560
Db 2162 TTAATGCTCTGGATTAATCTTGTGTGACACTTCTCTACACAGAGCTGCATATTTGTGTGATC 2221
Qy 1561 TACAAACCTGCCCGCTACTCCTGAGCTATGGGTGATCCCTAAATATATCCCTTCAGG 1620
Db 2222 TACAAACCTGCCCGCTACTCCTGAGCTATGGGTGATCCCTAAATATATATCCCTTCAGG 2281
Qy 1621 GCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCCTCCAGAGGGTATCT 1680
Db 2282 GCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCCTCCAGAGGGTATCT 2341
Qy 1681 CATTAAGTAAATTCAGAGGAGACAGACAAATTTGCTGGAAGCTGCCAAGGCTGGAGATGTCG 1740
Db 2342 CATTAAGTAAATTCAGAGGAGACAGACAAATTTGCTGGAAGCTGCCAAGGCTGGAGATGTCG 2401
Qy 1741 AAACGTGTAAGAAAAGCTGTACTGTTTCAGAGTGTCACATGTCAGAGACATTTGAAGGGCGTC 1800
Db 2402 AAACGTGTAAGAAAAGCTGTACTGTTTCAGAGTGTCACATGTCAGAGACATTTGAAGGGCGTC 2461
Qy 1801 AGTCTACACCACTTCATTTTTCAGCTGGGTATTAACAGAGTGTCCTCCCAAGGGTATCTGTC 1860
Db 2462 AGTCTACACCACTTCATTTTTCAGCTGGGTATTAACAGAGTGTCCTCCCAAGGGTATCTGTC 2521
Qy 1861 TACAGATGAGAGCTGATGTGATGCTAAAGATAAAGAGAGGCTTGTAACCTTTGACAAATG 1920
Db 2522 TACAGATGAGAGCTGATGTGATGCTAAAGATAAAGAGAGGCTTGTAACCTTTGACAAATG 2581
Qy 1921 CATGTTCTTATGGAATTAAGATGTCAGAGCTTCTGTTTAAACATGGAGCAGTAGTTA 1980
Db 2582 CATGTTCTTATGGAATTAAGATGTCAGAGCTTCTGTTTAAACATGGAGCAGTAGTTA 2641
Qy 1981 ATGTAGCTGATTTATGGAATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG 2040
Db 2642 ATGTAGCTGATTTATGGAATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG 2701
Qy 2041 AAATTTGCAAACTTCTGCTCCAGCATGTGTCAGACCTTACCAAAAAAAGGAGTGAA 2100
Db 2702 AAATTTGCAAACTTCTGCTCCAGCATGTGTCAGACCTTACCAAAAAAAGGAGTGAA 2761
Qy 2101 ATACTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGAG 2160
Db 2762 ATACTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGAG 2821
Qy 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGGAAGTGTGCTT 2220
Db 2822 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGGAAGTGTGCTT 2881
Qy 2221 CTCTCTGATAATGTAATTTGCCCGATACCCCAAGGAGCAGATTTCAACACCTTTTACATTTAG 2280
Db 2882 CTCTCTGATAATGTAATTTGCCCGATACCCCAAGGAGCAGATTTCAACACCTTTTACATTTAG 2941
Qy 2281 CAGCTGGTTATTAATTTTAGAATTTGCAGAGTATTTGTTACACACGAGCTGATGTGA 2340
Db 2942 CAGCTGGTTATTAATTTTAGAATTTGCAGAGTATTTGTTTACACACGAGCTGATGTGA 3001
Qy 2341 ATGCCCAAGACAAAGAGGAGCTTATTTCTTTTACATAATGTCAGATCTTTACGGGATGTAG 2400
Db 3002 ATGCCCAAGACAAAGAGGAGCTTATTTCTTTTACATAATGTCAGATCTTTACGGGATGTAG 3061
Qy 2401 ATGTAGCAGCTCTACTTAATAAGTATAATGCAATGTGTCAATGCCACGCAAAATGGGCTT 2460
Db 3062 ATGTAGCAGCTCTACTTAATAAGTATAATGCAATGTGTCAATGCCACGCAAAATGGGCTT 3121

Qy 2461 TCACACCTTTTGCAAGAGCAGCCCAAAGGACGAAACACAGCTTTTGTGCTTTTGTGCTAG 2520
Db 3122 TCACACCTTTTGCAAGAGCAGCCCAAAGGACGAAACACAGCTTTTGTGCTTTTGTGCTAG 3181
Qy 2521 CCCATGAGCTGAGCCCGACTCTTTAAAAATCAGGAAGGACAAACCTTTAGATTTAGTTT 2580
Db 3182 CCCATGAGCTGAGCCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTT 3241
Qy 2581 CAGCGATGATGTCAGCGCTCTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTT 2640
Db 3242 CAGCAGATGATGTCAGCGCTCTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTT 3301
Qy 2641 GTTACAAAGCTTCAAGTGTCTCAATGCTGTGAGAAAGCCAGAGACCACTGACAGATGCTCTCT 2700
Db 3302 GTTACAAAGCTTCAAGTGTCTCAATGCTGTGAGAAAGCCAGAGACCACTGACAGATGCTCTCT 3361
Qy 2701 CTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGAGCAGCAGCAGCTTTGACAACTTATCTG 2760
Db 3362 CTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGAGCAGCAGCAGCTTTGACAACTTATCTG 3421
Qy 2761 GGAGTTTTTCAGAACTGCTTTCAGTAGTTAGTTCAAGTGGACAGAGGGTCTTCCAGTT 2820
Db 3422 GGAGTTTTTCAGAACTGCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGGTCTTCCAGTT 3481
Qy 2821 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTCAGATAAATTCATTCGTAAAGGAATCTTG 2880
Db 3482 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTCAGATAAATTCATTCGTAAAGGAATCTTG 3541
Qy 2881 GACTTTGAGCACTTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTTAGTTG 2940
Db 3542 GACTTTGAGCACTTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTTAGTTG 3601
Qy 2941 AGATGGGGCACAGGAGCTGAGGAGATTTGGAATCAATGCTTATGGACATAGGCAAAAC 3000
Db 3602 AGATGGGGCACAGGAGCTGAGGAGATTTGGAATCAATGCTTATGGACATAGGCAAAAC 3661
Qy 3001 TAAITAAAGGAGTCGAGAGACTTATCTCCGAGCAACAAAGGCTTTAAACCATATTTAACTT 3060
Db 3662 TAAITAAAGGAGTCGAGAGACTTATCTCCGAGCAACAAAGGCTTTAAACCATATTTAACTT 3721
Qy 3061 TGAAACCTCTGTPAGTGGAAACAAATCTTATAGATCTGCTCTCTGATGATAAAGAGTTTC 3120
Db 3722 TGAAACCTCTGTPAGTGGAAACAAATCTTATAGATCTGCTCTCTGATGATAAAGAGTTTC 3781
Qy 3121 AGTCTGTGGAGAAAGATGCAAAAGTACAGTTTCAGAGCAGCAGAGATGGAGTCAATGAG 3180
Db 3782 AGTCTGTGGAGAAAGATGCAAAAGTACAGTTTCAGAGCAGCAGAGATGGAGTCAATGAG 3841
Qy 3181 GTGGAATCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAAACTAT 3240
Db 3842 GTGGAATCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAAACTAT 3901
Qy 3241 GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAGAGAAACCAACCATGCCATG 3300
Db 3902 GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAGAGAAACCAACCATGCCATG 3961
Qy 3301 AACGAATGCTATTTTCAATGGGTCTCTTTTGTGAATGCAATTTATCCAAAGAGCTTTGATG 3360
Db 3962 AACGAATGCTATTTTCAATGGGTCTCTTTTGTGAATGCAATTTATCCAAAGAGCTTTGATG 4021
Qy 3361 AAAGGCATGCTACATAGGTGTTATGTTGGAGCTGGCATTTATTTTGTCTGAAACTCTT 3420
Db 4022 AAAGGCATGCTACATAGGTGTTATGTTGGAGCTGGCATTTATTTTGTCTGAAACTCTT 4081
Qy 3421 CCAAAAGCAATCAATATGATATGGAATTTGGAGAGGTAAGTCTGGGTCTCCAGTTCAAAAG 3480
Db 4082 CCAAAAGCAATCAATATGATATGGAATTTGGAGAGGTAAGTCTGGGTCTCCAGTTCAAAAG 4141
Qy 3481 ACAGATCTGTGATCAATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAACTTGGGAAAGT 3540
Db 4142 ACAGATCTGTGATCAATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAACTTGGGAAAGT 4201

Db 1536 TGCTAAGAAAAGGAGCAACATCAATGAAAGACTAAAGAAATTCCTTGACTCCTCTGCACG 1595
Qy 1441 TGGCATCTGAGNAAGCTCATATGATGTGTGTTGAAGTAGTGTGTAAGCAATGNAAGCAAGG 1500
Db 1596 TGGCATCTGAGNAAGCTCATATGATGTGTGTTGAAGTAGTGTGTAAGCAATGNAAGCAAGG 1655
Qy 1501 TTAATGCTCTGATATCTTGCTGAGACTTCTCTACACAGAGCTGCATATTTGTGTGTCATC 1560
Db 1656 TTAATGCTCTGATATCTTGCTGAGACTTCTCTACACAGAGCTGCATATTTGTGTGTCATC 1715
Qy 1561 TACAAACCTTGGCGCTACTCTCTGAGCTATGGGTGTGATCCTTAAACATATATATCCCTTCAGG 1620
Db 1716 TACAAACCTTGGCGCTACTCTCTGAGCTATGGGTGTGATCCTTAAACATATATATCCCTTCAGG 1775
Qy 1621 GCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT 1680
Db 1776 GCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT 1835
Qy 1681 CATTAGGTAAATTCAGAGCGACAGACAAATTTGCTGGAAGCTGCAAGGCTGGAGATGTG 1740
Db 1836 CATTAGGTAAATTCAGAGCGACAGACAAATTTGCTGGAAGCTGCAAGGCTGGAGATGTG 1895
Qy 1741 AAACGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTTGAAAGGGCTC 1800
Db 1896 AAACGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTTGAAAGGGCTC 1955
Qy 1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATACAGAGTGTCCGTGTGGATATCTGC 1860
Db 1956 AGTCTACACCACTTCATTTTGCAGCTGGGTATACAGAGTGTCCGTGTGGATATCTGC 2015
Qy 1861 TACAGCATGGAGCTGATGTGATGCTAAAGATAAAGGAGGCTTGATCCTTTTGACAAATG 1920
Db 2016 TACAGCATGGAGCTGATGTGATGCTAAAGATAAAGGAGGCTTGATCCTTTTGACAAATG 2075
Qy 1921 CATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTAAACATCGAGCAGTAGTTA 1980
Db 2076 CATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTAAACATCGAGCAGTAGTTA 2135
Qy 1981 ATGTAGCTGATTTATGGAATTTACACCTTTACATGAAGCGACGACAAAGGAAAATATG 2040
Db 2136 ATGTAGCTGATTTATGGAATTTACACCTTTACATGAAGCGACGACAAAGGAAAATATG 2195
Qy 2041 AAATTTGCAAACTCTGCTCCAGCATGTGCAGACCTTACCAGGAGGAGGATGGA 2100
Db 2196 AAATTTGCAAACTCTGCTCCAGCATGTGCAGACCTTACCAGGAGGAGGATGGA 2255
Qy 2101 ATATCTCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAG 2160
Db 2256 ATATCTCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAG 2315
Qy 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGATGTGCTT 2220
Db 2316 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGATGTGCTT 2375
Qy 2221 CTCCTGATAATGTAATTTGCCCGCATACCAGGCGACATTTCAACACCTTTACATTTAG 2280
Db 2376 CTCCTGATAATGTAATTTGCCCGCATACCAGGCGACATTTCAACACCTTTACATTTAG 2435
Qy 2281 CAGCTGGTTATAATTAATTTAGAAAGTTGCAGAGTATTTGTTTACACACGAGCTGATGTA 2340
Db 2436 CAGCTGGTTATAATTAATTTAGAAAGTTGCAGAGTATTTGTTTACACACGAGCTGATGTA 2495
Qy 2341 ATGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGCGAGCATCTTACGGGCATGTAG 2400
Db 2496 ATGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGCGAGCATCTTACGGGCATGTAG 2555
Qy 2401 ATGTAGCAGCTCTACTAATAAAGTATAATGATGTTCAATGCTCCACGACGACAAATGGGCTT 2460
Db 2556 ATGTAGCAGCTCTACTAATAAAGTATAATGATGTTCAATGCTCCACGACGACAAATGGGCTT 2615
Qy 2461 TCACACCTTTGACGAAGCAGCCCAAAAGGAGCGAACACAGCTTTGTGCTTTGTGCTAG 2520
Db 2616 TCACACCTTTGACGAAGCAGCCCAAAAGGAGCGAACACAGCTTTGTGCTTTGTGCTAG 2675

Qy 2521 CCCATGCGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTT 2580
Db 2676 CCCATGCGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTT 2735
Qy 2581 CAGCGGATGATGTGAGCGCTCTTCTTGACAGCAGCCATGCCCCCCTCTGCTCTGCCCTCTT 2640
Db 2736 CAGCAGATGATGTGAGCGCTCTTCTTGACAGCAGCCATGCCCCCCTCTGCTCTGCCCTCTT 2795
Qy 2641 GTTACAAAGCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGAGGCCACTGCGAGATGCTCTCT 2700
Db 2796 GTTACAAAGCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGAGGCCACTGCGAGATGCTCTCT 2855
Qy 2701 CTTCAAGTCCATCTAGCCCATCAAGCCTTTCTGAGCGCAGCAGCTTGTGACAACTTATCTG 2760
Db 2856 CTTCAAGTCCATCTAGCCCATCAAGCCTTTCTGAGCGCAGCAGCTTGTGACAACTTATCTG 2915
Qy 2761 GGAGTTTTTCAAGAACTGTCTTCAAGTAGTATTCAAGTGGAAACAGAGGGTGTCTTCCAGTT 2820
Db 2916 GGAGTTTTTCAAGAACTGTCTTCAAGTAGTATTCAAGTGGAAACAGAGGGTGTCTTCCAGTT 2975
Qy 2821 TGGAAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAGGGAATCTTG 2880
Db 2976 TGGAAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAGGGAATCTTG 3035
Qy 2881 GACTTGAGCAGCTTAATGATATATTTGAGAGAGAAACAGATCACCTTTGGATGCTATTAGTTG 2940
Db 3036 GACTTGAGCAGCTTAATGATATATTTGAGAGAGAAACAGATCACCTTTGGATGCTATTAGTTG 3095
Qy 2941 AGATGGGGCAACAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGACACAAAC 3000
Db 3096 AGATGGGGCAACAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGACACAAAC 3155
Qy 3001 TAATTTAAAGAGTGCAGAGACTTATCTCCGGAACAAAGGCTTTAAACCATATTTAACTT 3060
Db 3156 TAATTTAAAGAGTGCAGAGACTTATCTCCGGAACAAAGGCTTTAAACCATATTTAACTT 3215
Qy 3061 TGAACACCTCTGTGAGTGGAAACAAATCTTATAGATCTGTCTCCTGTATGATAAAGAGTTTC 3120
Db 3216 TGAACACCTCTGTGAGTGGAAACAAATCTTATAGATCTGTCTCCTGTATGATAAAGAGTTTC 3275
Qy 3121 AGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAG 3180
Db 3276 AGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAG 3335
Qy 3181 GTGGAATCTTCAACAGATACAAATTTCTCAAGATTCAAGATTGTAAGAGGTTTGTAAAGAAACTAT 3240
Db 3336 GTGGAATCTTCAACAGATACAAATTTCTCAAGATTCAAGATTGTAAGAGGTTTGTAAAGAAACTAT 3395
Qy 3241 GGGAAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCAATG 3300
Db 3396 GGGAAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCAATG 3455
Qy 3301 AACGAATGCTATTTTCATGGGTCTCCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATG 3360
Db 3456 AACGAATGCTATTTTCATGGGTCTCCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATG 3515
Qy 3361 AAAGGATGCGTACATAGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACCTCTT 3420
Db 3516 AAAGGATGCGTACATAGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACCTCTT 3575
Qy 3421 CCAAAAGCAATCAATATGTAATGGAATTTGGAGGAGTACTGGGTGTCCAGTTCACAAAG 3480
Db 3576 CCAAAAGCAATCAATATGTAATGGAATTTGGAGGAGTACTGGGTGTCCAGTTCACAAAG 3635
Qy 3481 ACAGATCTTGTATCAATTTGCCACAGGAGCTGCTCTTTTTCGGGGTAAACCTTTGGGAAAGT 3540
Db 3636 ACAGATCTTGTATCAATTTGCCACAGGAGCTGCTCTTTTTCGGGGTAAACCTTTGGGAAAGT 3695
Qy 3541 CTTTCTCTGAGGTTCAAGTGAATGAAAATGGGACATTTCTCTCTCCAGGTCATCATCTAGTCA 3600
Db 3696 CTTTCTCTGAGGTTCAAGTGAATGAAAATGGGACATTTCTCTCTCCAGGTCATCATCTAGTCA 3755

[illegible]

1501 QY TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACAGAGCTGCTATATGTGGTCATC 1560
1656 Db TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACAGAGCTGCTATATGTGGTCATC 1715
1561 QY TACAAACCTGCCGCCCTACTCTCTGAGCTATGGGTGATCTTAACTATATCCCTTCAGG 1620
1716 Db TACAAACCTGCCGCCCTACTCTCTGAGCTATGGGTGATCTTAACTATATCCCTTCAGG 1775
1621 QY GCTTTACTGCTTTACAGATGGGAAATGAATAATGTCAGCAACTCTCCCAAGAGGGTATCT 1680
1776 Db GCTTTACTGCTTTACAGATGGGAAATGAATAATGTCAGCAACTCTCCCAAGAGGGTATCT 1835
1681 QY CATTAAGTAATTCAGAGGCAGACAGACAAATGCTGGAAGCTGCAAGGCTGGAGATGTCG 1740
1836 Db CATTAAGTAATTCAGAGGCAGACAGACAAATGCTGGAAGCTGCAAGGCTGGAGATGTCG 1895
1741 QY AAACCTGTAATAAATCTGTACTGTTTACAGAGTGTCAACTGCGAGAGCATTTGAAGGGCGTC 1800
1896 Db AAACCTGTAATAAATCTGTACTGTTTACAGAGTGTCAACTGCGAGAGCATTTGAAGGGCGTC 1955
1801 QY AGTCTACACCACTTCAATTTGAGCTGGGTATACAGAGTGTCCGCTGGTGAATATCTGC 1860
1956 Db AGTCTACACCACTTCAATTTGAGCTGGGTATACAGAGTGTCCGCTGGTGAATATCTGC 2015
1861 QY TACAGCATGGAGCTGATGTCATCTTAAAGATAAAGAGGCGCTTGTACCTTTGCAAAATG 1920
2016 Db TACAGCATGGAGCTGATGTCATCTTAAAGATAAAGAGGCGCTTGTACCTTTGCAAAATG 2075
1921 QY CATGTTCTTATGAGCATTAATGAAGTTGCGAATCTTGTGTTAAACATGAGCAGATGTTTA 1980
2076 Db CATGTTCTTATGAGCATTAATGAAGTTGCGAATCTTGTGTTAAACATGAGCAGATGTTTA 2135
1981 QY ATGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAGGAATATG 2040
2136 Db ATGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAGGAATATG 2195
2041 QY AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAAGAGGATGGA 2100
2196 Db AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAAGAGGATGGA 2255
2101 QY ATACTCTTTTGGATCTTGTGTTAAGATGGAGATACAGATATTCAGATCTGCTTAGGGAG 2160
2256 Db ATACTCTTTTGGATCTTGTGTTAAGATGGAGATACAGATATTCAGATCTGCTTAGGGAG 2315
2161 QY ATGCGAGCTTTGCTAGATGCTGCCAAGAGGTGTTTACGAGAGTGAAGAGTGTCTTT 2220
2316 Db ATGCGAGCTTTGCTAGATGCTGCCAAGAGGTGTTTACGAGAGTGAAGAGTGTCTTT 2375
2221 QY CTCCTGATTAATGTAATTCGCGATACCCAGGCGAGACATTCACACCTTTTACATTTAG 2280
2376 Db CTCCTGATTAATGTAATTCGCGGATACCCAGGCGAGACATTCACACCTTTTACATTTAG 2435
2281 QY CAGCTGGTTTATAATAATTAGATTGCGAGATTTGTTTGAACAACGAGCTGATGTA 2340
2436 Db CAGCTGGTTTATAATAATTAGATTGCGAGATTTGTTTGAACAACGAGCTGATGTA 2495
2341 QY ATGCCCCAAGACAAAGAGAGCTTATTCCTTTTACATTAATCGCAGATCTTACGGGATGTA 2400
2496 Db ATGCCCCAAGACAAAGAGAGCTTATTCCTTTTACATTAATCGCAGATCTTACGGGATGTA 2555
2401 QY ATGTAGCAGCTTACTTAATAAGTATAATGCTGTGTCATGTCACGCAAAATGGGCTT 2460
2556 Db ATGTAGCAGCTTACTTAATAAGTATAATGCTGTGTCATGTCACGCAAAATGGGCTT 2615
2461 QY TCACACCTTTGCAAGAGCAGGCCAAAGAGGACGAACAACAGCTTTGTGTTGCTAG 2520
2616 Db TCACACCTTTGCAAGAGCAGGCCAAAGAGGACGAACAACAGCTTTGTGTTGCTAG 2675
2521 QY CCCATGGAGCTGACCGACTCTTAAATAATCAGGAAGGACAAACCTTTTATAGTTT 2580
2676 Db CCCATGGAGCTGACCGACTCTTAAATAATCAGGAAGGACAAACCTTTTATAGTTT 2735
2581 QY CAGCGGATGATGTGAGCGCTCTTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTT 2640

2736 Db CAGCAGATGATGTGAGCGCTCTTCTGACAGAGCCATGCCCATCTGCTCTGCCCTCTT 2795
2641 QY GTTACAGGCTCAAGTGTCTCAATGCTGTGAGAGCCAGGAGCCACTGAGATGCTCTCT 2700
2796 Db GTTACAGGCTCAAGTGTCTCAATGCTGTGAGAGCCAGGAGCCACTGAGATGCTCTCT 2855
2701 QY CTTTCAAGTCTCATCTAGCCCATCAAGCCTTTCTGACAGCAGAGTCTTGTGACAACTTATCTG 2760
2856 Db CTTTCAAGTCTCATCTAGCCCATCAAGCCTTTCTGACAGCAGAGTCTTGTGACAACTTATCTG 2915
2761 QY GGAGTTTTCAGAACTGCTTTCAGTAGTGTAGTTCAAGTGGAAACAGAGGCTGCTTCAGTT 2820
2916 Db GGAGTTTTCAGAACTGCTTTCAGTAGTGTAGTTCAAGTGGAAACAGAGGCTGCTTCAGTT 2975
2821 QY TGGAGAAAAGAGGCTTCCAGGAGTAGATTTTGTAGCATTAATTCGTAAGGAATCTTG 2880
2976 Db TGGAGAAAAGAGGCTTCCAGGAGTAGATTTTGTAGCATTAATTCGTAAGGAATCTTG 3035
2881 QY GACTTTGAGCACCTAATGGATATATTTGAGAGAAACAGATCACTTTGGATGTATTAGTTG 2940
3036 Db GACTTTGAGCACCTAATGGATATATTTGAGAGAAACAGATCACTTTGGATGTATTAGTTG 3095
2941 QY AGATGGGCGCACAGGAGCTGAGGAGATTGGAATCAATGCTTTATGGACATAGGCAAAAC 3000
3096 Db AGATGGGCGCACAGGAGCTGAGGAGATTGGAATCAATGCTTTATGGACATAGGCAAAAC 3155
3001 QY TAAATTAAGGAGTCCAGAGACTTATCTCGGCAACAAGGCTTTAACCCATATTTAACTT 3060
3156 Db TAAATTAAGGAGTCCAGAGACTTATCTCGGCAACAAGGCTTTAACCCATATTTAACTT 3215
3061 QY TGAAACACCTCTGCTAGTGTGAACAAATTTCTATAGATCTGCTCTGATGATAAGAGTTTC 3120
3216 Db TGAAACACCTCTGCTAGTGTGAACAAATTTCTATAGATCTGCTCTGATGATAAGAGTTTC 3275
3121 QY AGTCTGTGGAGAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTTCATGCGAG 3180
3276 Db AGTCTGTGGAGAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTTCATGCGAG 3335
3181 QY GTGGATCTTCAACAGATACATATTTCTCAGATTCAGAGGTTTGTAAACAGAACTAT 3240
3336 Db GTGGATCTTCAACAGATACATATTTCTCAGATTCAGAGGTTTGTAAACAGAACTAT 3395
3241 QY GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAAACCAACACCATGCCAATG 3300
3396 Db GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAAACCAACACCATGCCAATG 3455
3301 QY AACGAATGCTATTTTCATGGGTCTCCTTTTGTGAATGCAATTCACAAAGGCTTTGATG 3360
3456 Db AACGAATGCTATTTTCATGGGTCTCCTTTTGTGAATGCAATTCACAAAGGCTTTGATG 3515
3361 QY AAAGCATGCGTACATAGGTGTATTTGAGCTGGCATTTATTTTGTGTAAGAACTCTT 3420
3516 Db AAAGCATGCGTACATAGGTGTATTTGAGCTGGCATTTATTTTGTGTAAGAACTCTT 3575
3421 QY CCABAAGCAATCAATATGTAATGGAATTGGAGGAGTACTGGGTGTCAGTTTCAAAAG 3480
3576 Db CCABAAGCAATCAATATGTAATGGAATTGGAGGAGTACTGGGTGTCAGTTTCAAAAG 3635
3481 QY ACAGATCTTGTTCATATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGT 3540
3636 Db ACAGATCTTGTTCATATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGT 3695
3541 QY CTTTCTGCGAGTTAGTGAATGAATAATGGGCAATCTCTCTCCAGTCTATCTAGTCA 3600
3696 Db CTTTCTGCGAGTTAGTGAATGAATAATGGGCAATCTCTCTCCAGTCTATCTAGTCA 3755
3601 QY CTGTGAGCCCGAGTGAATGCGCTAGCATTTAGCTGAATATGTTATTTTACAGAGGAGAAC 3660
3756 Db CTGTGAGCCCGAGTGAATGCGCTAGCATTTAGCTGAATATGTTATTTTACAGAGGAGAAC 3815
3661 QY AGGCTTATCTGAGTATTTTAAATTTACTTACCAGATTTATGAGGCTTGAAGGTATGTCGATG 3720

1621 GCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT 1680
1776 GCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT 1835
1681 CATTAGGTAAATCAGAGGCAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGCG 1740
1836 CATTAGGTAAATCAGAGGCAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGCG 1895
1741 AAACGTAAATAAATCTGCTACTGTTTCAGAGTGTCAACTGCGAGACATTTGAAGGGCGTC 1800
1896 AAACGTAAATAAATCTGCTACTGTTTCAGAGTGTCAACTGCGAGACATTTGAAGGGCGTC 1955
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VERSION AR584137.1 GI:56622263
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ORGANISM Unknown.
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1. (bases 1 to 6018)
AUTHORS Chen, Y.-T., Old, L.J., Scanlan, M.J. and Stockert, E.
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JOURNAL Patent: US 6794501-A 11 21-SEP-2004;
Ludwig Institute for Cancer Research and Cornell Research
Foundation, Inc.; New York, NY
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RESULT 15

AF305081 4295 bp mRNA linear PRI 17-APR-2001

LOCUS Homo sapiens tankyrase-related protein mRNA, partial cds.

DEFINITION AF305081

ACCESSION AF305081

VERSION AF305081.1 GI:10953951

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 4295)

AUTHORS Monz,D., Munnia,A., Contesse,N., Fischer,U., Steudel,W.I., Feiden,W., Glass,B. and Meese,E.U.

TITLE Novel tankyrase-related gene detected with meningioma-specific sera

JOURNAL Clin. Cancer Res. 7 (1), 113-119 (2001)

PUBMED 11205898

REFERENCE 2 (bases 1 to 4295)

AUTHORS Monz,D.W. and Meese,E.

TITLE Direct Submission

JOURNAL Submitted (12-SEP-2000) Human Genetics, Universitaet des Saarlandes, Geb. 60, Homburg 66421, Germany

FEATURES

source location/Qualifiers

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ORIGIN

Query Match 97.9%; Score 3737; DB 5; Length 4295;

Best Local Similarity 95.6%; Pred. No. 0;

Matches 3798; Conservative 1; Mismatches 7; Indels 8; Gaps 5;

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REFERENCE
AUTHORS

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The FANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)
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TITLE

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AUTHORS

RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium.

Antisense Transcription in the Mammalian Transcriptome

Science 309, 1564-1566 (2005)
7

TITLE

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REFERENCE
AUTHORS

The FANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).

The Transcriptional Landscape of the Mammalian Genome

Science 309, 1559-1563 (2005)
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TITLE

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REFERENCE
AUTHORS

(bases 1 to 1967)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

Direct Submission

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>.

Location/Qualifiers

FEATURES
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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsic.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

COMMENT

FEATURES

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Best Local Similarity 72.4%; Pred. No. 0;
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QY 2820 TTGGAGAAAAGGAG-----GTTCCAGAGTAGATTTTAGCATAACTCAATTCCTAGG 2873
Db 2418 GCAGAAAGGAAGGAAGGAGAGTTGGGGTCTTGACATGAACATCATCCAGTTCTCTTAAG 2477
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QY 3234 AAACATATGGAAAGATACACTCACCGGAGAAAAAGAGTTTCTGAAGAAAAACACAAACCAT 3293
Db 2838 AAGCTGAGGGAGCGATTCTGCCACAGACAAAGAGAGGTGTCTGAGGAGAACCAACAAACCAT 2897
QY 3294 GCCAATGAAAGAAAGCTATTTTCATGGGTCTCTCTTTGTAATGCAATTTATCCACAAAGGC 3353
Db 2898 CACAATGAGCCATGCTGTTCACGGTTCTCTTTTCAATTAATGCAATTTATTCATAAAGGG 2957
QY 3354 TTTGATGAAAGGCGATGCGTACATAGTGGTATGTTTGGAGCTGGCATTTATTTTCTCTGAA 3413
Db 2958 TTTGATGAGCAGCATGCTGATATTGGAGGATGTTTGGAGCTGGAATTTACTTTGCTGAA 3017
QY 3414 AACTCTTCCAAAAGCAATATGATATATGGAATTTGGAGGAGTACTGGGTGTCAGATT 3473
Db 3018 AACTCTTCAAAAAGCAATCAGTATGTTTATGGAATTTGGAGGAGAACAGGCTGTCCACA 3077
QY 3474 CACAAGACAGATCTTGTATCATTTGCCACAGGAGCTGCTTTTTCGCGGGTAACTTTG 3533
Db 3078 CACAAGACAGATCATGTTATATATGTCACAGACAAATGCTTTTCTGTAGAGTGACCTTT 3137
QY 3534 GGAAGCTTTTCTTCGAGTTCAGTGCATGCAATGGAATGGAATGGAATGGAATGGAATGGAAT 3593
Db 3138 GGAAGTCTTCTTCGATTCAGCACCATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 3197
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QY 3654 GGAGACAGGCTTATCTGAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3708
Db 3258 GGGGAACAGGCATATCCAGATATCTCATCACTACCTACCTACCTACCTACCTACCTACCTAC 3312

RESULT 3

AKI49368
LOCUS AKI49368 2226 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C73001F05 product:Tankyrase 2 (TC 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1-interacting ankryrin-related ADP-ribose polymerase 2) (Tankyrase-like protein) (Tankyrase-related protein) homolog [Homo sapiens], full insert sequence.
ACCESSION AKI49368
VERSION AKI49368.1 GI:74143548
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED REFERENCE AUTHORS	11076861	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Akawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojibori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Asahara, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staab, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayaashizaki, Y.
	4	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
		Functional annotation of a full-length mouse cDNA collection
	Nature 409 (6821), 685-690 (2001)	
PUBMED REFERENCE AUTHORS	11217851	5
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	Nature 420 (6915), 563-573 (2002)	
PUBMED REFERENCE AUTHORS	12466851	6
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	Science 309 (5740), 1559-1563 (2005)	
PUBMED REFERENCE AUTHORS	16141072	7
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		RIKEN Genome Exploration Research Group
		Antisense transcription in the mammalian transcriptome
	Science 309 (5740), 1564-1566 (2005)	
PUBMED REFERENCE AUTHORS	16141073	8
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		Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayaashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayaashizaki, Y.
		Direct Submission
PUBMED REFERENCE AUTHORS	16141074	9
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		CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
		Please visit our web site for further details.
PUBMED REFERENCE AUTHORS	16141075	10
		URL: http://genome.gsc.riken.jp/
		URL: http://fantom.gsc.riken.jp/
		Location/Qualifiers
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		/db_xref="taxon:10090"
		/clone="C730001F05"
PUBMED REFERENCE AUTHORS	16141078	13
		/sex="male"
		/cell_type="tumor"

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Qy 862 CTCCTATTACATTTGGCAGCAGGATATAACAGAGTAAGAGATTGTACAGCTGTTACTGCAAC 921
Db 1119 CTCGGTTACACCTGGCAGCAGGCTACACAGAGTTGCGATAGTTGAGTCTGTTCTACAGC 1178
Qy 922 ATGAGCTGATGTCATGCTAAAGATAAAGAGTGATCTGGTACCATTTACAAATGCTGTT 981
Db 1179 ATGGTGTGATGTCACGCGAAGACAAAGGTGGACTTGTACTCTCTCATATGATGCT 1238
Qy 982 CTTATGGCTATTAGAGTAAGTAACTGTAACCTTTGGTCAAGCAGTGGCTGTGTAATGCAA 1041
Db 1239 CATACGGACACTATGAGGTCAAGAACTGCTCTAAAGCATGGAGCTTGTGTCAACGCTA 1298
Qy 1042 TGGACTTTGGCAATTTCACTCTCTTTCATAGGCGAGCTTCTTAAGAACAGGGGTGTAAGTAT 1101
Db 1299 TGGATCTGTGGCAGTTTCAACCGCTGCATGAAGCTGCTTCAAGAACCGGGTAGAGTCT 1358
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Db 1359 GTTCTCTGTTACTTAGTCAAGGTGCGGATCCAACTTGGTCAATTTGCCATGGCAAAAGTG 1418
Qy 1162 CTATAGACTTGGCTCCACACACAGTTTAAAGAAAGATTAGCATATGAATTTAAAGGCC 1221
Db 1419 CTGTGCACATGGCTCCAACTCTGAGCTCCGGGAAAGACTGACATATGAATTTAAAGGCC 1478
Qy 1222 ACTGTTGCTGCAAGCTGCACAGAGAGCTGATGTTACTCGAATCAAAAACATCTCTCTC 1281
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Qy 1402 TCAATGAAAAGACTAAAGAAATTTTGACTCTCTGACGTGGCATCTGAGAAAGCTCAT 1461
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Db 2139 ATGCCAAAGACAAAGGTGGCTTGGTTCCCTTTCAAAATGCTGCTCTCTATGGACACTATG 2198

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Qy 2122 AAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAGATGCACTTTGCTAGATGCTG 2181
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RESULT 5
DQ034114
LOCUS

DQ034114 3612 bp DNA linear GSS 02-JUN-2005

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RESULT 6
DQ034115
LOCUS DQ034115 3107 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes TNKS gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ034115
VERSION DQ034115.1 GI:66885324
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
1 (bases 1 to 3107)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civallo, D.,
White, T.J., Sninsky, J.J., Adams, M.D., and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(ex) PLoS Biol. 3 (6), E170 (2005)
JOURNAL PUBMED 15869325
2 (bases 1 to 3107)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civallo, D.,


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Email: www.rzpd.de
RZPD; RZPdp9017K2313.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No.9017
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact:
Inge Artlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubenerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPdp9017K2313
contact RZPD (product- supporter@rzpd.de) for further information.
Primer name: qe3_4 , primer sequence: CGGATAACATTCACAG.
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NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-lymphocytes with a NotI - oligo(dT) primer [5'
GACTAGTCTAGATCGAGCGCGCCGCTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to SalI adaptors,
digested with NotI and cloned into the NotI and SalI sites
of the pQE80LSN cloned vector"

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Query Match	23.2%;	Score 884.4;	DB 8;	Length 888;
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RESULT 8
LOCUS CR987822 RZPD no. 9016 Homo sapiens cDNA clone RZPDp901611435 5',
DEFINITION mRNA sequence.
ACCESSION CR987822
VERSION CR987822.1 GI:68281707
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D.
AUTHORS Human T-Lymphocytes library
TITLE Unpublished (2005)
JOURNAL Contact: Inge Arlt
COMMENT RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPDp901611435.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No. 9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
Inge Arlt
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de

This clone is available from RZPD:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPDp901611435
contact RZPD (product- support@rzpd.de) for further information.
Primer name: qe3_4, Primer sequence: CGGATAACAATTCACACAG.

FEATURES
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NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-Lymphocytes with a NotI - oligo(dT) primer [5'
GACTAGTCTAGATCGAGCGCGCCCTTTTTTTTTTTT 3']
Double-stranded cDNA was ligated to Sali adaptors.
digested with NotI and cloned into the NotI and Sali sites
of the pQE80LSN_cloned vector"

ORIGIN
Query Match 22.5%; Score 859.6; DB 8; Length 926;
Best Local Similarity 98.6%; Pred. No. 4.2e-215;
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Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaudo, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, C., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Washima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

11217851

5

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaudo, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Knapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glasi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawagawa, Y., Kedzierski, R.M., King, B.L., Kongsaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Nunata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

PANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12466851

6

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L.,

Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Kall, M., Knapin, A., Katoh, M., Kawasawa, Y., Keiso, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Litano, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempke, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sincalir, B., Sperling, S., Stupka, E., Sugiu, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusci, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, K., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

PANTOM Consortium

The transcriptional landscape of the mammalian genome

Science 309 (5740), 1559-1563 (2005)

16141072

7

Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yagi, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.

RIKEN Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome

Science 309 (5740), 1564-1566 (2005)

16141073

8 (bases 1 to 1078)

Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

1. .1078

FEATURES
source

QY	871	ATTTCGACGAGGATATTAACAGAGTAAAGATTGTACAGCTTTTACTGCAACATGAGAGCTG	930
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DEFINITION	LB0173.CR_I04 GC_BGC-17 Bos taurus cDNA clone IMAGE:8121774 5'		
ACCESSION	DT808067		
VERSION	DT808067.1	GI:5739943	
KEYWORDS	EST.		
SOURCE	Bos taurus (cattle)		
ORGANISM	Bos taurus		
REFERENCE	Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Taniguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C., Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaliff, R., Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R., Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Stott, J., Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.		
TITLE	Bovine Genome Sequencing Program: Full-length cDNA Sequencing		
JOURNAL	Unpublished (2005)		
COMMENT	Contact: Robert Kirkpatrick Canada's Michael Smith Genome Sciences Centre BC Cancer Agency Suite 100, 570 West 7th Avenue, Vancouver, British Columbia, Canada, V5Z 4S6 Tel: 1-604-707-5900 x5406 Fax: 1-604-876-3561 Email: robertk@bcgs.ca Plate: LB0173 row: 1 column: 4 High quality sequence stop: 898.		
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Matches 824;	Conservative 0;	Mismatches 69;	Indels 2; Gaps 1;
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QY	2980	CTTATGGACATAGGCGACAACTAAATTAAGAGTTCGAGAGACTTATCTCCGGACCAACAG	3039
Db	61	CTTATGGACATAGGCGACAACTAAATTAAGAGTTCGAGAGACTTATCTCTGGACCAACAG	120

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 Qy CTCTGATGATTAAGAGTTTCAGTCTGTGGGGAAGAGTCAAGTACAGTTGCGAGC 3159
 Db CTCTGATGATTAAGAGTTTCAGTCTGTGGGGAAGAGTCAAGTACAGTTGCGAGC 240
 Qy ACAGAGATGAGGTCATGCGAGTGGATCTTCAACAGATACAAATATTTCTCAAGATTGAGA 3219
 Db ACAGAGATGAGGTCATGCGAGTGGATCTTCAACAGATACAAATATTTCTCAAGATTGAGA 300
 Qy AGTTTGTGTAACAGAACTATGGAAGATACATCTACCGGAGAGAAAGAGTTTCTGAAG 3279
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RESULT 12
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 DEFINITION 969630 MARC 4BOV Bos taurus cDNA 3', mRNA sequence.
 ACCESSION CK847047
 VERSION CK847047.1 GI:45208162
 KEYWORDS EST.
 SOURCE Bos taurus (cattle)

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 834)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
 Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A.,
 Chitko-McKown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F.,
 Quackenbush, J. and Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 11282978
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: 98 row: I column: 7
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 Location/Qualifiers
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 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from day 20 and day 40
 embryos."

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 Qy 1307 TCAACACATGAACACGATTTGCTGCTGCTGCTCATCTCCATATCCAAAAGAAAGCA 1366
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 Qy 1367 AATATGTGAATCTGTTGCTAAGAAAGGAGCAACATCAATGAAAGACTAAAGAAATCTT 1426
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 Qy 1487 ACATGAAGCAAGGTAAATGCTCTGGATTAATCTTGGTCAAGACTTCTCTACACAGAGTGC 1546
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LOCUS DN536421 848 bp mRNA linear EST 11-MAR-2005
 DEFINITION 1372517 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION DN536421

VERSION DN536421.1 GI:60988240

KEYWORDS EST.

SOURCE Bos taurus (cattle)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 848)

REFERENCE Smith, R.P.L., Roberts, A.J., Ehternkamp, S.E., Chitko-McKown, C.G.,
 Wray, J.E. and Keeler, J.W.
 TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
 JOURNAL Unpublished (2003)

COMMENT Contact: Smith, TPL

USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.

Plate: RLK8064 row: G column: 17

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FEATURES

source

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/notes="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including ovary, hindbrain, uterus, and day-30 whole

embryos."

ORIGIN

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 Matches 762; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

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QY 1668 CAAGAGGGTATCTCAATAGTAAATTCAGAGGGCAGACAGCAATTTGCTGGAAGCTGCAAG 1727

Db 75 CAAGAGGGTATCCCATAGTAAATTCAGAGGGCAGACAGACAGTTGCTGGAAGCTGCAAG 134

QY 1728 GCTGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCGAGAC 1787

Db 135 GCTGGAGATGTAGAAACCGTAAAAAAATTTGTCTACTGTTTCAGAGTGTCAACTGCGAGAC 194

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 QY 1908 CTTTGGCAATATGCAATGCTTTTATGACATTAATGAAGTTGCGAGAGCTTCTTGTAAAGCAT 1967
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 VERSION DN533094.1 GI:81281747
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 SOURCE Homo sapiens (human)
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 Homnidae; Homo.
 1 (bases 1 to 819)

REFERENCE Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Teuritani, K., Wakaqura, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 TITLE Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute

2-6-7 Kazuse-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@ifty.com

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
HRI.

```

FEATURES
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    Matches 763; Conservative 0; Mismatches 52; Indels 5; Gaps 4;
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Db 181 AAAGCTGGAGATGTGAAACCTGTAATAAACTGTGTACTCTTCAGAGTGTCAACTGCAG 240
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Db 241 AGACATTGAAGGGCGTCACTACACCACTTCATTTCGACCTGGGTATACAGAGTGC 300
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Db 301 CGTGTGGAATATCTGCTACAGCATGGAGCTGATGTGCATCTAAAGATAAAGAGGCGCT 360
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SOURCE
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    NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
    Unpublished (1999)
JOURNAL
    COMMENT
    Contact: Robert Strausberg, Ph.D.
    Email: rgs@nih.gov
    Tissue Procurement: Dr. David Rowe and Dr. Mina
    cDNA Library Preparation: Invitrogen Corp
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    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
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    directionally, priming method: Oligo-dT. cDNA enrichment:
    >1k bp. Average insert size 1.8k bp. Priming sequence:
    5'-GACTAGTTCTAGATCGAGCGCGCCCT(T) 3'. Tissue contributed
    by, David Rowe. Library constructed by ResGen, Invitrogen
    Corp."
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; Publication No. US2003032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
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US-09-972-115A-5

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Db	900	CAAGTGATGGCAGAAAGTCAACTCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGA	959
Qy	901	TTGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTTAAAGATAAAGGTGATCTGG	960
Db	960	TTGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTTAAAGATAAAGGTGATCTGG	1019
Qy	961	TACCATTACAAATGCGCTGTTCTTATGGTCAATTAAGAAGTAACTGAACTTTTGGTCAAGC	1020
Db	1020	TACCATTACAAATGCGCTGTTCTTATGGTCAATTAAGAAGTAACTGAACTTTTGGTCAAGC	1079
Qy	1021	ATGCTGCTGTGTTAAATGCAATGCACTTGTGGCAATTCATCTCTTCAATGAGGACGCTT	1080
Db	1080	ATGCTGCTGTGTTAAATGCAATGCACTTGTGGCAATTCATCTCTTCAATGAGGACGCTT	1139
Qy	1081	CTAGAACAGGGTTGAAGTATGTTCTCTTCTTAAGTTATGGTGCAGACCCACACTGC	1140
Db	1140	CTAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAGTTATGGTGCAGACCCACACTGC	1199
Qy	1141	TCAATTGTCACAATAAAGTGCTATAGACTTGGCTCCCAACACAGTAAAAAGAAAAGAT	1200
Db	1200	TCAATTGTCACAATAAAGTGCTATAGACTTGGCTCCCAACACAGTAAAAAGAAAAGAT	1259
Qy	1201	TAGCATATGAATTTAAAGGCCACTCGTTGTGCAAGCTGCAAGAGAGCTGATGTTACTC	1260
Db	1260	TAGCATATGAATTTAAAGGCCACTCGTTGTGCAAGCTGCAAGAGAGCTGATGTTACTC	1319

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Db	1320	GAATCAAAAAACATCTCTCTCTGGAATGGTGAATTTCAAGCATCTCTCAAAACATGAAA	1379
Qy	1321	CAGCATGCATTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTGAACTGT	1380
Db	1380	CAGCATTGCATTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTGAACTGT	1439
Qy	1381	TGCTAAGAAAGGAGCAAAACATCAATGAAAGACTAAAGAAATTTCTTGACTCTCTGCACG	1440
Db	1440	TGCTAAGAAAGGAGCAAAACATCAATGAAAGACTAAAGAAATTTCTTGACTCTCTGCACG	1499
Qy	1441	TGGCATCTGAGAAAGCTCATAAATGATGTTGTTGAAAGTAGTGGTGAACAATGAAGCAAAAG	1500
Db	1500	TGGCATCTGAGAAAGCTCATAAATGATGTTGTTGAAAGTAGTGGTGAACAATGAAGCAAAAG	1559
Qy	1501	TTAAATGCTCTGGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCAATC	1560
Db	1560	TTAAATGCTCTGGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCAATC	1619
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Db	1620	TACAAACCTGCCGCTACTCTCAGCTATGGGTGTGATCCTAACTATATATCCCTTCAGG	1679
Qy	1621	GCTTTACTGCTTTACAGATGGGAAATGAAAAATGTACAGCAACTCTCTCAAGAGGGTATCT	1680
Db	1680	GCTTTACTGCTTTACAGATGGGAAATGAAAAATGTACAGCAACTCTCTCAAGAGGGTATCT	1739
Qy	1681	CATTAGGTAAATCAGAGGCGACAGACAATGCTGTGGAAGCTGCAAGGCTGGAGATGTGCG	1740
Db	1740	CATTAGGTAAATCAGAGGCGACAGACAATGCTGTGGAAGCTGCAAGGCTGGAGATGTGCG	1799
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Db	1920	TACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGAGAGCCCTGTGATCTTTCACAAATG	1979
Qy	1921	CATGTTCTTATGCACATTTAGAGTTGCAGAACTTCTGTGTTAAACATGGAGCAGTAGTTA	1980
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Qy	2101	ATACTCCTTTGGATCTTGTGTTAAAGATGGAGATACAGTATTTCAAGTCTCTTAGGGGAG	2160
Db	2160	ATACTCCTTTGGATCTTGTGTTAAAGATGGAGATACAGTATTTCAAGTCTCTTAGGGGAG	2219
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Db	2340	CAGCTGGTTATAATTTAGAGTTGCAGAGTATTTGTTTACAAACGAGGAGCTGATGTGA	2399

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RESULT 4

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US-10-199-937-134
; Sequence 134, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 4992
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (876)..(4373)
US-10-199-937-134
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Query Match 99.4%; Score 3791.4; DB 7; Length 4992;
Best Local Similarity 99.8%; Pred No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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DB 1972 CAGCATTTGCTGCTGCTGCTATCTCCATAATCCCAAGAAAGCAATATGTGAATGT 2031
QY 1381 TGCTAAGAAAAAGGAGCAAAACATCAATGAAAAAGATTAAGAAATTTCTTGACCTCTCTGACG 1440
DB 2032 TGCTAAGAAAAAGGAGCAAAACATCAATGAAAAAGATTAAGAAATTTCTTGACCTCTCTGACG 2091
QY 1441 TGGCATCTGAGAAAGCTCATTAATGATGTTGTAAGTAGTGGTGAACATGAAGCAAGG 1500
DB 2092 TGGCATCTGAGAAAGCTCATTAATGATGTTGTAAGTAGTGGTGAACATGAAGCAAGG 2151
QY 1501 TTAATGCTCTGATTAATCTTTGCTCAGACTTCTCTACACAGAGCTGCATATTTGGTCAATC 1560
DB 2152 TTAATGCTCTGATTAATCTTTGCTCAGACTTCTCTACACAGAGCTGCATATTTGGTCAATC 2211
QY 1561 TACAAACCTGCCGCTATCTCTGAGCTATGGGTGATCTCTAAACATTAATATCTCTTCAGG 1620
DB 2212 TACAAACCTGCCGCTATCTCTGAGCTATGGGTGATCTCTAAACATTAATATCTCTTCAGG 2271
QY 1621 GCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAATCTCTCCAAAGAGGATCT 1680
DB 2272 GCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAATCTCTCCAAAGAGGATCT 2331
QY 1681 CATTAGGTAATTTACAGAGCAGACAGACAATTCGTGGAAGCTGCAAAAGGCTGGAGATGTCG 1740
DB 2332 CATTAGGTAATTTACAGAGCAGACAGACAATTCGTGGAAGCTGCAAAAGGCTGGAGATGTCG 2391
QY 1741 AAACGTAAAAAACTGTGTACTGTTTACAGAGTGTCAACTGCAGAGACATTTGAAAGGCGTC 1800
DB 2392 AAACGTAAAAAACTGTGTACTGTTTACAGAGTGTCAACTGCAGAGACATTTGAAAGGCGTC 2451
QY 1801 AGTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC 1860
DB 2452 AGTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC 2511
QY 1861 TACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGGAGGCTTTGACCTTTGCACAATG 1920
DB 2512 TACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGGAGGCTTTGACCTTTGCACAATG 2571
QY 1921 CATGTTCTTTATGGACATTAATGAAGTTGCAAGACTTCTTGTAAAAATGAGAGTAGTTA 1980
DB 2572 CATGTTCTTTATGGACATTAATGAAGTTGCAAGACTTCTTGTAAAAATGAGAGTAGTTA 2631
QY 1981 ATGTAGCTGATTTATGGAATTTTACACTTTTACATGAAGCAGCAGCAAAAGGAAATATG 2040
DB 2632 ATGTAGCTGATTTATGGAATTTTACACTTTTACATGAAGCAGCAGCAAAAGGAAATATG 2691
QY 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAAGCCCTACCAAAAAAACAAGGATGGA 2100
DB 2692 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAAGCCCTACCAAAAAAACAAGGATGGA 2751
QY 2101 ATACTCCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAG 2160
DB 2752 ATACTCCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAG 2811
QY 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTT 2220
DB 2812 ATGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTT 2871
QY 2221 CTCCTGATTAATGTAAATTTGCGCGATACCAAGGCGACATTCAAACACCTTTTACATTTAG 2280
DB 2872 CTCCTGATTAATGTAAATTTGCGCGATACCAAGGCGACATTCAAACACCTTTTACATTTAG 2931
QY 2281 CAGCTGGTTTATTAATATTTAGAAAGTTGCGAGATTTGTTTACAAACGAGGAGCTGATGTA 2340
DB 2932 CAGCTGGTTTATTAATATTTAGAAAGTTGCGAGATTTGTTTACAAACGAGGAGCTGATGTA 2991
QY 2341 ATGCCCAAGCAAAAGGAGCTTATTCCTTTACATATGAGCATCTTACGGGATGTA 2400
DB 2992 ATGCCCAAGCAAAAGGAGCTTATTCCTTTACATATGAGCATCTTACGGGATGTA 3051
QY 2401 ATGTAGCAGCTCTACTTAATAAAGTATAATGTCATGTCTCAATGCCAGCAGCAAAATGGGCTT 2460

Qy	3541	CTTTCCTGCAGTTCAGTGC	CAATGGAATGCGCATCTTCCTCCTCAGGTCATCACTCAGTCA	3600
Db	4192	CTTTCCTGCAGTTCAGTGC	CAATGGAATGCGCATCTTCCTCCTCAGGTCATCACTCAGTCA	4251
Qy	3601	CTGCTAGGCCCCAGTGTAAATGGCCTAGCATTTAGCTGAAATGTTATTTCACAGAGGAGAAC	3660	
Db	4252	CTGCTAGGCCCCAGTGTAAATGGCCTAGCATTTAGCTGAAATGTTATTTCACAGAGGAGAAC	4311	
Qy	3661	AGGCTTATCTCGAGTATTTAAATTTACTTACACAGATTTATAGCGCTCGAAGGTATGGTCCGATG	3720	
Db	4312	AGGCTTATCTCGAGTATTTAAATTTACTTACACAGATTTATAGCGCTCGAAGGTATGGTCCGATG	4371	
Qy	3721	GATATAATAGTGTATTTTAAAGAAAATTAATTCACATCGAACCTAAATCATCAAAGCAGCAGTGC	3780	
Db	4372	GATATAATAGTGTATTTTAAAGAAAATTAATTCACATCGAACCTAAATCATCAAAGCAGCAGTGC	4431	
Qy	3781	GCCTCTACGTTTTCCTCTTTCGTGAAAAAAA	3813	
Db	4432	GCCTCTACGTTTTCCTCTTTCGTGAAAAAAA	4464	

RESULT 5
US-10-199-937-132
; Sequence 132, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: Mcelligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199.937

Query Match	99.4%;	Score 3791.4;	DB 7;	Length 5002;				
Best Local Similarity	99.8%;	Pred. No. 0;						
Matches 3806;	Conservative	0;	Mismatches	6;	Indels	1;	Gaps	1;
Qy	1	CGCGCTGCTCCGCCCGCGGGGAGACCGGGGGGAGGGAGCCACGAGGAGGGGCGCGG	60					
Db	663	CGCGCTGCTCCGCCCGCGGGGAGCGGGGGGAGGGAGGCCACGAGGAGGGGCGCGG	722					
Qy	61	TGGCGCGGGGCCATGGAGCTGCGCCGGATCCGGGTGACAGCAGGAGAGCCAAAGCGGCCGGG	120					
Db	723	TGGCGCGGG-CCATGGGACTGCGCCGGANTCCGGTGAACAGCAGGAGAGCCAAAGCGGCCGGG	781					
Qy	121	CCCTGAGCGCGTCTTCTCCGGGGGGCGCTCGCCCTCCTGCTCGCGGGGCGGGGCTCCTGC	180					
Db	782	CCCTGAGCGCGTCTTCTCCGGGGGGCGCTCGCCCTCCTGCTCGCGGGGCGGGGCTCCTGC	841					
Qy	181	TCCGGTGTGCGCGCTGTGCTGTGCGCGCGGCCAGGATCATGTGCGGTGTCGCGCT	240					
Db	842	TCCGGTGTGCGCGCTGTGCTGTGCGCGCGGCCAGGATCATGTGCGGTGTCGCGCT	901					
Qy	241	GCGC CGGCGGGAGCGGCGCTGCGGAGCGCCCGCGCCCGAGGCCCTGTGGAGCGCGGCC	300					
Db	902	GCGC CGGCGGGAGCGGCGCTGCGGAGCGCCCGCGCCCGAGGCCCTGTGGAGCGCGGCC	961					

Qy	301	GAGAGCTGTTGAGGGCTGCGCGAAACGGGGACGTGGAAACAGATCAAGAGGCTGGTGAACG	360
Dd	962	GAGAGCTGTTGAGGGCTGCGCGAAACGGGGACGTGGAAACAGATCAAGAGGCTGGTGAACG	1021
Qy	361	CTGAGAGGTGAACAGCCGCGACACGCGCGGCGAGGAAATCCACCCGCTGCACTTCGCGG	420
Dd	1022	CTGAGAGGTGAACAGCCGCGACACGCGCGGCGAGGAAATCCACCCGCTGCACTTCGCGG	1081
Qy	421	CAGGTTTTGGCGGAAAGAGCTAGTTGAATATTTGCTTCCAGAAATGGTGCAAAATGTTCCAAG	480
Dd	1082	CAGGTTTTGGCGGAAAGAGCTAGTTGAATATTTGCTTCCAGAAATGGTGCAAAATGTTCCAAG	1141
Qy	481	CACGTGATGATGGGGGCTTATTCCTCTTCAATATGATGCTCTTTTGGTGCATGCTGAAG	540
Dd	1142	CACGTGATGATGGGGGCTTATTCCTCTTCAATATGATGCTCTTTTGGTGCATGCTGAAG	1201
Qy	541	TAGTCAATCTCCTTTTGGGACATGGTGCGACACCCCAATGCTCGAGATAAATGGAAATATA	600
Dd	1202	TAGTCAATCTCCTTTTGGGACATGGTGCGACACCCCAATGCTCGAGATAAATGGAAATATA	1261
Qy	601	CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTTGATGTTTGCATTTGCTGTTACAGC	660
Dd	1262	CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTTGATGTTTGCATTTGCTGTTACAGC	1321
Qy	661	ATGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCAATGGATTTAGCAGATC	720
Dd	1322	ATGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCAATGGATTTAGCAGATC	1381
Qy	721	CATCTGCGAAGCAGTCTTACTGCTGAATATAGAAAGATGAACCTTTAGAAAGTGCCA	780
Dd	1382	CATCTGCGAAGCAGTCTTACTGCTGAATATAGAAAGATGAACCTTTAGAAAGTGCCA	1441
Qy	781	GGAGTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATGTCACCACTGCCACG	840
Dd	1442	GGAGTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATGTCACCACTGCCACG	1501
Qy	841	CAAGTATGGCAGAAAGTCAAATCCATTAATGCTGAGGAGGAGATATAACAGATGAAGA	900
Dd	1502	CAAGTATGGCAGAAAGTCAAATCCATTAATGCTGAGGAGGAGATATAACAGATGAAGA	1561
Qy	901	TTGTACAGCTGTTACTCCACATGGAGCTGATGCCATGCTTAAGATAAAGGATGATCTGG	960
Dd	1562	TTGTACAGCTGTTACTCCACATGGAGCTGATGCCATGCTTAAGATAAAGGATGATCTGG	1621
Qy	961	TACCAATACCAATGCTGTTCTTATGGTCAATATGAAGTAACTGAACCTTTTGGTCAAGC	1020
Dd	1622	TACCAATACCAATGCTGTTCTTATGGTCAATATGAAGTAACTGAACCTTTTGGTCAAGC	1081
Qy	1021	ATGGTGCTGTGTAATGCAATGGACCTTGGGCAATTCACCTCTCTTCATGAGGAGCTTT	1080
Dd	1682	ATGGTGCTGTGTAATGCAATGGACCTTGGGCAATTCACCTCTCTTCATGAGGAGCTTT	1741
Qy	1081	CTAAGAACAGGTTGAAGTATGTTCTCTCTTAAGTATGTCAGAGACCCACACTGC	1140
Dd	1742	CTAAGAACAGGTTGAAGTATGTTCTCTCTTAAGTATGTCAGAGACCCACACTGC	1801
Qy	1141	TCAATTTGTCAAAATGAAGTGTATAGACTTTGGCTCCCAACCAACAGTAAAGAAAGAT	1200
Dd	1802	TCAATTTGTCAAAATGAAGTGTATAGACTTTGGCTCCCAACCAACAGTAAAGAAAGAT	1261
Qy	1201	TAGCATATGAATTAAGGGCCACTGTTGCTGCAAGCTGCAAGAGAGCTGATGTTACTC	1260
Dd	1862	TAGCATATGAATTAAGGGCCACTGTTGCTGCAAGCTGCAAGAGAGCTGATGTTACTC	1321
Qy	1261	GAATCAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCCCTCAACACATGAAA	1320
Dd	1921	GAATCAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCCCTCAACACATGAAA	1381
Qy	1321	CAGCATTTGCAATTTGCTGCTGCACTCTCATATCCCAAAAGAAAGCAATATGTTGCTGT	1380
Dd	1982	CAGCATTTGCAATTTGCTGCTGCACTCTCATATCCCAAAAGAAAGCAATATGTTGCTGT	2041

Qy	1381	TGCTAAGAAAAAGAGCAAAACATCAATGAAAAAGACTAAAGAAATCTTTGACTCCTCTGCACG	1440
Dd	2042	TGCTAAGAAAAAGAGCAAAACATCAATGAAAAAGACTAAAGAAATCTTTGACTCCTCTGCACG	2101
Qy	1441	TGSCATCTCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAG	1500
Dd	2102	TGSCATCTCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAG	2161
Qy	1501	TTAATGCTCTGGTAATCTTTGGTCAGACTTCTTACACAGAGCTGCATATTTGGTGCATC	1560
Dd	2162	TTAATGCTCTGGTAATCTTTGGTGCAGACTTCTTACACAGAGCTGCATATTTGGTGCATC	2221
Qy	1561	TACAAACCTGCCGCCCTACTCCTGAGCTATGGGTGTCATCTTAACATTTATATCCCTTCAGG	1620
Dd	2222	TACAAACCTGCCGCCCTACTCCTGAGCTATGGGTGTCATCTTAACATTTATATCCCTTCAGG	2281
Qy	1621	GCTTTACTGCTTTTACAGATGGGAAATGAAAAATGTACAGCAACTCCTCCAAGAGGGTATCT	1680
Dd	2282	GCTTTACTGCTTTTACAGATGGGAAATGAAAAATGTACAGCAACTCCTCCAAGAGGGTATCT	2341
Qy	1681	CATTAGGTAAATTCAGAGGACAGACAGCAATTTGCTGGAGCTGCAAGGCTGGAGATGTCG	1740
Dd	2342	CATTAGGTAAATTCAGAGGACAGACAGCAATTTGCTGGAGCTGCAAGGCTGGAGATGTCG	2401
Qy	1741	AACTCTAAAAAACTGTGTACTGTTTGCAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTC	1800
Dd	2402	AACTCTAAAAAACTGTGTACTGTTTGCAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTC	2461
Qy	1801	AGTCTACACCACTTTCATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGC	1860
Dd	2462	AGTCTACACCACTTTCATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGC	2521
Qy	1861	TACAGCATGGAGCTGATGTCATGCTTAAGATAAAGAGGSCCTTGACCTTTGCAACAATG	1920
Dd	2522	TACAGCATGGAGCTGATGTCATGCTTAAGATAAAGAGGSCCTTGACCTTTGCAACAATG	2581
Qy	1921	CATGTTCTTATGACATTAATGAAGTTGCAGAACTTCTTGTGTTAAACATGGAGCAGTAGTTA	1980
Dd	2582	CATGTTCTTATGACATTAATGAAGTTGCAGAACTTCTTGTGTTAAACATGGAGCAGTAGTTA	2641
Qy	1981	ATGTAGCTGATTTATGGAAATTTACACCTTTTACATGAAGCAGCAGCAAAAAGGAAATATG	2040
Dd	2642	ATGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAAGGAAATATG	2701
Qy	2041	AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACAAAAGGAAAGGAGTGAA	2100
Dd	2702	AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACAAAAGGAAAGGAGTGAA	2761
Qy	2101	ATACTCCTTTTGGATCTTGTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAG	2160
Dd	2762	ATACTCCTTTTGGATCTTGTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAG	2821
Qy	2161	ATGCAGCTTTTGTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTTGCTTT	2220
Dd	2822	ATGCAGCTTTTGTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTTGCTTT	2881
Qy	2221	CTCCTGATTAATGTAATTTGCGCGGATACCCAGGACAGATTTCAACCTTTTCAATTTAG	2280
Dd	2882	CTCCTGATTAATGTAATTTGCGCGGATACCCAGGACAGATTTCAACCTTTTCAATTTAG	2941
Qy	2281	CAGCTGGTATTAATTAATTTAGAAAGTTGACAGATATTTGTTTACAAACAGGAGCTGATGTA	2340
Dd	2942	CAGCTGGTATTAATTAATTTAGAAAGTTGACAGATATTTGTTTACAAACAGGAGCTGATGTA	3001
Qy	2341	ATGCCAAGACAAAGAGGAGCTTATTCCTTTTACATATGAGCATCTTTACGGGCATGTAG	2400
Dd	3002	ATGCCAAGACAAAGAGGAGCTTATTCCTTTTACATATGAGCATCTTTACGGGCATGTAG	3061
Qy	2401	ATGTAGCAGCTCTACTAATTAAGATTAATGATGTTGTCATGTCACCGACCAATATGGGCTT	2460
Dd	3062	ATGTAGCAGCTCTACTAATTAAGATTAATGATGTTGTCATGTCACCGACCAATATGGGCTT	3121
Qy	2461	TCACACCTTTTGCAAGAGCAGCCCAAAAGGACGACACACAGCTTTTGTGCTGTAG	2520

Db 3122 TCACACCTTTGACGAGCAGCCCAAGGAGCGAACACAGCTTTGTGCTTTGCTAG 3181
QY 2521 CCCATGGAGCTGACCGACTCTTTAAATAACAGGAGGACAAACACCTTTAGATTAGTTT 2580
Db 3182 CCCATGGAGCTGACCGACTCTTTAAATAACAGGAGGACAAACACCTTTAGATTAGTTT 3241
QY 2581 CAGCGGATGATGTCAGCGCTCTTTGACAGAGCCATGCCCCATCTGCTCTGCCCTCTT 2640
Db 3242 CAGCAGATGATGTCAGCGCTCTTTGACAGAGCCATGCCCCATCTGCTCTGCCCTCTT 3301
QY 2641 GTTACAGGCTCAAGTGCTCAATGGTGTGAGAGCCAGAGCCACTGCAGATGCTCTCT 2700
Db 3302 GTTACAGGCTCAAGTGCTCAATGGTGTGAGAGCCAGAGCCACTGCAGATGCTCTCT 3361
QY 2701 CTTTCAGGCTCATCTAGCCCATCAAGCTTTCTGACGACGAGCTCTTGACAACTTATCTG 2760
Db 3362 CTTTCAGGCTCATCTAGCCCATCAAGCTTTCTGACGACGAGCTCTTGACAACTTATCTG 3421
QY 2761 GGAGTTTTTTCAGAACTGCTCTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTGCTCCAGTT 2820
Db 3422 GGAGTTTTTTCAGAACTGCTCTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTGCTCCAGTT 3481
QY 2821 TGGAGAAAAGAGGTTCCAGGAGTAGATTAGCATAACTCAATTCGTAAGGAATCTTG 2880
Db 3482 TGGAGAAAAGAGGTTCCAGGAGTAGATTAGCATAACTCAATTCGTAAGGAATCTTG 3541
QY 2881 GACTTTGAGCCTTAATGGATATATTGAGAGAGACAGATCACTTTGGATGTATTAGTTG 2940
Db 3542 GACTTTGAGCCTTAATGGATATATTGAGAGAGACAGATCACTTTGGATGTATTAGTTG 3601
QY 2941 AGATGGGGCAACAGGAGCTGAAGGAGATTGGAATCAATCTTTATGGACATAGGCAAAAC 3000
Db 3602 AGATGGGGCAACAGGAGCTGAAGGAGATTGGAATCAATCTTTATGGACATAGGCAAAAC 3661
QY 3001 TAAATTAAGGAGTCGAGAGACTTATCTCCGGACAAACAGGCTTTAAACCATATTTAACTT 3060
Db 3662 TAAATTAAGGAGTCGAGAGACTTATCTCCGGACAAACAGGCTTTAAACCATATTTAACTT 3721
QY 3061 TGAACACCTCTGTTAGTGAAACAATCTTATAGATCTGCTCTGATGATGAAGATTTC 3120
Db 3722 TGAACACCTCTGTTAGTGAAACAATCTTATAGATCTGCTCTGATGATGAAGATTTC 3781
QY 3121 AGTCTGTGGAGGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCAATGAG 3180
Db 3782 AGTCTGTGGAGGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCAATGAG 3841
QY 3181 GTGGAATCTTCAACAGATACAAATATTTCAAGATTGAGAGGTTTGTAAACAGAAACTAT 3240
Db 3842 GTGGAATCTTCAACAGATACAAATATTTCAAGATTGAGAGGTTTGTAAACAGAAACTAT 3901
QY 3241 GGGAAAGATACACTCACCGGAGAAAGATTCTGAGAAACACCAACCATGCCAATG 3300
Db 3902 GGGAAAGATACACTCACCGGAGAAAGATTCTGAGAAACACCAACCATGCCAATG 3961
QY 3301 AACGAATGCTATTTCAATGGTCTCTTTGTCAATGCAATTTATTCACAAAGGCTTTGATG 3360
Db 3962 AACGAATGCTATTTCAATGGTCTCTTTGTCAATGCAATTTATTCACAAAGGCTTTGATG 4021
QY 3361 AAAGGAGTCGTPACATAGTGTTGTTGGAGCTGGCATTTATTTGCTGAAAACTCTT 3420
Db 4022 AAAGGAGTCGTPACATAGTGTTGTTGGAGCTGGCATTTATTTGCTGAAAACTCTT 4081
QY 3421 CCAAAAGCAATCAATATGATGAAATTTGAGAGGAGTACTGGGTGTCAGTTTCAAAAG 3480
Db 4082 CCAAAAGCAATCAATATGATGAAATTTGAGAGGAGTACTGGGTGTCAGTTTCAAAAG 4141
QY 3481 ACAGATCTGTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGT 3540
Db 4142 ACAGATCTGTTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGT 4201
QY 3541 CTTTCTGAGTTCAAGTCAATGAAATGGCAATTTCTCTCCAGGTCTATCTCAGTCA 3600

Db 4202 CTTTCTGCAAGTTCAAGTCAATGAAATGGCAATTTCTCTCCAGGTCACTCACTCAGTCA 4261
QY 3601 CTGCTAGGCCAGCTGTAATAGTCCCTAGCATTAAGTGAATATCTTTATACAGAGGAGAAC 3660
Db 4262 CTGCTAGGCCAGCTGTAATAGTCCCTAGCATTAAGTGAATATCTTTATACAGAGGAGAAC 4321
QY 3661 AGGCTTATCTGAGTATTTAAATTTACTTACAGATTATGAGGCTGAAGGTATGGTCAATG 3720
Db 4322 AGGCTTATCTGAGTATTTAAATTTACTTACAGATTATGAGGCTGAAGGTATGGTCAATG 4381
QY 3721 GATAAATAGTATTTTAAAGAACTAATTTCCACTGAACCTTAAATCATCAAGCAGCAGTG 3780
Db 4382 GATAAATAGTATTTTAAAGAACTAATTTCCACTGAACCTTAAATCATCAAGCAGCAGTG 4441
QY 3781 GCTCTAGCTTTTACTCTCTTTGCTCAAAAAAA 3813
Db 4442 GCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA 4474

RESULT 6
US-10-898-653-5
; Sequence 5, Application US/10898653
; Publication No. US20050143370A1
; GENERAL INFORMATION:
; APPLICANT: Helleday et al
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: J660-046
; CURRENT APPLICATION NUMBER: US/10/898,653
; CURRENT FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 6189
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-898-653-5

Query Match 99.4%; Score 3791.4; DB 10; Length 6189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 CGCGTGTCTCGCGCCCGCGCGGCGAGCCCGGGGGGACGGAGCCCGAGGAGGGCGCGG 60
Db 157 CGCGTGTCTCGCGCCCGCGCGGCGAGCCCGGGGGGACGGAGCCCGAGGAGGGCGCGG 216
QY 61 TGGCGCGCGCCCATGCGGACTCGCGGATCCGGTTCAGACAGCGGGAGCCAGCGGCGCGG 120
Db 217 TGGCGCGCGG-CCATGGGACTCGCGCGGATCCGGTTCAGACAGCGGGAGCCAGCGGCGCGG 275
QY 121 CCCTGAGCGGCTTTCTCGGGGGGCGCTCGCCCTCTCTGCTCGCGGGCGCGGGCTCTTGC 180
Db 276 CCCTGAGCGGCTTTCTCGGGGGGCGCTCGCCCTCTCTGCTCGCGGGCGCGGGCTCTTGC 335
QY 181 TCCGGTTGCTCGCGCTGTTGCTGGCTGGCGGGCGCGGATCATGTGCGGTCCCGCT 240
Db 336 TCCGGTTGCTCGCGCTGTTGCTGGCTGGCGGGCGCGGATCATGTGCGGTCCCGCT 395
QY 241 CGCGCGCGGGGAGCGGCTCGCGGAGCGCGCGGCGCGGCGCGGCGCGGCGCGGCG 300
Db 396 CGCGCGCGGGGAGCGGCTCGCGGAGCGCGCGGCGCGGCGCGGCGCGGCGCGGCG 455
QY 301 GAGAGCTGTTTCGAGCGTTCGCAACCGGGAGCTGGAAACGAGTCAAGAGGCTGGTGACGC 360
Db 456 GAGAGCTGTTTCGAGCGTTCGCAACCGGGAGCTGGAAACGAGTCAAGAGGCTGGTGACGC 515
QY 361 CTGAGAGGTTGAACAGCGCGCACCGCGGAGGAAATCCACCCCGCTGCACTTCGCGCG 420
Db 516 CTGAGAGGTTGAACAGCGCGCACCGCGGAGGAAATCCACCCCGCTGCACTTCGCGCG 575
QY 421 CAGGTTTGGCGGAAAGACGCTAGTTGAATATTTGCTTTCAGAAATGTCGAAATGTCGAAAG 480
Db 576 CAGGTTTGGCGGAAAGACGCTAGTTGAATATTTGCTTTCAGAAATGTCGAAATGTCGAAAG 635
QY 481 CACGTGATGATGGGGGCTTATCTCTTCATATGATGCTCTTTTGGTTCATGCTGAAG 540

Db	636	 CAGGTGATGATGGGGCTTTATTCCTCTTCATAATGCATGCTCTTTTGGTCAATGCTGAAG	695
Qy	541	TAGTCAATCTCCTTTTGGCGACATGGTGCAGACCCCAATGCTCGAGATAAATTGGAAATTATA	600
Db	696	TAGTCAATCTCCTTTTGGCGACATGGTGCAGACCCCAATGCTCGAGATAAATTGGAAATTATA	755
Qy	601	CTCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATATGATGTTTGCATTTGTCTGTACAGC	660
Db	756	CTCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATATGATGTTTGCATTTGTCTGTACAGC	815
Qy	661	ATGAGCTGAGCCAA CCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATC	720
Db	816	ATGAGCTGAGCCAA CCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATC	875
Qy	721	CATCTGCCAAAGCAGTCTTACTTGCTGAATATTAAGAAAGATGAATCTTTAGAAGTGCCCA	780
Db	876	CATCTGCCAAAGCAGTCTTACTTGCTGAATATTAAGAAAGATGAATCTTTAGAAGTGCCCA	935
Qy	781	GGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACATTAAATGTCAACTGCCACG	840
Db	936	GGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACATTAAATGTCAACTGCCACG	995
Qy	841	CAAGTGATGCGAAGTCAACTCCATTACATTTGGCAGCAGGATATACAGAGTTAAAGA	900
Db	996	CAAGTGATGCGAAGTCAACTCCATTACATTTGGCAGCAGGATATACAGAGTTAAAGA	1055
Qy	901	TTGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTTAAGATAAAGTGATCTGG	960
Db	1056	TTGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTTAAGATAAAGTGATCTGG	1115
Qy	961	TACCATTACACAATGCCGTGTTCTTATGGTCAATTATGAAGTAACTGAACCTTTTGGTCAAGC	1020
Db	1116	TACCATTACACAATGCCGTGTTCTTATGGTCAATTATGAAGTAACTGAACCTTTTGGTCAAGC	1175
Qy	1021	ATGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTCACCTCTCTTCATGAGCGAGCTT	1080
Db	1176	ATGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTCACCTCTCTTCATGAGCGAGCTT	1235
Qy	1081	CTAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAAGTTATGGTGCAGACCCCAACTGC	1140
Db	1236	CTAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAAGTTATGGTGCAGACCCCAACTGC	1295
Qy	1141	TCAATTGTCAAAATAAAGTGCTATAGACTTGGCTCCACACACACAGTTAAAAAGAAAGAT	1200
Db	1296	TCAATTGTCAAAATAAAGTGCTATAGACTTGGCTCCACACACACAGTTAAAAAGAAAGAT	1355
Qy	1201	TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAGCTGATGTTACTC	1260
Db	1356	TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAGCTGATGTTACTC	1415
Qy	1261	GAATCAAAAAACATCTCTCTGGAATATGGTGAATTCACAGCATCTTCAACACATGAAA	1320
Db	1416	GAATCAAAAAACATCTCTCTGGAATATGGTGAATTCACAGCATCTTCAACACATGAAA	1475
Qy	1321	CAGATTGTCATTTGCTGCTGCATCTCCATATCCCAAAGAAAGCAAAATATGTGAATCTG	1380
Db	1476	CAGATTGTCATTTGCTGCTGCATCTCCATATCCCAAAGAAAGCAAAATATGTGAATCTG	1535
Qy	1381	TGCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTTAAAGAAATTTCTTGACCTCTGCACG	1440
Db	1536	TGCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTTAAAGAAATTTCTTGACCTCTGCACG	1595
Qy	1441	TGGCATCTGAGAAAGCTCATATGATGTTGTTGAGTAGTGGTGAACATGAAGCAAAAGG	1500
Db	1596	TGGCATCTGAGAAAGCTCATATGATGTTGTTGAGTAGTGGTGAACATGAAGCAAAAGG	1655
Qy	1501	TTAATGCTCTGGGATAATCTTGTGTCAGACTTCTCTACACAGAGCTGCGATATTTGTGGTCATC	1560
Db	1656	TTAATGCTCTGGGATAATCTTGTGTCAGACTTCTCTACACAGAGCTGCGATATTTGTGGTCATC	1715
Qy	1561	TACAAACCTCGCGCTACTCCTGAGCTATGGGTGTGATCCCTAACATTATATCCCTTCAGG	1620

1716	TACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTTAACATTATATACCTTTCAGG	1771	TACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTTAACATTATATACCTTTCAGG
1621	GCCTTTACTGCTTTTACAGATGGGAAATGAAATATGTACAGCAACTCCTCCAAGAGGGTATCT	1680	GCCTTTACTGCTTTTACAGATGGGAAATGAAATATGTACAGCAACTCCTCCAAGAGGGTATCT
1776	GCCTTTACTGCTTTTACAGATGGGAAATGAAATGTAACAGCAACTCCTCCAAGAGGGTATCT	1835	GCCTTTACTGCTTTTACAGATGGGAAATGAAATGTAACAGCAACTCCTCCAAGAGGGTATCT
1681	CATTAGGTAAATTACAGAGGCAGACAGACAATTGTCTGGAAGCTGCAAAAGGCTGGAGATGTGC	1740	CATTAGGTAAATTACAGAGGCAGACAGACAATTGTCTGGAAGCTGCAAAAGGCTGGAGATGTGC
1836	CATTAGGTAAATTACAGAGGCAGACAGACAATGTCTGGAAGCTGCAAAAGGCTGGAGATGTGC	1895	CATTAGGTAAATTACAGAGGCAGACAGACAATGTCTGGAAGCTGCAAAAGGCTGGAGATGTGC
1741	AAACTGTAAAAAACHTGTGTACTGTTTCAGAGTCTCAACTGCACAGACATTTGAAGGGCGCTC	1800	AAACTGTAAAAAACHTGTGTACTGTTTCAGAGTCTCAACTGCACAGACATTTGAAGGGCGCTC
1896	AAACTGTAAAAAACHTGTGTACTGTTTCAGAGTCTCAACTGCACAGAGCAATTTGAAGGGCGCTC	1955	AAACTGTAAAAAACHTGTGTACTGTTTCAGAGTCTCAACTGCACAGAGCAATTTGAAGGGCGCTC
1801	AGTCTACACACATTCATTTTTCAGAGCTGGGTATAAACAGAGTGTCCGTGGTGGAAATATCTGC	1860	AGTCTACACACATTCATTTTTCAGAGCTGGGTATAAACAGAGTGTCCGTGGTGGAAATATCTGC
1956	AGTCTACACACATTCATTTTTCAGAGCTGGGTATAAACAGAGTGTCCGTGGTGGAAATATCTGC	2015	AGTCTACACACATTCATTTTTCAGAGCTGGGTATAAACAGAGTGTCCGTGGTGGAAATATCTGC
1861	TACAGCATGAGCTGATGTGCATGCTTAAAGATAAAGAGAGGCCCTGTACCTTTGCACAAATG	1920	TACAGCATGAGCTGATGTGCATGCTTAAAGATAAAGAGAGGCCCTGTACCTTTGCACAAATG
2016	TACAGCATGAGCTGATGTGCATGCTTAAAGATAAAGAGAGGCCCTGTACCTTTGCACAAATG	2075	TACAGCATGAGCTGATGTGCATGCTTAAAGATAAAGAGAGGCCCTGTACCTTTGCACAAATG
1921	CATGTTCTTATGACACATTATGAAGTTGCAGAACTCTTGTTAAACATGGAGCAGTAGTTA	1980	CATGTTCTTATGACACATTATGAAGTTGCAGAACTCTTGTTAAACATGGAGCAGTAGTTA
2076	CATGTTCTTATGACACATTATGAAGTTGCAGAACTCTTGTTAAACATGGAGCAGTAGTTA	2135	CATGTTCTTATGACACATTATGAAGTTGCAGAACTCTTGTTAAACATGGAGCAGTAGTTA
1981	ATGTAGCTGATTTATGGAAATTTTACACCTTTTATCAATGAAGCAGACGACAAAAGGAAAATATG	2040	ATGTAGCTGATTTATGGAAATTTTACACCTTTTATCAATGAAGCAGACGACAAAAGGAAAATATG
2136	ATGTAGCTGATTTATGGAAATTTTACACCTTTTATCAATGAAGCAGACGACAAAAGGAAAATATG	2195	ATGTAGCTGATTTATGGAAATTTTACACCTTTTATCAATGAAGCAGACGACAAAAGGAAAATATG
2041	AAATTTGCAAACTTCTCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGGATGGAA	2100	AAATTTGCAAACTTCTCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGGATGGAA
2196	AAATTTGCAAACTTCTCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGGATGGAA	2255	AAATTTGCAAACTTCTCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGGATGGAA
2101	ATACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAG	2160	ATACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAG
2256	ATACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAG	2315	ATACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAG
2161	ATCAGCTTTTGTCTAGATGCTGCCAAGAAGGTTGTTTATGCCAGAGTGAAGAAATGTTCTT	2220	ATCAGCTTTTGTCTAGATGCTGCCAAGAAGGTTGTTTATGCCAGAGTGAAGAAATGTTCTT
2316	ATGCAGCTTTGTCTAGATGCTGCCAAGAAGGTTGTTTATGCCAGAGTGAAGAAATGTTCTT	2375	ATGCAGCTTTGTCTAGATGCTGCCAAGAAGGTTGTTTATGCCAGAGTGAAGAAATGTTCTT
2221	CTCCTGATTAATGTAATGCCGCGATACCCAAGGCAGACATTCAAACCTTTTACATTTAG	2280	CTCCTGATTAATGTAATGCCGCGATACCCAAGGCAGACATTCAAACCTTTTACATTTAG
2376	CTCCTGATTAATGTAATGCCGCGATACCCAAGGCAGACATTCAAACCTTTTACATTTAG	2435	CTCCTGATTAATGTAATGCCGCGATACCCAAGGCAGACATTCAAACCTTTTACATTTAG
2281	CAGCTGGTTAATAATTTAGAGATTTGCAGAGTATTTGTTTACAACGAGAGCTGATGTGA	2340	CAGCTGGTTAATAATTTAGAGATTTGCAGAGTATTTGTTTACAACGAGAGCTGATGTGA
2436	CAGCTGGTTAATAATTTAGAGATTTGCAGAGTATTTGTTTACAACGAGAGCTGATGTGA	2495	CAGCTGGTTAATAATTTAGAGATTTGCAGAGTATTTGTTTACAACGAGAGCTGATGTGA
2341	ATGCCAAGACAAGGAGGACTTTATTCCTTTTACATAATGCAGCATCTTACCGGCATGTAG	2400	ATGCCAAGACAAGGAGGACTTTATTCCTTTTACATAATGCAGCATCTTACCGGCATGTAG
2496	ATGCCAAGACAAGGAGGACTTTATTCCTTTTACATAATGCAGCATCTTACCGGCATGTAG	2555	ATGCCAAGACAAGGAGGACTTTATTCCTTTTACATAATGCAGCATCTTACCGGCATGTAG
2401	ATGTAGCAGCTCTACTAATAAAGTATAATGTCATGTGTCAATGCCAGGACAAATGGGCTT	2460	ATGTAGCAGCTCTACTAATAAAGTATAATGTCATGTGTCAATGCCAGGACAAATGGGCTT
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2616	TCACACCTTTTGCAGAGACGCCCAAAAGGGAGCAACACAGCTTTGTGCTTTGTGCTAG	2675	TCACACCTTTTGCAGAGACGCCCAAAAGGGAGCAACACAGCTTTGTGCTTTGTGCTAG
2521	CCCATGGAGCTGACCGGACTCTTAAAAATCAGGAAGGACAAAAACACTTTTAGATTTAGTTT	2580	CCCATGGAGCTGACCGGACTCTTAAAAATCAGGAAGGACAAAAACACTTTTAGATTTAGTTT
2676	CCCATGGAGCTGACCGGACTCTTAAAAATCAGGAAGGACAAAAACACTTTTAGATTTAGTTT	2735	CCCATGGAGCTGACCGGACTCTTAAAAATCAGGAAGGACAAAAACACTTTTAGATTTAGTTT
2581	CAGCGGATGATGTACGGCTCTTTCTGACAGACGCCATGCCCCCATCTGCTCTGCCCTCTT	2640	CAGCGGATGATGTACGGCTCTTTCTGACAGACGCCATGCCCCCATCTGCTCTGCCCTCTT
2736	CAGCAGATGATGTACGGCTCTTTCTGACAGACGCCATGCCCCCATCTGCTCTGCCCTCTT	2795	CAGCAGATGATGTACGGCTCTTTCTGACAGACGCCATGCCCCCATCTGCTCTGCCCTCTT
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QY 2821 TGGAGAAAAGAGGTTCCAGAGGTAGATTCTGAGATACCTCAATTCGTAAGGAATCTTG 2880
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; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 3803; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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Db 3120 CTGTGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGACAGAGATGGAGTCAATGCAAGTG 3179
QY 3184 GAATCTTCAACAGATACAAATATTTCTCAAGATTGGAAGGTTTGTAAACAAGAACTATGGG 3243
Db 3180 GAATCTTCAACAGATACAAATATTTCTCAAGATTGGAAGGTTTGTAAACAAGAACTATGGG 3239
QY 3244 AAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAACACAAACCATGCAATGAAC 3303
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QY 3304 GAATGCTATTTCATGGTCTCTTTTGTGAATGCAATATATCACAAGAGCTTTTGTATGAA 3363
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QY 3424 AAGCAATCAATATGATATGAAATGGAGAGGTACTGGGTGTCAGTTTCAAAAGACA 3483
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QY 3544 TCCTGCAGTTCAAGTCAATGAAATGGCAATTTCTCTCCAGGTCACTCAGTCACTG 3603
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Db 3780 TCTAGCTTTTACTCTCTTGTGCGAAAAAAA 3809

RESULT 8

US-10-302-172-556
; Sequence 556, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids and
FILE REFERENCE: 803.1CNCp
CURRENT APPLICATION NUMBER: US/10/302,172
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 556
LENGTH: 5075
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (253)..(3750)
US-10-302-172-556

Query Match 98.8%; Score 3770.8; DB 8; Length 5075;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3800; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 1 CGCGCTGCTCCGCGCCGCGCGGCGAGCCGCGGGGCGAGCGCGGGGGGAGCCCGAGGAGGGCGCGCG 60
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QY 61 TGGGGCGCGCCCATGGGACTGCGCCGCGATTCGGTGAACAGAGGAGGCCAAGCGCGCGCGG 120
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QY 121 CCCTGAGCGCGCTTCTCCGCGGGGCGCTCGCCCTCCTCTCT-CCGCGGGGCGCGGGGCTCTCTG 179
Db 148 CCCTGAGCGCGCTTCTCCGCGGGGCGCTCGCCCTCCTCTCTCTCCCGGGGCGCGGGGCTCTCTG 207
QY 180 CTCGCGTTGCTGGCGCTGTTGCTGCTGTCGCGCGGCGGCGAGGATCATGTGCGGGTGCCTGCG 239
Db 208 CTCGCGTTGCTGGCGCTGTTGCTGCTGCGCGGCGGCGAGGATCATGTGCGGGTGCCTGCGCG 267
QY 240 TCGCGCGCGGGGAGCGGCGCTGCGAGCGCGCGCGCGCGGCGGCGGCGCGCGCGCGCG 299
Db 268 TCGCGCGCGGGGAGCGGCGCTGCGAGCGCGCGCGCGCGGCGGCGGCGGCGCGCGCGCG 327
QY 300 CGAGAGCTGTTTCGAGGCGTCCGCAACCGGGGACGTTGGAAACGAGTCAAGAGGCTGGTGAGG 359
Db 328 CGAGAGCTGTTTCGAGGCGTCCGCAACCGGGGACGTTGGAAACGAGTCAAGAGGCTGGTGAGG 387
QY 360 CCTGAGAGGTGAACAGCGCGGACACAGCGGGGCGAGGAAATCCACCCCGCTGCACCTTCGCG 419
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QY 420 GCAGGTTTGGCGGAGAAAGACGTAGTTGAAATATTTGCTTCAGAAATGGTGCAGAAATGTCGAA 479
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QY 480 GCAGGATGATGGGGCGCTTATTCCTCTTCAATGATGCTCTCTTTTGGTCAATGCTGAA 539
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QY 540 GTAGTCAATCTCTTTTTCGACATGGTGCAGACCCCAATGCTCCAGAGATAATTTGGAATAT 599
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QY 960 GTACCATTTACAAATGCCCTGTTCTTATGGTCAATTAAGAAGTAACCTGAACTTTTGGTCAAG 1019
DB 988 GTACCATTTACAAATGCCCTGTTCTTATGGTCAATTAAGAAGTAACCTGAACTTTTGGTCAAG 1047
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QY 1620 GGCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCCCAAGAGGATATC 1679
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DB 1828 CAGTCTACACCACCTTCATTTTTCAGCTGGGTATAACAGAGTGTCCGTGTGGTAATCTG 1887
QY 1860 CTACAGCATGAGCTGATGTGCATCTAAAGATAAAGGAGGCTTTGTACCTTTGCACAAT 1919
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QY 1980 AATGTAGCTGATTTTATGAAAAATTTACACTTTTACATGAAGCAGCAGCAAAAAGAAATAT 2039
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QY 2100 AATAGTCTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTTAGGGGA 2159
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RESULT 9

US-10-199-937-100

; Sequence 100, Application US/10199937

; Publication No. US20030190739A1

; GENERAL INFORMATION:

; APPLICANT: Christenson, Erik

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; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: PANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 4127
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3508)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (3509)..(4127)
; US-10-199-937-100
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Query Match 94.2%; Score 3595.8; DB 7; Length 4127;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3597; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 935 CCATGCTTAAAGATAAAGGCTGATCTGTGTACCAATACACAATGCCCTGTCTTATGCTCATTA 994
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QY 721 CCATGCTTAAAGATAAAGGCTGATCTGTGTACCAATACACAATGCCCTGTCTTATGCTCATTA 780
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QY 841 ATTCACTCTCTTCATGAGCAGCTCTTAAGACAGGGTTGAAGTATGTTCTCTCTCTT 900
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QY 1621 CAGAGTCTCGGTGGTGAATATCTGCTACAGCATGGAGCTGATGTGCATGCTAAAGATAA 1680
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QY 1895 AGGAGGCTTGACCTTTGCAAAATGCAATGCAATGTTCTTATGGAATATGAGAGTGTGCAAACT 1954
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QY 1681 AGGAGGCTTGACCTTTGCAAAATGCAATGCAATGTTCTTATGGAATATGAGAGTGTGCAAACT 1740
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QY 1955 TCTTGTAAACATGGAGCAGTATGTTAATGTAGCTGATTTATGGAAATTTACACCTTTACA 2014

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QY 2015 TGAAGCAGCAGCAAAAAGGAAAATATGAAAATTTGCAAACTTCTGCTCCAGCATGGTGAGA 2074
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QY 1801 TGAAGCAGCAGCAGCAAAAAGGAAAATATGAAAATTTGCAAACTTCTGCTCCAGCATGGTGAGA 1860
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QY 2075 CCTACCAAAAAAACAAGGATGGAATACTCTTTTGGATCTTTGTTAAAGATGGAGATAC 2134
DB |||||
QY 1861 CCTACCAAAAAAACAAGGATGGAATACTCTTTTGGATCTTTGTTAAAGATGGAGATAC 1920
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QY 2135 AGATATTTCAAGATCTGCTTAGGGGAGATGCAAGCTTTGCTAGATGCTGCCAAGAGGGTGT 2194
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QY 1921 AGATATTTCAAGATCTGCTTAGGGGAGATGCAAGCTTTGCTAGATGCTGCCAAGAGGGTGT 1980
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DB |||||
QY 1981 TTTTAGCCAGAGTGAAGAAGTTGTCTTCTCTGATAATGTAAATTTGCCGCGATACCCCAAGG 2040
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QY 2675 CCAGAGAGCCACTGCAGATGCTCTCTTCAGGTCCAATCTAGCCCATCAAGCCCTTTCTGCG 2734
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QY 2461 CCAGAGAGCCACTGCAGATGCTCTCTTCAGGTCCAATCTAGCCCATCAAGCCCTTTCTGCG 2520
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Db 1681 AGGAGGCTTGTACCTTTGCACAAATGCATGCTTTTATGGACATTAAGAAGTTCGAGAACT 1740
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RESULT 12

US-10-616-101-1
; Sequence 1, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-616-101-1

Query Match 88.9%; Score 3393.4; DB 10; Length 3797;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1382 GCTAAGAAAAGGAGCAAAACATCAATGAAGACCTAAAGAAATTTCTTGACTCTCTGCGAGT 1441
Db 1363 GCTAAGAAAAGGAGCAAAACATCAATGAAGAAAGCTAAAGAAATTTCTTGACTCTCTGCGAGT 1422
Qy 1442 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTGTGTAAGCAATGAAGCAAAAGGT 1501
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Db 1483 TAATGCTCTGATTAATCTTGGTCAAGCTTCTACACAGAGCTGCATATTTGTTGTCATCT 1542
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Db 1603 CTTTACTGCTTTACAGATGGAAATGTAAGTGTACAGCACTCTCCAAAGAGGTATCTC 1662
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Db 1663 ATTAGGTAATTCAGAGGCGAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCGA 1722
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Qy 1862 ACAGCATGGAGCTCATGTGATGCTTAAAGATAAAGAGGAGGCTTGTACCTTTGCAAAATGC 1921
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Qy 1922 ATGTTCTTATGCAATTTAAGAGTTGAGAACTTCTTGTGTTAAACATGAGGAGTAGTTAA 1981
Db 1903 ATGTTCTTATGCAATTTAAGAGTTGAGAACTTCTTGTGTTAAACATGAGGAGTAGTTAA 1962
Qy 1982 TGTAGCTGATTTTAAAGAAATTTACACCTTTTACATGAAGCAGCAGCAAAAGAAATATGA 2041
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Qy 2042 AATTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAAA 2101

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2222	Qy	TCCTGATAATGTAAATTTGCCGCGNATACCCAAAGCAGACATTTCAACACTTTACATTAGC	2281
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2282	Qy	AGCTGGTTTAATAATTTAGAAAGTTGCAGAGTATTTGTTACACACAGGAGCTGATGTGA	2341
2263	Db	AGCTGGTTTAATAATTTAGAAAGTTGCAGAGTATTTGTTACACACAGGAGCTGATGTGA	2322
2342	Qy	TGCCAAGAACAAGGAGACTTATTCCTTTACATAATGACGACATCTTACGGGATGTTAGA	2401
2323	Db	TGCCAAGAACAAGGAGACTTATTCCTTTACATAATGACGACATCTTACGGGATGTTAGA	2382
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2383	Db	TGTAGCAGCTCTACTAATAAAGTATAATGATGTGTCAATTGCCACGGACAATATGGGCTTT	2442
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2923	Db	GATGGGGCACAAGGAGCTGAAGGAGATTGGAATCAATGCTTTATGGACATAGGCACAAACT	2982
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3043	Db	GAACACTCTGGTAGTGGACAATTTCTTATAGATCTGCTCTCCTGATGATAAGAGTTTCA	3102
3122	Qy	GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCATGCAGG	3181

Db	3103	GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCAATGCAGG	3162
Qy	3182	TGGAATCTTCAACAGAGATACAATATCTCAAGATTTCAGAAGTTTGTAAACAAGAAACTATG	3241
Db	3163	TGGAATCTTCAACAGAGATACAATATCTCAAGATTTCAGAAGTTTGTAAACAAGAAACTATG	3222
Qy	3242	GGAAGATACACTCACCGGAGAAAGAGTTCGTGAAGAAACCAACAACATGCCAATGA	3301
Db	3223	GGAAGATACACTCACCGGAGAAAGAGTTCGTGAAGAAACCAACAACATGCCAATGA	3282
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Db	3283	ACGAATGCTATTTTCATGGGTCTCCTTTTGTGAATGCAATTATCCACAAGAGCCTTTGCATGA	3342
Qy	3362	AAGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTCTGAAACCTCTTC	3421
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Db	3403	CAAAAGCAATCAATATGTATATGGAATTGGAGAGGTACTTGGGTGTCCAGTTCACAAAGA	3462
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Qy	3542	TTTTCCTGCAGTTCAGTGCATGAAATGCGACATTTCTCTCCAGGTCATCAGTCAGTCAC	3601
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Qy	3602	TGTTAGGCCCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGGAGAACA	3661
Db	3583	TGTTAGGCCCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGGAGAACA	3642
Qy	3662	GGCTTATCTGAGTATTTAAATTACTTACAGATTTATGAGGCGTGAAGGTTATGTCATGG	3721
Db	3643	GGCTTATCTGAGTATTTAAATTACTTACCAGATTTATGAGGCGCTGAAGGTTATGTCATGG	3702
Qy	3722	ATAAATAGTATTTTAAAGAACTTAA'TTCACTGAACTTAAATCATCAAGCAGCAGTGG	3781
Db	3703	ATAAATAGTATTTTAAAGAACTTAA'TTCACTGAACTTAAATCATCAAGCAGCAGTGG	3762
Qy	3782	CTCTCAGTTTTTACTCCTTTGCTGAAAAAATAA	3816
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RESULT 13
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  Sequence 3, Application US/09972115A
  Publication No. US20030032769A1
  GENERAL INFORMATION:
  APPLICANT: Geron Corporation
  APPLICANT: Gregg, Morin B.
  APPLICANT: Walter, Funk D.
  APPLICANT: Mieczyslaw, Platuszek A.
  TITLE OF INVENTION: A Second Mammalian Telomerase
  FILE REFERENCE: 080/003C
  CURRENT APPLICATION NUMBER: US/09/972.115A
  CURRENT FILING DATE: 2001-10-05
  PRIOR APPLICATION NUMBER: US 60/128,577
  PRIOR FILING DATE: 2000-04-10
  PRIOR APPLICATION NUMBER: US 60/129,123
  PRIOR FILING DATE: 1999-04-13
  NUMBER OF SEQ ID NOS: 64
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO 3
  LENGTH: 4297
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(3801)

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Qy	181	TCGGTTGTGCGCGCTGTTGCTGTGTGCGGGGGCCAGGATCATGTCCGGT	CGCGCT	240
Db	254	TCGGTTGTGCGCGCTGTTGCTGTGTGCGGGGGCCAGGATCATGTCCGGT	CGCGCT	313
Qy	241	GGCGGGGGGGGAGCGGCGTGCAGACGCGCGGGCGGAGCGCGTGCAGCG	CGCGCGCGCC	300
Db	314	GGCGGGGGGGGAGCGGCGTGCAGACGCGCGGGCGGAGCGCGTGCAGCG	CGCGCGCGCC	373
Qy	301	GAGAGCTGTTTCAGGCGTGC CGCAA CGGGGACGTGGAA CGAGTCAA	GAGAGCTGCTGACGC	360
Db	374	GAAANCCTGTTCCAGACGTGCGCAA CGGGGACGTGGAA CGANTCAA	GAGAGCTGCTGACGC	433
Qy	361	CTGAGAAAGGTGAACAGCGCGGACACGCGGGCAGGAAATCCACCCCG	CTGCACCTTGC	420
Db	434	CTGARAAGGTGAACAGCGCGGACACGCGGGCAGGAAATCCACCCCG	CTGCACCTTGC	493
Qy	421	CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGT	GCAATGTC	480
Db	494	CANGTTTTGGCGGAAAGACGTANTTAAATATTTGCTTCANNAATGGT	GCAATGTC	553
Qy	481	CACGTGATGATGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGT	GTCATGCTCAAG	540
Db	554	CACGTGATGATGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGT	GTCATGCTCAAG	613
Qy	541	TAGTCAATCTCCTTTTGGACATGGTGCAGACCCCAATGCTCGAGATAA	TTGGAATTTATA	600
Db	614	NTATCNATCTCCTTTTGCNACATNGTCANAMCCCAATGCTCGAGATAA	TTGGAATTTATA	673
Qy	601	CTCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATTTTGCAATT	GCTGCTGTTACAGC	660
Db	674	CTCCTCNATGAAGCTGCAATTTAAAGGAAAGATTGANNNTTGCATT	GCTGCTGTTACAGC	733
Qy	661	ATGAGCTGAGCCCAACCATCCGAAATACAGATGAAGGACAGCATTCG	ATTTAGCACATC	720
Db	734	ATGAGCTGAGCCCAACCATCCGAAATACAGATGAAGGACAGCATTCG	ATTTAGCACATC	793
Qy	721	CATCTGCCAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACCT	TTAGAAAGTGCCA	780
Db	794	CATCTGCCAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACCT	TTAGAAAGTGCCA	853
Qy	781	GGAGTGGCAATGAAGAAAAATGATGGCTTACTCACACCATTTAAAT	TGTCACCTGCCACG	840
Db	854	GGAGTGGCAATGAAGAAAAATGATGGCTTACTCACACCATTTAAAT	TGTCACCTGCCACG	913
Qy	841	CAAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAA	CACAGAGTAAAGA	900
Db	914	CAAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAA	CACAGAGTAAAGA	973
Qy	901	TTGTACAGCTGTTACTGCAACAATGGAGCTGATGCCATGCTTAAAGATAA	AGAGTGCATCTGG	960
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Qy	961	TACATTACAAATGCCCTGTTCTTATGGTCAATTAAGATTAACCTGAA	ACTTTTGGTCAAGC	1020
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Qy	1021	ATGGTGCTGTGTAATGCAATGCACTTGGGCAATTCACCTCTTTCATGAG	CAGCAGCTT	1080
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Db	1154	CTAAGAACAGGGTTGAAGTATGTTCTCTTCTTTAAAGTTATGGTGCAGAC	CCCAACACTGCG	1213
Qy	1141	TCAATTTGTCAAAATAAAGTGCTATAGACTTTGGTCTCCACACCAACAG	TTAAAGAAAGAT	1200
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1274	Db	TAGCATAATGAATTTAAAGGCCACTCTCTTGCTGCAAGCTGC	CACGAGAAGCTGATGTTACTCTC	1333
1261	Qy	GAATCAAAAACCATCTCTCTGGAATGGTGAATTTCAAGCAT	CTCTCAAAACATGAAA	1320
1334	Db	GAATCAAAAACCATCTCTCTGGAATGGTGAATTTCAAGCAT	CTCTCAAAACATGAAA	1393
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1454	Db	TGCTAAGAAAAGAGCAAAACATCAATGAAAGACTAAAGAA	TTCTTTGACTCTCTGCAAG	1513
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1514	Db	TGCGATCTGAGAAAGCTCATATGATGTTGTTGAAAGTAG	TGGTGAACATGAAAGCAAGG	1573
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1561	Qy	TACAAACCTGCCCTACTCTCTGAGCTATGGGTGTGATC	CTTAACTATATCCCTTCAGG	1620
1634	Db	TACAAACCTGCCCTACTCTCTGAGCTATGGGTGTGATC	CTTAACTATATCCCTTCAGG	1693
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1694	Db	GCTTTACTGCTTTACAGATGGGAAATGAAATGTCACAG	CAATCTCTCCAAGAGGCTATCT	1753
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1754	Db	CATTAGGTAATTCAGAGGGCAGACAGACAATTCCTGGA	AGCTGCAAAAGGCTGGAGATGTCG	1813
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1814	Db	AAACTGTAAAAAATCTGTGTACTGTTTCAGAGTCTCAA	CTGCAGAGACATTTGAAGGCGCTC	1873
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1874	Db	AGTCTACACACTTTCATTTTGCAGCTGGGTATTAACAG	AGTGTCCGTGGTGGAAATATCTGC	1933
1861	Qy	TACAGCATGAGCTGATGTGCATGCTTAAAGATAAAGAG	GSCCTTGTACCTTTGCACAATG	1920
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1994	Db	CATGTTCTTATGCAACATTAAGAGTTGCAGAACTTCT	TGTTTAAACATGGAGCAGTAGTTA	2053
1981	Qy	ATGTAGCTGATTTATGGAAATTTACACCTTTTACATGA	AGCAGCAGCAAAAAGGAAAATATG	2040
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2101	Qy	ATACTCTCTTTGGATCTTGTTTAAAGATGGAGATACAG	ATATTTCAAGATCTCGCTTAGGGGAG	2160
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2161	Qy	ATGCAGCTTTTGCATGCTGCCAAGAAAGGGTTGTTT	TAGCCAGAGTGGAAGAGTTGTCCTT	2220
2234	Db	ATGCAGCTTTTGCATGCTGCCAAGAAAGGGTTGTTT	TAGCCAGAGTGGAAGAGTTGTCCTT	2293
2221	Qy	CTCCTGATGATGTAATTTGCCGGGATACCACAGGCAG	ACATTTCAACACCTTTTACATTTAG	2280
2294	Db	TTCTCTGATGATGTAATTTGCCGGGATACCACAGGCAG	ACATTTCAACACCTTTTACATTTAG	2353
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[illegible]

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; Patent No. US20020037582A1			
; GENERAL INFORMATION:			
; APPLICANT: DALY, Roger J.			
; APPLICANT: SUTHERLAND, Robert L.			
; TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling			
; TITLE OF INVENTION: Proteins			
; FILE REFERENCE: 1871-129			
; CURRENT APPLICATION NUMBER: US/09/509,196A			
; CURRENT FILING DATE: 2000-03-23			
; PRIOR APPLICATION NUMBER: P09388			
; PRIOR FILING DATE: 1997-09-23			
; PRIOR APPLICATION NUMBER: PCT AU98/00795			
; PRIOR FILING DATE: 1998-09-23			
; NUMBER OF SEQ ID NOS: 2			
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; TYPE: DNA			
; ORGANISM: Homo sapiens			
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Best Local Similarity 99.7%; Pred. No. 0;			
Matches 3303; Conservative 0; Mismatches 10; Indels 0; Gaps 0;			
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Qy 1761 ACTGTTGAGAGTGTCAACTGCAGAGACATTTGAAGGGGTGAGTCTACACCACTTCAATTTT 1820
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US-09-972-115A-1

Query Match 79.6%; Score 3039; DB 3; Length 4493;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 3101; Conservative 1; Mismatches 375; Indels 27; Gaps 2;

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Db	587	AACCATTCNNAGGCTGGTGACCCCTGANAAGGTNAACANCCNCAACACGNGGCGAGGA	646
Qy	397	AATCCACCCCGCTGCACCTTCGCCGACGTTTGGCGGAAGAGCTAGTTGAATATTTGC	456
Db	647	AATCCACCCCGCTGCACCTTCGCCGACGTTTGGCGGAAGAGCTAGTTGAATATTTGC	706
Qy	457	TTCAAGATGTGCAAAATGTCCAAGCAAGTGAATGAGGGGCTTATTCCTCTTCATATG	516
Db	707	TTCAAAATGTGCAAAATNTCCANCACTTTATAATGGGGGCTTATTCCTCTTCATATG	766
Qy	517	CATGCTCTTTTGGTCATGCTGAGTAGTCAATCTCTTTTGGACATGTTGACACCCCA	576
Db	767	CATGCTCTTTTGGTCATGCTGAGTAGTCAATCTCTTTTGGACATGTTGACACCCCA	826
Qy	577	ATGCTTCAGATAATTGGAAATTTATCTCTCTCCATGAAGCTGCATTTAAAGGAAGATTG	636
Db	827	ATGCTTCAGATAATTGGAAATTTATCTCTCTCCATGAAGCTGCATTTAAAGGAAGATTG	886
Qy	637	ATGTTTCATATGCTGTTACAGATCGAGCTGAGCCAAACATCCGAAATACAGATGAA	696
Db	887	ATGTTTCATATGCTGTTACAGATCGAGCTGAGCCAAACATCCGAAATACAGATGAA	946
Qy	697	GGACAGATTTGGATTTAGCAGATCCATCTGCCAAGCAGTCTACTGTGGAATATAGA	756
Db	947	GGACAGATTTGGATTTAGCAGATCCATCTGCCAAGCAGTCTACTGTGGAATATAGA	1006
Qy	757	AAGATGAACCTCTTAGAAGTGCAGAGAGTGGCAATGAAGAAAAATGATGGCTTACTCA	816
Db	1007	AAGATGAACCTCTTAGAAGTGCAGAGAGTGGCAATGAAGAAAAATGATGGCTTACTCA	1066
Qy	817	CACCATTAATGTCAACTGCCACGCAAGTGAAGTCAACTCCATTAATTTGG	876
Db	1067	CACCATTAATGTCAACTGCCACGCAAGTGAAGTCAACTCCATTAATTTGG	1126
Qy	877	CAGCAGGATATACAGAGTAAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGCC	936

Db	1127	CACGAGATATAACAGAGTAAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGCC	1186
Qy	937	ATGCTAAAGATAAAGTGATCTCGGTACCAATTAACAATGCTGTTCTTATGGTCATTATG	996
Db	1187	ATGCTAAAGATAAAGTGATCTCGGTACCAATTAACAATGCTGTTCTTATGGTCATTATG	1246
Qy	997	AAGTAATGAACCTTTTGGTCAACATGGTGCCTGTGTAAATGCAATGGACTTGTGGCAAT	1056
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Qy	1057	TCACCTCTCTTCATGAGGAGCTTCTAAGAACAGGGTGTGAAGTATGTTCTCTCTTAA	1116
Db	1307	TCACCTCTCTTCATGAGGAGCTTCTAAGAACAGGGTGTGAAGTATGTTCTCTCTTAA	1366
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Db	1487	CTGCACGAGAGCTGATGTTTACTCGAATCAAAAAACATCTCTCTCTGAAAAATGGTGAAT	1546
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Db	1727	TAGTGTGAAACATGAAGCAAAAGTTAATGCTCTGGATAATCTTGGTCAGACTTCTCTAC	1786
Qy	1537	ACAGAGCTGATATTTGGTGCATCAAAACCTGCCCTACTCCCTGAGCTATGGGTGTG	1596
Db	1787	ACAGAGCTGATATTTGGTGCATCAAAACCTGCCCTACTCCCTGAGCTATGGGTGTG	1846
Qy	1597	ATCCTAACATTTATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAAATGTAC	1656
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Qy	1717	AAGTGCAAAGGCTGGAGATGTCGAACTGTAATAAAGCTGTGACTGTTTCAGAGTGTCA	1776
Db	1967	AAGTGCAAAGGCTGGAGATGTCGAACTGTAATAAAGCTGTGACTGTTTCAGAGTGTCA	2026
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Db	2027	ACTGCAGAGACATTTGAAGGGCGTCAGTCTACCACTTCATTCTTTTTCAGCTGGGTATAACA	2086
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Db	2147	GAGGCTTGTACCTTGTGCAAAATGCTGTTTATGGACATTAAGAGTTCGCAACTTC	2206
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Qy 2137 ATATTCAAGATCTGTTAGGGAGATGCACTTTGCTAGATGCTGCCAAGAGGGTGT 2196
Db 2387 ATATTCAAGATGCTTAGGGAGATGCACTTTGCTAGATGCTGCCAAGAGGGTGT 2446
Qy 2197 TAGCAGAGTGAAGAAGTTGTCTCTCTGATAATGTAATTTGCCGCGATACCCCAAGGCA 2256
Db 2447 TAGCAGAGTGAAGAAGTTNTTTCTTGATTAATTTGCCGNGATACCCCAAGGCA 2506
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Db 2567 NNN 2626
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Db 2627 NNN 2686
Qy 2431 CATGTGTCAAATGCCAGCAAAATGGGCTTTACACACCTTTGCAAGAGCAGCCCAAGG 2490
Db 2687 NNN 2746
Qy 2491 GACGAACACAGCTTTGTGCTTTGTTGCTAGCCATGGAGCTGACCCGACTCTTAAAAATC 2550
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Qy 2551 AGGAAGGACAAACACCTTTAGATTTAGTTTACGCGATGTGTAGCGCTCTCTTGACAG 2610
Db 2807 NNN 2866
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DB 576 CAGGTTTGGCGGAAAGACGTAGTTGAATATTTGCTTTCAGATGGTGCGAAATGTCGCAAG 635
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DB 636 CACGTGATGATGGGGGCTTATCTCTTCATATGATGCTCTTTTGGTTCATGCTGCTGAAG 695
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QY 1381 TGTAAAGAAAGGAGCAAAACATCAATGAAAGAACTAAAGAAATTTCTTGACCTCTCGCACG 1440
DB 1536 TGTAAAGAAAGGAGCAAAACATCAATGAAAGAACTAAAGAAATTTCTTGACCTCTCGCACG 1595
QY 1441 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAAAATGAAAGCAAGG 1500
DB 1596 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAAAATGAAAGCAAGG 1655
QY 1501 TTAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTTGTCATC 1560
DB 1656 TTAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTTGTCATC 1715
QY 1561 TACAACACTGCGCCCTACTCTGAGCTATGGGTGTGATCTCTAAACATPATATATCCCTTCAGG 1620
DB 1716 TACAACACTGCGCCCTACTCTGAGCTATGGGTGTGATCTCTAAACATPATATATCCCTTCAGG 1775
QY 1621 GCTTTACTGCTTTACAGATGGGAAAATGAAAATGTAACGAACTCTCTCAAGAGGGTATCT 1680
DB 1776 GCTTTACTGCTTTACAGATGGGAAAATGAAAATGTACAGCAACTCTCTCAAGAGGGTATCT 1835
QY 1681 CATTAGTAAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGCG 1740
DB 1836 CATTAGTAAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGCG 1895
QY 1741 AAACCTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAAATGTCAGAGACATTTGAAGGGCGTC 1800
DB 1896 AAACCTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAAATGTCAGAGACATTTGAAGGGCGTC 1955
QY 1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCG 1860
DB 1956 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCG 2015
QY 1861 TACAGCATGAGCTGTATGTCATGCTAAAGATAAAGAGGCGCTTGTACCTTTGTCACAATG 1920
DB 2016 TACAGCATGAGCTGTATGTCATGCTAAAGATAAAGAGGCGCTTGTACCTTTGTCACAATG 2075
QY 1921 CATGTTCTTTATGGACATTAATGAAGTTGCAGAACTTTCTTTTAAACATGAGAGCTAGTTA 1980
DB 2076 CATGTTCTTTATGGACATTAATGAAGTTGCAGAACTTTCTTTTAAACATGAGAGCTAGTTA 2135
QY 1981 ATGTAGCTGATTTTATGGAATTTACACCTTTTACATGAGGACGAGCAAAAGGAAATATG 2040
DB 2136 ATGTAGCTGATTTTATGGAATTTTACACCTTTTACATGAGGACGAGCAAAAGGAAATATG 2195
QY 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTCAGACCTTACCAAAAAAAGAGGATGGAA 2100
DB 2196 AAATTTGCAAACTTCTGCTCCAGCATGGTCAGACCTTACCAAAAAAAGAGGATGGAA 2255
QY 2101 ATACTCTCTTTGGATCTTTTAAAGATGAGATACAGATATTCAGATCTGCTTAGGGAG 2160
DB 2256 ATACTCTCTTTGGATCTTTTAAAGATGAGATACAGATATTCAGATCTGCTTAGGGAG 2315
QY 2161 ATGAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTGTCTT 2220
DB 2316 ATGAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTGTCTT 2375
QY 2221 CTCTGTATAATGTAAATTTGCCGCGATACCCAAAGCGACATTCACACCTTTACATTTAG 2280

Db 2376 CTCCTGATAATGTAATTCGCCGATACCCAGGCGAGCAATTCACACCTTTACATTTAG 2435
Qy 2281 CAGCTGGTTATAATTAATTTAGAAAGTTGACAGTATTTCTGTACACACCGAGCTGATGGA 2340
Db 2436 CAGCTGGTTATAATTAATTTAGAAAGTTGACAGTATTTCTGTACACACCGAGCTGATGGA 2495
Qy 2341 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATTCGACATCTTTACGGGCAATGTAG 2400
Db 2496 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATTCGACATCTTTACGGGCAATGTAG 2555
Qy 2401 ATGTAGCAGCTCTACTATAAAGTATAATGCAATGTCATGTCATGTCACGCAAAATGGGCTT 2460
Db 2556 ATGTAGCAGCTCTACTATAAAGTATAATGCAATGTCATGTCATGTCACGCAAAATGGGCTT 2615
Qy 2461 TCACACCTTTGACACGAGCAGCCCAAGGAGGACGACAGCTTTGCTGTTGCTGCTAG 2520
Db 2616 TCACACCTTTGACACGAGCAGCCCAAGGAGGACGACAGCTTTGCTGTTGCTGCTAG 2675
Qy 2521 CCCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTT 2580
Db 2676 CCCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTT 2735
Qy 2581 CAGCGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCGCCCATCTGCTCTGCCCTCTT 2640
Db 2736 CAGCAGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCGCCCATCTGCTCTGCCCTCTT 2795
Qy 2641 GTTACAGCCTCAAGTGTCAATGTGTGAGAGCCGAGGACCACTCCAGATGCTCTCT 2700
Db 2796 GTTACAGCCTCAAGTGTCAATGTGTGAGAGCCGAGGACCACTCCAGATGCTCTCT 2855
Qy 2701 CTTCAAGTCCATCTAGCCCATCAAGCCTTCTGACGACGAGCTCTTGACAACTTATCTG 2760
Db 2856 CTTCAAGTCCATCTAGCCCATCAAGCCTTCTGACGACGAGCTCTTGACAACTTATCTG 2915
Qy 2761 GGAGTTTTCAGAACTGCTTTCAGTAGTGTTCAGTGGAAACAGAGGGTGTCTCCAGTT 2820
Db 2916 GGAGTTTTCAGAACTGCTTTCAGTAGTGTTCAGTGGAAACAGAGGGTGTCTCCAGTT 2975
Qy 2821 TGGAGAAAAGGAGGTTCCAGAGTAGATTTTTCAGTAACTCAATTCGTAAAGGAATCTTG 2880
Db 2976 TGGAGAAAAGGAGGTTCCAGAGTAGATTTTTCAGTAACTCAATTCGTAAAGGAATCTTG 3035
Qy 2881 GACTTTGAGCCTTAATGATATTTTGGAGAGACAGATCACTTTGGATGATTTAGTTG 2940
Db 3036 GACTTTGAGCCTTAATGATATTTTGGAGAGACAGATCACTTTGGATGATTTAGTTG 3095
Qy 2941 AGATGGGCAACAGGAGCTGAAAGGAGATTGGAATCAATGCTTATGGAATAGGCAAAAC 3000
Db 3096 AGATGGGCAACAGGAGCTGAAAGGAGATTGGAATCAATGCTTATGGAATAGGCAAAAC 3155
Qy 3001 TAAATTAAGGAGTCAGAGACTTATCTCGGACAAAGGCTTTAAACCATATTTAACTT 3060
Db 3156 TAAATTAAGGAGTCAGAGACTTATCTCGGACAAAGGCTTTAAACCATATTTAACTT 3215
Qy 3061 TGACACCTCTGCTAGTGAAACAAATCTTATAGATCTGCTCTCATGATAAGAGTTTC 3120
Db 3216 TGACACCTCTGCTAGTGAAACAAATCTTATAGATCTGCTCTCATGATAAGAGTTTC 3275
Qy 3121 AGCTGTGTGAGGAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAG 3180
Db 3276 AGCTGTGTGAGGAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAG 3335
Qy 3181 GTGGAAATCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTAT 3240
Db 3336 GTGGAAATCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTAT 3395
Qy 3241 GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAACCAACCAATGCAATG 3300
Db 3396 GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAACCAACCAATGCAATG 3455
Qy 3301 AACGAATGCTATTTCATGGGCTCTCTTTGTAATGCAATTTATCCACAAAGGCTTTGATG 3360
Db 3456 AACGAATGCTATTTCATGGGCTCTCTTTGTAATGCAATTTATCCACAAAGGCTTTGATG 3515

Qy 3361 AAAGCATGCGTACATAGGTGGTATGTTTGAGCTGGCATTTATTTTGCTGAAAACTCTT 3420
Db 3516 AAAGCATGCGTACATAGGTGGTATGTTTGAGCTGGCATTTATTTTGCTGAAAACTCTT 3575
Qy 3421 CCAAAAGCAATCAATATGATATGGAATTTGAGAGGATCTGGGTGTCAGATTCAAAAG 3480
Db 3576 CCAAAAGCAATCAATATGATATGGAATTTGAGAGGATCTGGGTGTCAGATTCAAAAG 3635
Qy 3481 ACAGATCTTGTACATTTGCCACAGGAGCTGCTTTTTCGGGGTAACCTTTGGGAAAGT 3540
Db 3636 ACAGATCTTGTACATTTGCCACAGGAGCTGCTTTTTCGGGGTAACCTTTGGGAAAGT 3695
Qy 3541 CTTTCTGTCAGTTCAGTGTCAATGGAATTTGCAATTTCTCTCCAGGTCATCACTCAGTCA 3600
Db 3696 CTTTCTGTCAGTTCAGTGTCAATGGAATTTGCAATTTCTCTCCAGGTCATCACTCAGTCA 3755
Qy 3601 CTGTAGGCCCAGTGTAAATGGCCCTAGCATTTAGTGAATATGTTTATACAGAGGAGAAC 3660
Db 3756 CTGTAGGCCCAGTGTAAATGGCCCTAGCATTTAGTGAATATGTTTATACAGAGGAGAAC 3815
Qy 3661 AGGCTTATCTGAGTATTTAAATTTACTTACCAGATTTATGAGGCTTGAAGGTATGTCGATG 3720
Db 3816 AGGCTTATCTGAGTATTTAAATTTACTTACCAGATTTATGAGGCTTGAAGGTATGTCGATG 3875
Qy 3721 GATAAATAGTATTTTAAAGAACTAAATTCCTCACTGAACCTTAAATCATCAAAAGCAGCAGTG 3780
Db 3876 GATAAATAGTATTTTAAAGAACTAAATTCCTCACTGAACCTTAAATCATCAAAAGCAGCAGTG 3935
Qy 3781 GCCTCTACGTTTTACTCCTTTGCTGAAAAAAA 3813
Db 3936 GCCTCTACGTTTTACTCCTTTGCTGAAAAAAA 3968

RESULT 2

US-11-266-748A-23602
; Sequence 23602, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 23602
; LENGTH: 3815
; TYPE: DNA
; ORGANISM: Homo Sapiens

Query Match 97.6%; Score 3724.8; DB 8; Length 3815;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 3726; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Qy	86	GGATCCGGTGA	CAGCAGGAGC	CAAGCGGCCCGG	CCCTGAGCGCGTCTTCTCCGGGGG 145
Db	1	GGATCCGGTGA	CAGCAGGAGC	CAAGCGGCCCGG	CCCTGAGCGCGTCTTCTCCGGGGG 60
Qy	146	CCTCGCCCTCT	GTCTGCGGGGCG	GGGCTCTCTGCT	CGGGTGTGCGGCTGTGCTGGC 205
Db	61	CCTCGCCCTCT	GTCTGCGGGGCG	GGGCTCTCTGCT	CGGGTGTGCGGCTGTGCTGGC 120
Qy	206	TGTGGCGCGCC	CAGGATCATG	TGCGGGTCCGCG	CGCGCGGAGCGGCTCGC 265
Db	121	TGTGGCGCGCC	CAGGATCATG	TGCGGGTCCGCG	CGCGCGGAGCGGCTCGC 180
Qy	266	GAGCGCGCGCC	CGAGCGGTG	AGCGCGCGCG	CGCGCGGAGCGGCTCGC 325
Db	181	GAGCGCGCGCC	CGAGCGGTG	AGCGCGCGCG	CGCGCGGAGCGGCTCGC 240
Qy	326	CGGGGACGTGA	ACGAGCTG	GTGAGCGCTG	AGAGGTGAACGCCGAC 385
Db	241	CGGGGACGTGA	ACGAGCTG	GTGAGCGCTG	AGAGGTGAACGCCGAC 300
Qy	386	GGCGGCGAGAA	ATCCACCCGCT	GCACCTCGCG	CGAGGTTTGGCGGGAAGCGTAGT 445
Db	301	GGCGGCGAGAA	ATCCACCCGCT	GCACCTCGCG	CGAGGTTTGGCGGGAAGCGTAGT 360
Qy	446	TGAATATTTGCT	TGAGATGGT	GCAATGTCT	CAAGCAGCTGATGGGGCCCTTATTC 505
Db	361	TGAATATTTGCT	TGAGATGGT	GCAATGTCT	CAAGCAGCTGATGGGGCCCTTATTC 420
Qy	506	TCCTCATAGTC	ATGCTTTTGG	TGATGCTG	GAAGTAGTCAATCTCTTTTGCACATGG 565
Db	421	TCCTCATAGTC	ATGCTTTTGG	TGATGCTG	GAAGTAGTCAATCTCTTTTGCACATGG 480
Qy	566	TGCAGACCCCA	ATGCTGAGAT	AAATGGAATTA	TACTCTCCATGAAGCTGCAATTTAA 625
Db	481	TGCAGACCCCA	ATGCTGAGAT	AAATGGAATTA	TACTCTCCATGAAGCTGCAATTTAA 540
Qy	626	AGGAAGATTGAT	GTGTGCTGTT	ACAGCATGG	AGCTGAGCCCAACCATCCGAAA 685
Db	541	AGGAAGATTGAT	GTGTGCTGTT	ACAGCATGG	AGCTGAGCCCAACCATCCGAAA 600
Qy	686	TACAGATGGA	AGGACAGAT	TGATTTAG	CAGATCCATCTGCGCAAGAGTCTACTGG 745
Db	601	TACAGATGGA	AGGACAGAT	TGATTTAG	CAGATCCATCTGCGCAAGAGTCTACTGG 660
Qy	746	TGAATATAAGA	AGATGAATCT	TAGAAAGTGC	AGGAGTGGCAATGAAGAAAATGAT 805
Db	661	TGAATATAAGA	AGATGAATCT	TAGAAAGTGC	AGGAGTGGCAATGAAGAAAATGAT 720
Qy	806	GGCTCTACTCA	CACCATTAAT	GTCAACTGCC	CAAGTATGAGCAAAAGTCAACTCC 865
Db	721	GGCTCTACTCA	CACCATTAAT	GTCAACTGCC	CAAGTATGAGCAAAAGTCAACTCC 780
Qy	866	ATTACATTTGC	CAGCAGATTA	ACAGATTAAG	ATTTGATAGCTGTATCTGCAACATGG 925
Db	781	ATTACATTTGC	CAGCAGATTA	ACAGATTAAG	ATTTGATAGCTGTATCTGCAACATGG 840
Qy	926	AGCTGATGTCA	TGTAAGATAA	AGGTGATCT	TGTACCATTTACACAATGCTGTCTTA 985
Db	841	AGCTGATGTCA	TGTAAGATAA	AGGTGATCT	TGTACCATTTACACAATGCTGTCTTA 900
Qy	986	TGGTCATTATG	AAGTAACTTT	TGGTCAAG	CATGGTCCCTGTGTAAATGCAATGGA 1045
Db	901	TGGTCATTATG	AAGTAACTTT	TGGTCAAG	CATGGTCCCTGTGTAAATGCAATGGA 960
Qy	1046	CTTGTGGCAAT	TCACTCTCTT	CATGAGG	AGCTTCTAAGAACAGGGTGAAGTATGTT 1105
Db	961	CTTGTGGCAAT	TCACTCTCTT	CATGAGG	AGCTTCTAAGAACAGGGTGAAGTATGTT 1020
Qy	1106	TCCTCTCTTAA	GTATGTG	CAGACCCCA	CACTGCTCAATTTGTCAATAAAGTGCTAT 1165
Db	1021	TCCTCTCTTAA	GTATGTG	CAGACCCCA	CACTGCTCAATTTGTCAATAAAGTGCTAT 1080

Qy	1166	AGACTTGGCTCC	CACACACAGCT	TAAAGAAAG	ATTAGCATATGAATTTAAAGCCACTC 1225
Db	1081	AGACTTGGCTCC	CACACACAGCT	TAAAGAAAG	ATTAGCATATGAATTTAAAGCCACTC 1140
Qy	1226	GTGTGCTCAAG	CTGCGAGAG	CTGATGTTA	CTCGAATCAAAAAACATCTCTCTGGA 1285
Db	1141	GTGTGCTCAAG	CTGCGAGAG	CTGATGTTA	CTCGAATCAAAAAACATCTCTCTGGA 1200
Qy	1286	AATGGTGAATTT	CAAGCATCTC	CAACACATG	AAACAGCAATTCGATGTGCTGCAATC 1345
Db	1201	AATGGTGAATTT	CAAGCATCTC	CAACACATG	AAACAGCAATTCGATGTGCTGCAATC 1260
Qy	1346	TCATATCCCAA	AGAAAGCAAA	TATGTGAAC	TGTGCTAAGAAAAGGAGCAACATCAA 1405
Db	1261	TCATATCCCAA	AGAAAGCAAA	TATGTGAAC	TGTGCTAAGAAAAGGAGCAACATCAA 1320
Qy	1406	TGAAAGACTTAA	AGAAATTTCT	GACTCTCTC	TCGACGTGGCATCTGAGAAAGCTCAATGA 1465
Db	1321	TGAAAGACTTAA	AGAAATTTCT	GACTCTCTC	TCGACGTGGCATCTGAGAAAGCTCAATGA 1380
Qy	1466	TGTTGTTGAAG	TAGTGGTGA	AAACATGA	AGCAAGGTTAATGCTCTGATTAATCTGTC 1525
Db	1381	TGTTGTTGAAG	TAGTGGTGA	AAACATGA	AGCAAGGTTAATGCTCTGATTAATCTGTC 1440
Qy	1526	GACTTCTCTAC	ACAGAGCTGC	ATATTGTG	TCATCTCAACAACTGCCCTCTCTGAG 1585
Db	1441	GACTTCTCTAC	ACAGAGCTGC	ATATTGTG	TCATCTCAACAACTGCCCTCTCTGAG 1500
Qy	1586	CTATGGGTGAT	CTTAAACAT	TATATCCCT	TCAGGGCTTTACTGCTTTACAGATGGGAAA 1645
Db	1501	CTATGGGTGAT	CTTAAACAT	TATATCCCT	TCAGGGCTTTACTGCTTTACAGATGGGAAA 1560
Qy	1646	TGAAATGTAC	AGCACTCTC	CAAGAGG	GTATCTCATTAGGTAAATTCAGAGGCAGAC 1705
Db	1561	TGAAATGTAC	AGCACTCTC	CAAGAGG	GTATCTCATTAGGTAAATTCAGAGGCAGAC 1620
Qy	1706	ACAAATTCCTG	GAAGCTGCA	AAAGGCTG	GAGATGTGCAAACTGTAAAAAACCTGTACTGT 1765
Db	1621	ACAAATTCCTG	GAAGCTGCA	AAAGGCTG	GAGATGTGCAAACTGTAAAAAACCTGTACTGT 1680
Qy	1766	TCAGAGTGTCA	ACTGACAG	ACATTTGA	AGGCGTCACTACACACTTCATTTTGACGC 1825
Db	1681	TCAGAGTGTCA	ACTGACAG	ACATTTGA	AGGCGTCACTACACACTTCATTTTGACGC 1740
Qy	1826	TGGGTATAACA	GAGTGTCC	GTGGTGG	AAATATCTGCTACAGATGGAGCTGATGTCATGC 1885
Db	1741	TGGGTATAACA	GAGTGTCC	GTGGTGG	AAATATCTGCTACAGATGGAGCTGATGTCATGC 1800
Qy	1886	TAAAGATAAAG	GAGGCTTGT	ACCTTTTGC	CAATGCAATGCAATGCTTTATGCAATTTAGAT 1945
Db	1801	TAAAGATAAAG	GAGGCTTGT	ACCTTTTGC	CAATGCAATGCAATGCTTTATGCAATTTAGAT 1860
Qy	1946	TGCAGAACTCT	TTGTTAAACA	TGAGCAG	TAGTTAATGTAGCTGATTTATGAAAATTTAC 2005
Db	1861	TGCAGAACTCT	TTGTTAAACA	TGAGCAG	TAGTTAATGTAGCTGATTTATGAAAATTTAC 1920
Qy	2006	ACCTTTTACAT	GAAGCAGC	AGCAAAAG	AAATATGAATAATTTGCAAACTTCCTGCTCCAGCA 2065
Db	1921	ACCTTTTACAT	GAAGCAGC	AGCAAAAG	AAATATGAATAATTTGCAAACTTCCTGCTCCAGCA 1980
Qy	2066	TGGTGACAGCT	TACCAAAAA	AAACAGGG	ATGGAATACCTCTTTGGATCTTGTTTAAGA 2125
Db	1981	TGGTGACAGCT	TACCAAAAA	AAACAGGG	ATGGAATACCTCTTTGGATCTTGTTTAAGA 2040
Qy	2126	TGGAGATACAG	ATATCAAG	ATCTGCT	TAGGGAGATGCACTTTGTAGATGCTGCCAA 2185
Db	2041	TGGAGATACAG	ATATCAAG	ATCTGCT	TAGGGAGATGCACTTTGTAGATGCTGCCAA 2100
Qy	2186	GAAGGGTGT	TTAGCCAG	AGTGAAGA	AGTGTCTCTCTGATTAATGTAAATTCGCCGGA 2245
Db	2101	GAAGGGTGT	TTAGCCAG	AGTGAAGA	AGTGTCTCTCTGATTAATGTAAATTCGCCGGA 2160

QY 2246 TACCAAGGACAGATCAACACCTTTTACATTTAGCAGCTGGTTATATAATTTAGAAGT 2305
 Db 2161 TACCCAAAGGACAGATCAACACCTTTTACATTTAGCAGCTGGTTATATAATTTAGAAGT 2220
 QY 2306 TGCAGAGTATTTGTTTAAACACGAGCTGATGTGAATGCCCCAAGAACGAGGACTTAT 2365
 Db 2221 TGCAGAGTATTTGTTTAAACACGAGCTGATGTGAATGCCCCAAGAACGAGGACTTAT 2280
 QY 2366 TCCCTTACATATGAGCATCTTACGGGCATGTAGATGTAGCAGCTCTACTAATAAAGTA 2425
 Db 2281 TCCCTTACATATGAGCATCTTACGGGCATGTAGATGTAGCAGCTCTACTAATAAAGTA 2340
 QY 2426 TAATGATGTGTCAATGCCCACGACAAATGGGCTTTTACACCTTTTGCACGAGCAGCCCA 2485
 Db 2341 TAATGATGTGTCAATGCCCACGACAAATGGGCTTTTACACCTTTTGCACGAGCAGCCCA 2400
 QY 2486 AAAGGAGCGAACACAGCTTTGTGTTGTGTAGCCCATGAGCTGACCCGACTCTTAA 2545
 Db 2401 AAAGGAGCGAACACAGCTTTGTGTTGTGTAGCCCATGAGCTGACCCGACTCTTAA 2460
 QY 2546 AAATCAGGAGGACAAACACCTTTAGATTTTTCAGGGATGATGTCAGGCTCTTCT 2605
 Db 2461 AAATCAGGAGGACAAACACCTTTAGATTTTTCAGGGATGATGTCAGGCTCTTCT 2520
 QY 2606 GACAGCAGCCATGCCCCATCTGCTCTGCCCTTTTACAGCCCTCAAGTCTCAATGG 2665
 Db 2521 GACAGCAGCCATGCCCCATCTGCTCTGCCCTTTTACAGCCCTCAAGTCTCAATGG 2580
 QY 2666 TGTGAGAGCCGAGGAGCCATGCGAGATGCTCTCTTCAAGTCCATCTAGGCCCATCAAG 2725
 Db 2581 TGTGAGAGCCGAGGAGCCATGCGAGATGCTCTCTTCAAGTCCATCTAGGCCCATCAAG 2640
 QY 2726 CCTTTCTGAGCAGCAGCTTTTGACAACTTATCTGGAGTTTTCAGAACTGTCTTCAGT 2785
 Db 2641 CCTTTCTGAGCAGCAGCTTTTGACAACTTATCTGGAGTTTTCAGAACTGTCTTCAGT 2700
 QY 2786 AGTTAGTTCAAGTGAACAGAGGCTTCCAGTTTGGAGAAAAAGGAGTTCCAGGAGT 2845
 Db 2701 AGTTAGTTCAAGTGAACAGAGGCTTCCAGTTTGGAGAAAAAGGAGTTCCAGGAGT 2760
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 QY 2906 TGAGAGAGACAGATCACTTTGGATGTATTAGTTGAGTGGGCGACAGGAGCTCAAGA 2965
 Db 2821 TGAGAGAGACAGATCACTTTGGATGTATTAGTTGAGTGGGCGACAGGAGCTCAAGA 2880
 QY 2966 GATTCGAATCAATGCTTATGGACATAGGCACAACTTAATTAAGGAGTGCAGAGACTTAT 3025
 Db 2881 GATTCGAATCAATGCTTATGGACATAGGCACAACTTAATTAAGGAGTGCAGAGACTTAT 2940
 QY 3026 CTCGGGACAAAGGCTTTAAACCCATATTTAACTTTGAAACCTCTGGTAGTGGAACTAT 3085
 Db 2941 CTCGGGACAAAGGCTTTAAACCCATATTTAACTTTGAAACCTCTGGTAGTGGAACTAT 3000
 QY 3086 TCTTATAGATCTGCTCTGTATGATTAAGAGTTTCACTGTGGAGGAGAGATGCAAG 3145
 Db 3001 TCTTATAGATCTGCTCTGTATGATTAAGAGTTTCACTGTGGAGGAGAGATGCAAG 3060
 QY 3146 TACAGTTCCAGAGCAGAGATGGAGTCTATGAGTGAATCTTCAACAGATACAATAT 3205
 Db 3061 TACAGTTCCAGAGCAGAGATGGAGTCTATGAGTGAATCTTCAACAGATACAATAT 3120
 QY 3206 TCTCAAGATTCAAGAGTTTGTAAACAAGAAAACTATGGGAAAGATACACTCACCGGAGAA 3265
 Db 3121 TCTCAAGATTCAAGAGTTTGTAAACAAGAAAACTATGGGAAAGATACACTCACCGGAGAA 3180
 QY 3266 AGAAGTTCTGAAGAAAAACCAACCATGCGCAATGAAGTCTATTTTCATGGGTCTCC 3325
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 QY 3326 TTTTGTGAATGCAATTTATCCACAAGGCTTTGATGAAGGCGATGCGTACATAGGTGGTAT 3385

Db 3241 TTTTGTGAATGCAATTTATCCAAAGGCTTTGATGAAGGCGATGCTACATAGGTGGTAT 3300
 QY 3386 GTTTGGAGCTGGCATTTATTTTGTCTGAAAACCTTTCCAAAAGCAATCAATATGATATGG 3445
 Db 3301 GTTTGGAGCTGGCATTTATTTTGTCTGAAAACCTTTCCAAAAGCAATCAATATGATATGG 3360
 QY 3446 AATTGGAGGAGGTACTGGGTGTCCAGTTTCAAAAAGACAGATCTTGTTCATTTGCCACAG 3505
 Db 3361 AATTGGAGGAGGTACTGGGTGTCCAGTTTCAAAAAGACAGATCTTGTTCATTTGCCACAG 3420
 QY 3506 GCAGTGTCTTTTGGCCGGGTAACTTGGGAAAGTCTTTCTCGAGTTTCAGTGCATGAA 3565
 Db 3421 GCAGTGTCTTTTGGCCGGGTAACTTGGGAAAGTCTTTCTCGAGTTTCAGTGCATGAA 3480
 QY 3566 AATGGCACAATCTCTCCAGGTCTCACTCAGTCACTGTTAGGCGCCAGTGTAAATGGCCT 3625
 Db 3481 AATGGCACAATCTCTCCAGGTCTCACTCAGTCACTGTTAGGCGCCAGTGTAAATGGCCT 3540
 QY 3626 AGCATTAGTCAATATGTTTATTACAGAGGAGAAACAGGCTTTATCTGAGTATTTAATTAC 3685
 Db 3541 AGCATTAGTCAATATGTTTATTACAGAGGAGAAACAGGCTTTATCTGAGTATTTAATTAC 3600
 QY 3686 TTACAGATTTAGGCGCTGAAAGGTATGTTGATGATGATGATGATGATGATGATGATGAT 3745
 Db 3601 TTACAGATTTAGGCGCTGAAAGGTATGTTGATGATGATGATGATGATGATGATGATGAT 3660
 QY 3746 ATTCCACTGAACCTTAATATCATCAAGCAGAGTGGCGCTCTACGTTTACTCTTTGCTG 3805
 Db 3661 ATTCCACTGAACCTTAATATCATCAAGCAGAGTGGCGCTCTACGTTTACTCTTTGCTG 3720
 QY 3806 AAAAAAAA 3813
 Db 3721 AAAAAAAA 3728

RESULT 3
 US-11-266-748A-29428
 ; Sequence 29428, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcription Microarray Technology and
 ; TITLE OF INVENTION: Methods of Using the Same
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266.748A
 ; CURRENT FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 29428
 ; LENGTH: 4134
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-29428

Db 2607 AAGGTGGTAAATTCCTCTTCAATATCGCGCATCTTATGGGCATGTTGACATAGCGCT 2666
Qy 2412 CTACTAATAAGTATAATGCAATGCTCAATGCGGCAATGCGCTTTCACACCTTTG 2471
Db 2667 TTAATGATAAATAACAACGCTGTGTAATGCAACAGATAAGTGGCGTCTTACTCCCTC 2726
Qy 2472 CACGAAGCAGCCCAAAAGGAGCAACACAGCTCTTGTCTTGTCTAGCCCATGGAGCT 2531
Db 2727 CATGAAGCAGCCCAAAAGGAGGACGAGCTGTGCGCCCTCTCTAGCGCATGTCGA 2786
Qy 2532 GACCCGACTCTTAAATAACAGGAAGCAAAACCTTTAGATTTAGTTTTCAGCGGATGAT 2591
Db 2787 GACCCCAACCATGAAGAACAGGAAGGCGCAGCGCTCTGGATCTGGCAACAGCTCAGCAT 2846
Qy 2592 GTGAGGCTCTTCTGACAGCAGCATGCCCATCTGCTCTGCGCTCTTGTGTACAGGCT 2651
Db 2847 ATCAGAGCTTTGCTGATGATGCCATGCCCGGAGGCGCTTACCTACCTGTTTAAACCT 2906
Qy 2652 CAAGTGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGCGAGATGCTCTCTTTCAGGTCCA 2711
Db 2907 CAGG-----CTACTGTAGTGAGTGCCTCTCTGATCTCACCAGCA 2945
Qy 2712 TCTAGCCCAATCAAGCTTTCTGCGCAGCAGTCTTGACAACTTATCTGGGAGTTTTCOA 2771
Db 2946 TCCACCCCTCTCTGCTCTCGGCTGCGCAGCAGCATAGACAACTCACTGGCCCTTTAGCA 3005
Qy 2772 GAACTGCTCTCAGTAGTAGTTCAAGTGGAAACAGAGGCTGCTTCAGTTTGGAGAAAG 2831
Db 3006 GAGTTGGCGGTAGGAGGAGCCCTCAATGCGAGGATGCGCGCGGCAACAGAAAGGAG 3065
Qy 2832 -----GAGGTTTCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGAACTCTCGACTT 2885
Db 3066 GAAGAGAGTTGCTGGTCTTGACATGATATCAGCCCAATTTCTAAAGAGCTTGGCCTT 3125
Qy 2886 GAGCACCTTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTTAGTTGAGATG 2945
Db 3126 GAACACCTTCGGGATATCTTTGAAACAGAACAGATTAACATACTAGATGTGTGGCTGATG 3185
Qy 2946 GGGCACAGGAGCTCAAGAGATTGGATCAATGCTTATGGACATAGGACACAACTAAT 3005
Db 3186 GGTCAATGAAGAGTTGAAGAATAGGCATCAATGATATGGGCACCGCCACAAATTAATC 3245
Qy 3006 AAAGAGTTCGAGAGACTTATCTCCGCAACAAAGGTCTTAAACCCATATTTAACTTTGAAC 3065
Db 3246 AAAGAGTAGAAGACTCTTAGGTGCAACAAAGGCAACCACTCTTATTTGACTTTTAC 3305
Qy 3066 ACCTCTGGTAGTGGAACTTTATAGATCTGTCTCTGATGATAAGAGTTTCAGTCT 3125
Db 3306 TGTGTTAATCAGGGAACGATTTTGTGGATCTTGTCTCAGAGATTAAGAAATATCAGTCA 3365
Qy 3126 GTGGAGGAGAGATGCAAGATACAGTTGAGAGACAGAGATGGAGTTCATGCGAGTGA 3185
Db 3366 GTGGAAGAGAGATGCAAGATACAGTTTGTGAGAACAGAGATGGTGAATGCTGGCGGC 3425
Qy 3186 ATCTTTCAACAGATACAAATTTCTCAAGATTTCAGAGTTTGAAGAGTTTGAACAACTATGGGAA 3245
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Qy 3306 ATGCTATTTCATGGGTCTCTTTTGTGAATGCAATTTCCAAAGGCTTGTGATGAAGG 3365
Db 3546 ATGTTGTTTCATGGTCTCTTTCTTCAATTAATGTCATTTATTAAGGGTGTGATGAGCGA 3605
Qy 3366 CATGCGTACATAGTGGTATGTTTGGAGCTGCAATTTATTTTGTGAAACCTCTTCCAAA 3425
Db 3606 CATGCAATACATAGGAGGATGTTTGGGCGCGGATTTATTTTGTGAAACCTCTTCAAAA 3665
Qy 3426 AGCAATCAATATGTATGGAAATGGAGGAGTACTGGGTGCTCAGTTTCACAAAGACAGA 3485
Db 3666 AGCAACCAATATGTTTATGGAATTCGAGGAGGAAACAGGCTGCCCTTACACAAAGCAGG 3725

Qy 3486 TCTTGTACATTTGCGCAGGAGCTGCTCTTTTGGCCGGTAACCTTGGGAAAGTCTTTC 3545
Db 3726 TCATGCTATATATGTCACAGACAAATGCTCTTCTGTAGAGTGACCTTGGGAAATCCTTT 3785
Qy 3546 CTGAGTTCACTGCAATGAAATGGCAATTTCTCTCCAGGTCACTCACTAGTCACTGCT 3605
Db 3786 CTGAGTTTAGCACCATGAAATGGCCAGCGCTCCAGGGCACCACTCACTAGTCACTGCT 3845
Qy 3606 AGGCCAGTGTAAATGGCTAGCATTAAGTCAATATGTTTATACAGAGGAGAACAGCT 3665
Db 3846 AGACCGAGCTCAATGGGCTGGCATATGCTGAATATGTCATCTACAGAGGAGAACAGCA 3905
Qy 3666 TATCTGAGTATTTAAATTTACTTACAGATTTAGGCGCTGAAG 3708
Db 3906 TACCAGAGTATCTTATCACTTACCAGATCATGAAGCCAGAG 3948

RESULT 4
US-11-266-748A-22929
; Sequence 22929, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266.748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22929
; LENGTH: 8901
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-22929

Query Match 47.1%; Score 1796.4; DB 8; Length 8901;
Best Local Similarity 72.5%; Pred. No. 0;
Matches 2366; Conservative 0; Mismatches 871; Indels 27; Gaps 2;

Qy 451 ATTTGCTTTCAGAAATGGTGCAATGTCACAGCAGTATGGGGGCTTATTCCTCTTC 510
Db 2 ACTTACTACAGATGGTGTCTAATGTCACGCTCGTGATGATGGAGTCTCATCCGCTTC 61
Qy 511 ATATGCAATGCTCTTTTGGTCACTGAGTAGTCAATCTCTTTTGGACATGCTGCG 570
Db 62 ATATGCTGTTCTTTTGGCCATGCTGAGTGTGAGTCTGTTATTTGCGCAAGAGCTG 121
Qy 571 ACCCAATGCTCGAGATAATGGAAATATATCTCTCCATGAAGCTCAATTTAAAGAA 630
Db 122 ATCCAAATGCCAGGATTAACCTGGAACACTATACCTCTGATGAAGCTCTTATTAAGGA 181
Qy 631 AGATTGATGTTTGCATTTGCTGTTTACAGCATGGAGCTGAGCCCAACCAATCCGAATACAG 690

Db 182 AGATCGATGTGCTGCTGCTGCAGCAGCGAGCTGACCCAAACATTCGGAACTG 241
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691 ATGGAAGGACAGCATTTGGATTTAGCAGATCCATCTGCCAAAGCAGTGCCTTACTGGTGAAT 750
Db
242 ATGGGAATCAGCCCTGGACCTGGCAGATCCTTCAGCAAAAGCTGTCTTTACAGGTTGAAT 301
Qy
751 ATAGAAGATGAACCTTTAGAAAGTCCAGGAGTGCCAAATGAGAAATAATGATGCTC 810
Db
302 ACAAGAAGACGAACCTCTAGAAGCTCTAGGAGTGGTATGATGAAGAAATAATGATGCTT 361
Qy
811 TACTCACACCATTAATATGTCACCTGCCAGCAAGTGTATGGCAGAAAGTCAACTCCATTAC 870
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362 TACTGACTCTCTAATATGTAATGTCATGCGATGCGAGTGTATGGCGAAAGTGCAGCTCCCTTAC 421
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871 ATTTGGCAGCAGGATATAACAGAGTAAGATGTPACAGCTGTTACTGCAACATGAGAGCTG 930
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422 ATCTAGCAGCGGGCTACAACAGAGTTGGAATAGTTTCAGCTTCTTCTTCAGCATGGTCTG 481
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991 ATTATGAAGTAACGAACTTTTGGTCAAGCATGGTCTGTGTAAATGCAATGAGCTTGT 1050
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542 ATATGAAGTCAAGAACTGCTACTAAAGCATGAGAGCTTGTATGATGCCATGGATCTCT 601
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1051 GGCAATTCACCTCTTCATGAGCAGCTTCTAAGAACAGGGTTGAAGTATGTTCTCTTC 1110
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1111 TCITTAAGTTATGGTGAGACCCAAACACTGCTCAATTTGTCACAATAAAGTGCTATAGACT 1170
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662 TACTTAGCCATGGCGCTGATCCTACGTTAGTCAACTGCCCATGGCAAAAGTGTGTGGATA 721
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1231 TGCAGCTGCA CGAAGAGCTGATGTTACTCGAATCAAAAAACAFCTCTCTCTGGAATGG 1290
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782 TACAAGCAGCAGAGAAGCAGACTTAGCTAAAGTTAAATAAAACACTCGCTCTGGAAATCA 841
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1291 TGAATTTCAAGCTCTTCAACACATGAAACAGTATGCTTGGCTGCTGCATCTCCAT 1350
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1351 ATCCCAAAAGAAAGCAATAATGTGAATGTTGCTTAAGAAAGGAGCAAAACATCAATGAAA 1410
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1411 AGACTAAAGAAATCTTCACTCTCTGCAAGTGGCATCTGAGAAAGCTCATAAATGATTTG 1470
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1651 ATGTACAGCAACTCTCCAGAGGGTATCTCATTTAGTGAATTTACAGAGCAGACAGCAAT 1710
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1202 CAGTGCAGCAGATTTCTGAGTGAGATGACACCTATACGTACTTCTGATGTTGATTTATCGAC 1261
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1711 TGCCTGGAAGCTGCAAGGCTGGAGATGTCGAAACTGTAAAAAAACTGTGTACTGTTTCAGA 1770
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1262 TCTTAGAGGCATCTTAAGCTGGAGACTTGGAAACTGTGAGCAACTTTGAGCTCTCAAA 1321

Qy 1771 GTGTCAACTGCAGACATTTGAAGGGGTCAGTCTACACCACTTCATTTTGCAGCTGGT 1830
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Qy 1831 ATAAACAGAGTGTCCGTGGTGAATATCTGTACAGCATGAGCTGATGTGCATGCTCTAAAG 1890
Db 1382 ACAACCGGTGTCTGTGTAGAGTACTGTCTACACACGGTGCAGATGTCATGCCAAAG 1441
Qy 1891 ATAAAGGAGGCTTGTACTCTTTGCACAAATGCTGTTCTTATGGACATTTATGAAGTTGAG 1950
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Qy 1951 AACTTCTTGTAAACATGGAGCAGTAGTTAAATGCTAGTGAATTTATGAAATTTTACACCTT 2010
Db 1502 AGCTTTTAGTAAGGCATGGGCTTCTGTCAATGTGGCGGACTTATGGAATTTTACCCCTC 1561
Qy 2011 TACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGGT 2070
Db 1562 TCCATGAGCAGCAGCTTAAAGGAAAGTATGAAATCTGCAAGCTCCTTTTAAACATGGAG 1621
Qy 2071 CAGACCTTACCAAAAAAACAAGGATGGAATACTCCTTTGGATCTTGTTTAAAGATGGAG 2130
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Qy 2311 AGTATTTGTTACAACGAGCTGATGTGAATGCCCAAGCAAAAGGAGGACTTTATTCCTT 2370
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Qy 2611 CAGCCATGCCCCCATCTGCTCTGCTCTTGTTCATAAGCCTCAAGTGTCTAATGGTGTGA 2670
Db 2162 ATGCCATGCCCCCAGAGGCTTACCTACCTGTTTAAAACTCAGG----- 2206
Qy 2671 GAAGCCAGGAGCCATGCGAGATGCTCTCTTTCAGGTCCATCTAGCCCACTCAAGCCCTT 2730
Db 2207 -----CTACTGTAGTGAAGTGCCTCTCTGATCTCACAGCATCCACCCCTCTCGCTCT 2260
Qy 2731 CTGAGCCAGCAGCTCTTGCAAACTTATCTGGAGTGTCTTTCAGAACTGTCTTCAGTAGTTA 2790
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Db 2321 CCTCCAAATGAGGGGATGGCGCGCGGAAACAGAAAGGAAGGAGAGAGTTGCTGTC 2380


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QY 2845 TAGATTTAGCAATACTCAATTCGTAAGAAATCTTGGACTTGAGCACTTAATGGATATAT 2904
Db 2381 TTGACATGAATCAGCCAAATTTCTAAAGAGCTTGGCTTGAACACACTTCGGATATCT 2440
QY 2905 TTGAGAGAGACAGATCACTTTGGATGATTAATTTGAGATGGGACACAGAGCTGAGG 2964
Db 2441 TTGAACACAGAACAGATTAACACTAGATGTTTGGCTGATATGGGTATGAAGAGTTGAAG 2500
QY 2965 AGATTGGAATCAATGCTTATGACATAGGCACAACTAATTAAGGAGTCGAGAGACTTA 3024
Db 2501 AATAGGCATCAATGATGATGGCCACCGCCCAAAATTAATCAAGAGTAGAAGACTCT 2560
QY 3025 TCTCCGAGCAACAGAGCTTTAAACCATATTTAACTTTGAACACTCTCTGGTAGTGAACAA 3084
Db 2561 TAGGTGGACAAACAGGACCAATCTTATTTGACTTTTCACTGTGTAACTAGGGAACGA 2620
QY 3085 TTTCTATAGATCTCTCTCTGATGATTAAGAGTTTTCAGTCTGTGGAGGAGAGATGCAA 3144
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QY 3145 GTACAGTTTCGAGAGCACAGAGATGAGGTCATGACAGTGGAACTTTCAACAGATACAATA 3204
Db 2681 GTACTATTTCGAGAACACAGAGATGTTGTAATGCTGGCGGATCTTCAACAGATACAATG 2740
QY 3205 TTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATGGGAAAGATACACTTCAACGAGAA 3264
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Db 2801 AGGAAGTCTCTGAGGAGAAATCAACCACTCAACATGAGCGCATGTTGTTTCATGGTTCTC 2860
QY 3325 TTTTGTGATGCAATTAATCCAAAGGCTTTGATGAAAGGCATCGTACATAGTGGTA 3384
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QY 3625 TAGCATAGCTGAATATGTTATTTTACAGAGGAAACAGGCTTATCTTCAATTTAATTA 3684
Db 3161 TGGCATATGCTGAATATGCTATCTACAGAGGAAACAGGCTATCCAGAGATCTTATCA 3220
QY 3685 CTTACAGATTTATGAGGCTGAAG 3708
Db 3221 CTTACAGATTTATGAAGCGAAG 3244
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RESULT 5

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US-11-266-748A-251004
; Sequence 251004, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55915-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
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; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 251004
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-251004
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Query Match 17.4%; Score 663.8; DB 8; Length 675;
Best Local Similarity 99.0%; Pred. No. 1.3e-151;
Matches 568; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2436 GTCAATGCCAGCAAAATGGCTTTACACCTTTGCGACGAGCCAAAGGAGCA 2495
Db 1 GTCATGCCAGCAAAATGGCTTTACACCTTTGCGACGAGCCAAAGGAGCA 60
QY 2496 ACACAGCTTTGCTGCTTTGCTGAGCCATGAGCTGACCGACTCTTAAATCAGNA 2555
Db 61 ACACAGCTTTGCTGCTTTGCTGAGCCATGAGCTGACCGACTCTTAAATCAGNA 120
QY 2556 GGACAAACACCTTTAGATTTAGTTTACGGCTGATGTCAGCGCTCTTCTGACAGCAGCC 2615
Db 121 GGACAAACACCTTTAGATTTAGTTTACGGCTGATGTCAGCGCTCTTCTGACAGCAGCC 180
QY 2616 ATGCCCCCATCTGCTGCTGCTTCTGTTTACAGGCTCAAGTCTCAATGGTGTGAAGC 2675
Db 181 ATGCCCCCATCTGCTGCTGCTTCTGTTTACAGGCTCAAGTCTCAATGGTGTGAAGC 240
QY 2676 CCAGAGCCACTGACAGATGCTCTCTTCAGGTCCATCAGCCCATCAAGCCTTTCTGCA 2735
Db 241 CCAGAGCCACTGACAGATGCTCTCTTCAGGTCCATCAGCCCATCAAGCCTTTCTGCA 300
QY 2736 GCCAGAGCTTTGACAACTTATCTGGGAGTTTTCAGAACTGTCTTCAGTAGTTAGTTCA 2795
Db 301 GCCAGAGCTTTGACAACTTATCTGGGAGTTTTCAGAACTGTCTTCAGTAGTTAGTTCA 360
QY 2796 AGTGGACAGAGGCTGCTTCCAGTTTGGAGAAAAGGAGGTTCCAGGAGTAGATTTAGC 2855
Db 361 AGTGGACAGAGGCTGCTTCCAGTTTGGAGAAAAGGAGGTTCCAGGAGTAGATTTAGC 420
QY 2856 ATAACCTCAATTCGTAAGGAATCTTGGACTTCAGACCTTAATGGATATATTTGAGAGAA 2915
Db 421 ATAACCTCAATTCGTAAGGAATCTTGGACTTCAGACCTTAATGGATATATTTGAGAGAA 480
QY 2916 CAGATCACTTTGGATGATTAATAGTTGAGATGGGACAGAGGAGCTGAAGAGATTCGAATC 2975
Db 481 CAGATCACTTTGGATGATTAATAGTTGAGATGGGACAGAGGAGCTGAAGAGATTCGAATC 540
QY 2976 AATGCTTATGACATAGGCAAACTAATTAAGGAGTCGAGAGACTTTATCTCCGACAA 3035
Db 541 AATGCTTATGACATAGGCAAACTAATTAAGGAGTCGAGAGACTTTATCTCCGACAA 600
QY 3036 CAAGGCTTTAAACCATATTTAACTTTGAACACCTCTGCTGAGTGGAAACAAATTTCTTATAGAT 3095
Db 601 CAAGGCTTTAAACCATATTTAACTTTGAACACCTCTGCTGAGTGGAAACAAATTTCTTATAGAT 660
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QY 3096 CTGCTCCTGATGAT 3110
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Db 661 CTGCTCCTGATGAT 675

RESULT 6
US-11-266-748A-311521/c
; Sequence 311521, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
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; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 311521
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-311521

Query Match 17.4%; Score 663.8; DB 8; Length 675;
Best Local Similarity 99.0%; Pred. No. 1.3e-151;
Matches 668; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2436 GTCATGCCAGGACAAATGGGCTTTTCACCTTTGCGAGAGCAGCCCAAAAGGAGCA 2495
| | | | | | | | | |
Db 675 GTCATGCCAGGACAAATGGGCTTTTCACCTTTGCGAGAGCAGCCCAAAAGGAGCA 616

QY 2496 ACACAGCTTTGTGCTTTGTGCTAGCCCATGAGCTGACCCGACTTTAAAAATCAGGAA 2555
| | | | | | | | | |
Db 615 ACACAGCTTTGTGCTTTGTGCTAGCCCATGAGCTGACCCGACTTTAAAAATCAGGAA 556

QY 2556 GGACAAACACCTTTAGATTTAGTTTTCAGGGATGATGTCAGGCTCTTCTGACAGCAGCC 2615
| | | | | | | | | |
Db 555 GGACAAACACCTTTAGATTTAGTTTTCAGGGATGATGTCAGGCTCTTCTGACAGCAGCC 496

QY 2616 ATGCCCCCATCTGCTCTGCCCTCTTGTTCACAGCCTCAAGTCTCAATGGTGTGAGAAGC 2675
| | | | | | | | | |
Db 495 ATGCCCCCATCTGCTCTGCCCTCTTGTTCACAGCCTCAAGTCTCAATGGTGTGAGAAGC 436

QY 2676 CCAGGAGCCATGCGAGATGCTCTCTTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGCA 2735
| | | | | | | | | |
Db 435 CCAGGAGCCATGCGAGATGCTCTCTTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGCA 376

QY 2736 GCCAGCAGCTCTGCAACTATCTGGAGTCTTTCAGAACTGCTCTCAGTAGTAGTTCA 2795
| | | | | | | | | |
Db 375 GCCAGCAGCTCTGCAACTATCTGGAGTCTTTCAGAACTGCTCTCAGTAGTAGTTCA 316

QY 2796 AGTGAACAGAGGGTGTCTTCCAGTTTGGAGAAAAGGAGTTTCCAGGAGTAGATTTTAC 2855
| | | | | | | | | |
Db 315 AGTGAACAGAGGGTGTCTTCCAGTTTGGAGAAAAGGAGTTTCCAGGAGTAGATTTTAC 256
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QY 2856 ATAACTCAATTCGTAAGGAATCTTGACCTTGAGCACCTAATGATATATTTTGAGAGAA 2915
| | | | | | | | | |
Db 255 ATAACTCAATTCGTAAGGAATCTTGACCTTGAGCACCTAATGATATATTTTGAGAGAA 196

QY 2916 CAGATCACCTTTGGATGCTATTAGTTGAGATGGGGCAACAAGAGCTGAAGGAGATTGGAATC 2975
| | | | | | | | | |
Db 195 CAGATCACCTTTGGATGCTATTAGTTGAGATGGGGCAACAAGAGCTGAAGGAGATTGGAATC 136

QY 2976 AATGCTTATGGACATAGGCACAACTAATTAAGGAGTGGAGAGCTTATCTCCGGACAA 3035
| | | | | | | | | |
Db 135 AATGCTTATGGACATAGGCACAACTAATTAAGGAGTGGAGAGCTTATCTCCGGACAA 76

QY 3036 CAAGGCTTTAAACCCATATTTAACTTTGAACACCTCTGCTAGTGGAAACAATTTCTATAGAT 3095
| | | | | | | | | |
Db 75 CAAGGCTTTAAACCCATATTTAACTTTGAACACCTCTGCTAGTGGAAACAATTTCTATAGAT 16

QY 3096 CTGCTCCTGATGAT 3110
| | | | | | | | | |
Db 15 CTGCTCCTGATGAT 1

RESULT 7
US-11-266-748A-99554
; Sequence 99554, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99554
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-99554

Query Match 14.9%; Score 570; DB 8; Length 594;
Best Local Similarity 99.7%; Pred. No. 8.9e-129;
Matches 592; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 3213 ATTCAGAAGGTTTGTAAACAAG-AACTATGGGAAAGATACACTCACCGG-AGAAAAAG 3270
| | | | | | | | | |
Db 1 ATTCAGAAGGTTTGTAAACAAGAACTATGGGAAAGATACACTCACCGGAAAGAAAG 60

QY 3271 TTTCTGAAGAAAAACCAACCATGCGCAATGAACGAATGCTATTTTCATGGGTCTCTTTTG 3330
| | | | | | | | | |
Db 61 TTTCTGAAGAAAAACCAACCATGCGCAATGAACGAATGCTATTTTCATGGGTCTCTTTTG 120

QY 3331 TGAATGCAATTTATCCCAAAAGGCTTTGATGAAGGCAATGCTACATAGGTGGTATGTTG 3390
| | | | | | | | | |
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Db 121 TGAATGCAATTAATCCACAAGGCTTTGATGAAAGGCATGCGGTACATAGGTGGTATGTTG 180
Qy 3391 GAGCTGGCAATTAATTTCTGAAACTCTTCCAAAGCAATCAATATATATATGGAATTG 3450
Db 181 GAGCTGGCAATTAATTTCTGAAACTCTTCCAAAGCAATCAATATATATGGAATTG 240
Qy 3451 GAGGAGGTACTGGGTGTCAGGTTCAAAAGACAGATCTTGTACATTTGGCCACAGGCAGC 3510
Db 241 GAGGAGGTACTGGGTGTCAGGTTCAAAAGACAGATCTTGTACATTTGGCCACAGGCAGC 300
Qy 3511 TGCTCTTTGGCGGTAACTTGGGAAAGTCTTCTCGAGTTCAGTGCATGAAATGG 3570
Db 301 TGCTCTTTGGCGGTAACTTGGGAAAGTCTTCTCGAGTTCAGTGCATGAAATGG 360
Qy 3571 CACATTTCTCCAGGTCACTCAGTCAGTGGTGGCCAGTGAATGSCCTTAGCAT 3630
Db 361 CACATTTCTCCAGGTCACTCAGTCAGTGGTGGCCAGTGAATGSCCTTAGCAT 420
Qy 3631 TAGCTGAAATATGTTATTTACAGAGGAGAACAGGCTTATCTCGAGTATTTAAATTAATACC 3690
Db 421 TAGCTGAAATATGTTATTTACAGAGGAGAACAGGCTTATCTCGAGTATTTAAATTAATACC 480
Qy 3691 AGATTATGAGGCTGAAAGTATGTCGATGGAATAATAGTATTTAAAGAACTAAATACC 3750
Db 481 AGATTATGAGGCTGAAAGTATGTCGATGGAATAATAGTATTTAAAGAACTAAATACC 540
Qy 3751 ACTGAACCTAAATCATCAAGCAGCAGTGGCTCTAGCTTTTACTCCTTTGCT 3804
Db 541 ACTGAACCTAAATCATCAAGCAGCAGTGGCTCTAGCTTTTACTCCTTTGCT 594

RESULT 8

US-11-266-748A-152365/c
; Sequence 152365, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152365
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-152365

Query Match 14.9%; Score 570; DB 8; Length 594;
Best Local Similarity 99.7%; Pred. No. 8.9e-129;
Matches 592; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 3213 ATTCAGAGGTTTGTAAACAG-AAACTATGGAAAGATACACTACCGG-AGAAAAGAG 3270

Db 594 ATT CAGAAGGTTTGTAAACAGAAACTATGGAAGATACACTCACCGGAAGAAAAGAG 535
Qy 3271 TTTCTGAGAAAACCAACCAATGCCAATGCAATGCAATGCTATTTTCATGGGTCTCCTTTTG 3330
Db 534 TTTCTGAGAAAACCAACCAATGCCAATGCAATGCAATGCTATTTTCATGGGTCTCCTTTTG 475
Qy 3331 TGAATGCAATTAATCCACAAGGCTTTGATGAAAGGCATGCGGTACATAGGTGGTATGTTG 3390
Db 474 TGAATGCAATTAATCCACAAGGCTTTGATGAAAGGCATGCGGTACATAGGTGGTATGTTG 415
Qy 3391 GAGCTGGCAATTAATTTCTGTAAGAACTCTTCCAAAGCAATCAATATATGTAATGGAATTG 3450
Db 414 GAGCTGGCAATTAATTTCTGTAAGAACTCTTCCAAAGCAATCAATATATGTAATGGAATTG 355
Qy 3451 GAGGAGGTACTGGGTGTCAGTTCACAAGACAGATCTTGTACATTTGGCCACAGGCAGC 3510
Db 354 GAGGAGGTACTGGGTGTCAGTTCACAAGACAGATCTTGTACATTTGGCCACAGGCAGC 295
Qy 3511 TGCTCTTTGGCGGTAACTTGGGAAAGTCTTCTCGAGTTCAGTGCATGAAATGG 3570
Db 294 TGCTCTTTGGCGGTAACTTGGGAAAGTCTTCTCGAGTTCAGTGCATGAAATGG 235
Qy 3571 CACATTTCTCCAGGTCACTCAGTCAGTGGTGGCCAGTGAATGSCCTTAGCAT 3630
Db 234 CACATTTCTCCAGGTCACTCAGTCAGTGGTGGCCAGTGAATGSCCTTAGCAT 175
Qy 3631 TAGCTGAAATATGTTATTTACAGAGGAGAACAGGCTTATCTCGAGTATTTAAATTAATACC 3690
Db 174 TAGCTGAAATATGTTATTTACAGAGGAGAACAGGCTTATCTCGAGTATTTAAATTAATACC 115
Qy 3691 AGATTATGAGGCTGAAAGTATGTCGATGGAATAATAGTATTTAAAGAACTAAATACC 3750
Db 114 AGATTATGAGGCTGAAAGTATGTCGATGGAATAATAGTATTTAAAGAACTAAATACC 55
Qy 3751 ACTGAACCTAAATCATCAAGCAGCAGTGGCTCTAGCTTTTACTCCTTTGCT 3804
Db 54 ACTGAACCTAAATCATCAAGCAGCAGTGGCTCTAGCTTTTACTCCTTTGCT 1

RESULT 9

US-11-266-748A-189602
; Sequence 189602, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189602
; LENGTH: 929

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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-189602

Query Match      14.0%; Score 535.6; DB 8; Length 929;
Best Local Similarity 74.0%; Pred. No. 2.8e-120;
Matches 679; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

QY 1707 CAATTGCTGGAAGCTGCAAAAGCTGGAGATGTCGAAACTGTAAATAAACTGTGTACTGTT 1766
Db 12 CGACTCTTAGAGGCATCTAAAGCTGGAGACTTGGAACTGTGAAGCAACTTTTGCAGCTCT 71
QY 1767 CAGAGTCACTGACAGACACTTGAAGGGCTCAGTCTACACCACTTCACTTTTGCAGCT 1826
Db 72 CAAAATGTGAATTGTAGAGACTTAGAGGGCCGCGCATTCACGCCCTTACACTTCGACGCA 131
QY 1827 GGGTATAACAGAGTGTCCCTGGTGGAAATATCTGTACACATGGAGCTCATGTGCATGCT 1886
Db 132 GGCTACACCGGTGTCTGTGTAGAGTACCTGTACACACAGGTGCCATGTCCATGCC 191
QY 1887 AAAGATAAAGGAGGCTTGTACTTTGCAATGCAATGTTCTTTATGGAATTTAGAGTT 1946
Db 192 AAAGACAAGGGTGGCTTGTGTCGCCCTTCATAATGCCCTTCATATGGACACTATGAGGTG 251
QY 1947 GCAGAACTTCTTTTAAACATGGACGAGTATTTATGTAGCTGATTTATGGAAATTTACA 2006
Db 252 GCTGAGCTTTTATAGTAAGGCATGGGGCTTCTGTCAATGTGGCGGACTTATGGAATTTACC 311
QY 2007 CTTTATACATGAAGCAGCAGCAAAAGGAAATATGAATTTGCAAACTTCTGCTCCAGCAT 2066
Db 312 CTTCTCCATGAAGCAGCAGCTAAGGAAAGTATGAATTCGACGCTCTTTTAAACAT 371
QY 2067 GGTGACAGCCCTTACCAAAAAAACAAGGATGGAATACTCTTTGGATCTTGTAAAGAT 2126
Db 372 GGAGCAGATCCAACTAAAAAAGAACAGAGATGGAATACACCTTTGGATTTGGTAAAGGAA 431
QY 2127 GGAGATACAGATATTTCAAGATCTGCTTAGGGAGATGCAAGCTTTGCTAGATGCTGCCAG 2186
Db 432 GGAGACACAGATATTTCAAGACTTACTTGAGAGGGGATGCTGCTTTGGATGCTGCCAAG 491
QY 2187 AAGGGTGTGTAGCCAGAGTGAAGAGTGTCTTCTCTCTGATAATGTAAATTTGCCCGCAT 2246
Db 492 AAGGCTGCTGCGCAAGAGTGCNAGAGCTCTGTACCCACAGAGATATCACTGCAGAGAC 551
QY 2247 ACCAAGGACAGATTTCAACACTTTTACATTTAGCAGCTGGTTATTAATTTAGAGTT 2306
Db 552 ACCCAGGGCAGAAATTTCAACCCCTCTGCACCTGGCAGCAGGCTATATAAATCCTGGAAGTA 611
QY 2307 GCAGAGATTTGTATACACACGAGCTGATGTGAAATGCCCCAAGACAAAGGAGACTTATT 2366
Db 612 GCTGAATATCTTTAGAGCATGGAGCTGATGTAAATGCCCCCAGACAAAGGGTGGTTAAAT 671
QY 2367 CCTTTACATAATGACAGCATCTTACGGGCATGTAGATGTAGAGCTCTACTATAAAGTAT 2426
Db 672 CCTCTTCATATGCGGCATCTTATGGCATGTGTACATAGCGCTTTATTTGATAAATAC 731
QY 2427 AATGATGTCTCAATGCGCAGCAAAATGGGCTTTTACACTTTTGCACGAAGCAGCCCAA 2486
Db 732 AACACGTGTGTAATGCAACAGATAAGTGGGCGTTTACTCCCTCCATGAAGCAGCCAG 791
QY 2487 AAGGACGACACAGCTTTGTCTTTGTTGCTAGGCCATGGAGCTGACCCGACTCTTAA 2546
Db 792 AAAGGAAGACGACGTGTGCGCCCTCTCTTAGGCGATGGTGCAGACCCCAACCATGAAG 851
QY 2547 AATCAGGAAGCAAAACACTTTTATGATTTTGTAGCGGATGATGTACAGCGCTCTTCTG 2606
Db 852 AACCGAAGGCGGACGAGCGCTCTGGATCTGGCAACAGCTGACGATATCAGAGCTTGTCTG 911
QY 2607 ACAGCAGCCATGCCCCA 2624
Db 912 ATAGATGCCATGCCCCA 929
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RESULT 10
US-11-266-748A-55144
; Sequence 55144, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55144
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-55144
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Query Match      14.0%; Score 533.6; DB 8; Length 564;
Best Local Similarity 99.3%; Pred. No. 6.5e-120;
Matches 536; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3274 CTGAAGAAACACCAACCAATGCCAATGAACGAATGCTATTTCATGGTCTCTCTTTGTA 3333
Db 1 CTGAAGAAACACCAACCAATGCCAATGAACGAATGCTATTTCATGGTCTCTCTTTGTA 60
QY 3334 ATGCAATTATCCACAAAGGCTTTGATGAAAGGATGCGTACATAGTGTGTTGGAG 3393
Db 61 ATGCAATTATCCACAAAGGCTTTGATGAAAGGATGCGTACATAGTGTGTTGGAG 120
QY 3394 CTGGCATTTATTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGTATATGGAATTTGGAG 3453
Db 121 CTGGCATTTATTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGTATATGGAATTTGGAG 180
QY 3454 GAGGTACTGGGTGCTCCAGTTTCAAAAGACAGATCTTGTACATTTGGCAGGAGCTGC 3513
Db 181 GAGGTACTGGGTGCTCCAGTTTCAAAAGACAGATCTTGTACATTTGGCAGGAGCTGC 240
QY 3514 TCTTTTCCGGGTAACTCTTGGGAAAGTCTTTCTCGAGTTTCAGTCAATGAAATGGCAC 3573
Db 241 TCTTTTCCGGGTAACTCTTGGGAAAGTCTTTCTCGAGTTTCAGTCAATGAAATGGCAC 300
QY 3574 ATTCTCTCCAGTTCATCACTCAGTCACTGGTAGGCCAGTGTAAATGGCTAGCATTAG 3633
Db 301 ATTCTCTCCAGTTCATCACTCAGTCACTGGTAGGCCAGTGTAAATGGCTAGCATTAG 360
QY 3634 CTGAATATGTTATTTACAGAGGAGAAACAGGCTTTATCTCTGAGTATTTAAATTTACCAGA 3693
Db 361 CTGAATATGTTATTTACAGAGGAGAAACAGGCTTTATCTCTGAGTATTTAAATTTACCAGA 420
QY 3694 TTATGAGGCTGAAAGTATGGTTCGATGGATGAATAGTATTTTAAAGAAATCAATTTCACT 3753
Db 421 TTATGAGGCTGAAAGTATGGTTCGATGGATGAATAGTATTTTAAAGAAATCAATTTCACT 480
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QY 3754 GAACCTAAATCATCAAAAGCAGCAGTGGCTCTAGCTTTTACTCTCTGCTGAAAAAAA 3813
Db 481 GAACCTAAATCATCAAAAGCAGCAGTGGCTCTAGCTTTTACTCTCTGCTGAAAAAAA 540

RESULT 11
US-11-266-748A-217436
; Sequence 217436, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 217436
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-217436

Query Match 14.0%; Score 533.6; DB 8; Length 564;
Best Local Similarity 99.3%; Pred. No. 6.5e-120;
Matches 536; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3274 CTGAAGAAAAACACCAACCATGCAATGCAATGCTATTTTCATGGGTCTCTTTGTGA 3333
Db 1 CTGAAGAAAAACCAACCATGCAATGCAATGCTATTTTCATGGGTCTCTTTGTGA 60

QY 3334 ATGCAATTATCCACAAGGCTTTGATGAAGGCATGCGTACATAGTGGTATGTTGGAG 3393
Db 61 ATGCAATTATCCACAAGGCTTTGATGAAGGCATGCGTACATAGTGGTATGTTGGAG 120

QY 3394 CTGGCAATTTATTTTCTGAAACTCTTCCAAAGCAATCAATGATATATGAAATTTGAG 3453
Db 121 CTGGCAATTTATTTTCTGAAACTCTTCCAAAGCAATCAATGATATATGAAATTTGAG 180

QY 3454 GAGGTACTGGGTCTCAGTTCAAAAGACAGATCTTTGTTACATTTGCCACAGGAGCTGC 3513
Db 181 GAGGTACTGGGTCTCAGTTCAAAAGACAGATCTTTGTTACATTTGCCACAGGAGCTGC 240

QY 3514 TCTTTTGGGGTACCTTGGGAAAGTCTTCTCAGTTCAATGCAATGAATGGCAC 3573
Db 241 TCTTTTGGGGTAACTTGGGAAAGTCTTCTCAGTTCAATGCAATGAATGGCAC 300

QY 3574 ATTCCTCCAGTCACTCAGTCACTGGTGGCCAGTGTAAATGGCCCTAGCATTTAG 3633
Db 301 ATTCCTCCAGTCACTCAGTCACTGGTGGCCAGTGTAAATGGCCCTAGCATTTAG 360

QY 3634 CTGAATATGTTATTTACAGAGAGAACAGGCTTATCCTGAGTATTAATTAATTAACCCAGA 3693
Db 361 CTGAATATGTTATTTACAGAGAGAACAGGCTTATCCTGAGTATTAATTAATTAACCCAGA 420

QY 3694 TTATGAGCCTGAAGGTATGTCGATGATAAATAGTTATTTTAAGAACTAATTCCTACT 3753
Db 421 TTATGAGCCTGAAGGTATGTCGATGATAAATAGTTATTTTAAGAACTAATTCCTACT 480

QY 3754 GAACCTAAATCATCAAAAGCAGCAGTGGCTCTAGCTTTTACTCTCTGCTGAAAAAAA 3813
Db 481 GAACCTAAATCATCAAAAGCAGCAGTGGCTCTAGCTTTTACTCTCTGCTGAAAAAAA 540

RESULT 12
US-11-266-748A-165504/c
; Sequence 165504, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 165504
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (220)..(228)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-165504

Query Match 13.5%; Score 515.6; DB 8; Length 668;
Best Local Similarity 97.6%; Pred. No. 1.7e-115;
Matches 518; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1663 TCCTCCAGAGGGTATCTCATTAGTAAATTCAGAGGCAGACAGCAATTCGTGGAAGCTG 1722
Db 646 TCCTACAGAGGGTATCTCATTAGTAAATTCAGAGGCAGACAGCAATTCGTGGAAGCTG 587

QY 1723 CAAAGGCTGGAGATGTCGAAACTGTGTAATAAAGCTGTGTTCTGAGAGTGTCAAAGTCA 1782
Db 586 CAAAGGCTGGAGATGTCGAAACTGTGTAATAAAGCTGTGTTCTGAGAGTGTCAAAGTCA 527

QY 1783 GAGCATTTGAAGGGCGTCACTACACCTTCATTTCAGCTGGGTATTAACAGAGTGT 1842
Db 526 GAGCATTTGAAGGGCGTCACTACACCTTCATTTCAGCTGGGTATTAACAGAGTGT 467

QY 1843 CCGTGGTGGATATCTGCTACAGCATGGAGCTGATGTCATGCTGCTAAAGATAAGAGGCC 1902
Db 466 CCGTGGTGGATATCTGCTACAGCATGGAGCTGATGTCATGCTGCTAAAGATAAGAGGCC 407

QY 1903 TTGTACCTTTTGCACAATGCTATTTCTTATGCAATTTATGAAGTTGCAAGACTTCTTTGTA 1962

Db 406 TTGTACCTTTGCACAAATGCAATGCTTCTTATGGACATTAATGAGCTTCAGAACTTCTTGTTA 347
QY 1963 AACATGGAGCAGTAGTAAATGATGAGCTGATTTATGGAATTTACACTTTACATGAAGCAG 2022
Db 346 AACATGGAGCAGTAGTAAATGATGAGCTGATTTATGGAATTTACACTTTTACATGAAGCAG 287
QY 2023 CAGCAAAAGGAAATATGAAATTTCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCA 2082
Db 286 CAGCCAAAGGAAATATGAAATTTGAAACTTCTGCTCCAGCATGGTGCAGACCCCTACNN 227
QY 2083 AAAAAACAGGATGGAATATACTCCCTTTGGATCTTGTAAAGATGGAGATACAGATATTC 2142
Db 226 NNNNNNCAGGATGGAATATACTCTTTGGATCTTGTAAAGATGGAGATACAGATATTC 167
QY 2143 AAGATCTGCTTAGGGAGATGAGCTTTGCTAGATGCTGCCAAGAGGGTT 2193
Db 166 AAGATCTGCTTAGTGGAGATGAGCTTTGCTAGATGCTGCCAAGAGGGTT 116

RESULT 13

US-11-266-748A-244089
; Sequence 244089, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 244089
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (441)..(449)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-244089

Query Match 13.5%; Score 515.6; DB 8; Length 668;
Best Local Similarity 97.6%; Pred. No. 1.7e-115;
Matches 518; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1663 TCCTCCAGAGGGTATCTCATTAGGTAAATTCAGAGGCAGACAGACAAATGCTGGAGCTG 1722
Db 23 TCCTACAGAGGGTATCTCATTAGGTAAATTCAGAGGCAGACAGACAAATGCTGGAGCTG 82
QY 1723 CAAAGGCTGGAGATGTCGAAACTGTAAAAAATCTGTGTACTGTTTCAGAGTGTCAACTGCA 1782
Db 83 CAAAGGCTGGAGATGTCGAAACTGTAAAAAATCTGTGTACTGTTTCAGAGTGTCAACTGCA 142
QY 1783 GAGACATTGAAGGGGCTCAGTCTACACCACTTCATTTTGCAGCTGGGTATACAGAGTGT 1842

Db 143 GAGACATTGAAGGGGCTCAGTCTACACCTTCATTTTGCAGCTGGGTATACAGAGTGT 202
QY 1843 CCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTCATGCTAAAGATAAAGAGGCC 1902
Db 203 CCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTCATGCTAAAGATAAAGAGGCC 262
QY 1903 TTGTACCTTTGCACAAATGCAATGCTTCTTATGGACATTAATGAGTTCAGAACTTCTTGTTA 1962
Db 263 TTGTACCTTTGCACAAATGCAATGCTTCTTATGGACATTAATGAGTTCAGAACTTCTTGTTA 322
QY 1963 AACATGGAGCAGTAGTAAATGATGAGCTGATTTATGGAATTTACACTTTTACATGAAGCAG 2022
Db 323 AACATGGAGCAGTAGTAAATGATGAGCTGATTTATGGAATTTACACTTTTACATGAAGCAG 382
QY 2023 CAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCA 2082
Db 383 CAGCCAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACNN 442
QY 2083 AAAAAACAGGATGGAATATACTCCCTTTGGATCTTGTAAAGATGGAGATACAGATATTC 2142
Db 443 NNNNNNCAGGATGGAATATACTCTCTTTGGATCTTGTAAAGATGGAGATACAGATATTC 502
QY 2143 AAGATCTGCTTAGGGAGATGAGCTTTGCTAGATGCTGCCAAGAGGGTT 2193
Db 503 AAGATCTGCTTAGTGGAGATGAGCTTTGCTAGATGCTGCCAAGAGGGTT 553

RESULT 14

US-11-266-748A-116071
; Sequence 116071, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116071
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-116071

Query Match 13.2%; Score 503.2; DB 8; Length 1000;
Best Local Similarity 76.2%; Pred. No. 2.3e-112;
Matches 619; Conservative 0; Mismatches 193; Indels 0; Gaps 0;
QY 2897 GGATATATTGAGAGAGAACAGATCATTCTTTGGATGTATTGATTGAGATGGGGCACAAGGA 2956
Db 3 GGATATCTTTGAAACAGAACAGATTACACTAGATGTGTTGGCTGATATGGGTATGGAAGA 62

2957	QY	GCTGAAGGAGATTGGAAATCAATGCTTATGACATATAGGCAAAACTAATTAAGAGAGTCGA	3016
63	Db	GTTGAAGAATAAGGCATCAATGCGCATATGGGCAACCGCACAAATTAATCAAAGGAGTAGA	122
3017	QY	GAGACTTATCTCGGACAAACAAGGCTCTTAACCCATATTAACTTTGAAACACCTCTGTAG	3076
123	Db	AAGACTTTAGGTGGACACAGGCCAATCTCTATTGACCTTTCACTGTGTTAATCA	182
3077	QY	TGGAACAATTTCTTATAGATCTGTCTCTGATGATAAAGAGTTTCAGTCTGTGGAGGAAGA	3136
183	Db	GGGAACGATTTTGTGCGATCTTGCTCAGGAAGATAAAGAATATACAGTCAGTGAAGAAGA	242
3137	QY	GATGCAAAAGTACAGTTCGAGAGCACAGAGATGAGGTCATGCGAGTGGAAATCTTCAACAG	3196
243	Db	GATGCAAAAGTACTATTGCGAAGCACAGAGATGGTGTAACTGCTGGCGGCATCTTCAACAG	302
3197	QY	ATACAAATATTCTCAAGATTCAGAAGGTTTGTAAACAAGAACTATGGGAAGATACACTCA	3256
303	Db	ATACAAATGTCATTCGAATTCMAAAGTTGTCAACAGNAGTTGAGGAGCGGTTCTGCCA	362
3257	QY	CCGAGAGAAAAGAAGTTTCTGAAGAAAAACCAACCATGCCAATCAACGAATGCTATTCTCA	3316
363	Db	CCGACAGAAGGAGTGTCTGAGGAGATCAACACCATCACAATGAGCGCATGTTGTTTCA	422
3317	QY	TGGGTCTCCTTTTGTGAAATGCAATTATCCACAAGGCTTTTGATGAAGGCGATGGGTACAT	3376
423	Db	TGGTTCTCCTTTTCATTAAATGCCATTATTCATAAAGGGTTTGTAGAGCGCATGCTACAT	482
3377	QY	AGGTGGTATGTTTGGAGCTGCATTTATTTTGTGTAAGAACTCTTCCAAAAGCAATCAATA	3436
483	Db	AGGAGGAATGTTTGGGCGCGGATTTATTTTGTGTAAGAACTCTTCCAAAAGCAATCAATA	542
3437	QY	TGTATATGGAATTTGGAGAGGTACTGGGTGTCCAGTTTCACAAAAGACAGATCTTTGTTACAT	3496
543	Db	TGTTTATGGAATTTGGAGAGGAACAGGCTGCCCTACACACAGACAGGTCATGCTATAT	602
3497	QY	TTGCGACAGGAGCTGCTCTTTTTCGCGGTAACTTTGGGAAGAGTCTTTCTGCAGATTTCAG	3556
603	Db	ATGTCAAGACAAATGCTCTTCTGTAGAGTGAACCCCTTGGGAAATCCCTTTCTGCAGTTTAG	662
3557	QY	TGCAATGAAATGGCACATTTCTCTCCAGGTCACTCACTAGTCACTGGTAGGCCAGTGT	3616
663	Db	CACCATGAAATGGCCCAACCGGCTCTCAGGGCACCACTCAGTCAATTGGTAGACCGAGCGT	722
3617	QY	AAATGGCCTAGCATTTAGCTGAATATGTTATTTTACAGAGGAACAGGCTTTATCTCGATGA	3676
723	Db	CAATGGGCTGGCATATGCTCGAATATGTCATCTACAGAGGAGACAGGCATACCCAGATGA	782
3677	QY	TTTAAATTACTTACAGATTAATGAGGCTCTGAAG	3708
783	Db	TCATTACACTTACCAGATCATGAAGCCAGGAAG	814

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RESULT 15
US-11-266-748A-158235/c
; Sequence 158235, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION: Paul
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transciptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (313189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0

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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 158235
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-158235

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Query Match	13.2%	Score 503.2	DB 8	Length 1000
Best Local Similarity	76.2%	Pred. No. 2.3e-112		
Matches 619	Conservative	0	Mismatches 193	Indels 0
Qy	2897	GGATATATTGACAGAGAACAGATCACTTTGGAGTGATTAGTTGAGATGGGACACAGGA	2956	
Db	998	GGATATCTTTTGAACACAGACAGATTACATAGATGTGTGGCTGATATGGGTATGAAGA	939	
Qy	2957	GCTCAAGGAGATTGGAATCAATCTTTATGACATATGGCAACAACTAATTAAAGGAGTCGA	3016	
Db	938	GTTGAAAGAAATAGGCATCAATGCATATGGCACCGCCACAAATTAATCAAGAGAGTAGA	879	
Qy	3017	GAGACTTATCTCGGACACACAGGCTTTAAACCCATATTAACTTTGCAACACCTCTGGTAG	3076	
Db	878	AAGACTCTTAGTGGGACCAACAGGCCAACATCCCTATTATTGACTTTTCACTGTGTTAATCA	819	
Qy	3077	TGAAACAAATCTTTATAGATCTGTCTCTGATATAAAGAGTTTTCAGTCTGTGGAGGAAGA	3136	
Db	818	GGGACGATTTTCTGTGGATCTTCTCCAGACAGATAAAGAAATATCACTCAGTGGGAAGAGA	759	
Qy	3137	GATGCAAAAGTACAGTTTCGAGAGCACAGATGAGAGTGCATGCAAGTGGGAATCTTCAACAG	3196	
Db	758	GATGCAAAAGTACTATTTCGAGAACACAGAGATGGTGTGTAATGCTGGGGCGCATCTTCAACAG	699	
Qy	3197	ATACAAATATTTCAAGATTACAGAGGTTTGTAACACAGAAACATATGGAAGATACACTCA	3256	
Db	698	ATCAATGTCAATTCGAATCTCAAAAGTTGTCAACAGAAAGTTGAGGGAGCGGTTCTGCCA	639	
Qy	3257	CCGGAGAAAAGAAAGTTTCTGAAGAAAACCAACCAATGCCAATGAACGAATGCTATTTCA	3316	
Db	638	CCGACAGAAAGAAAGTGTCTGAGGAGAATCACACCAATCACAATGAGCGCATGTGTGTTCA	579	
Qy	3317	TGGGTCTCTTTTGTGAAATGCAATTAATCCACAAAGGCTTTTGATGAAGGGCATCGGTACAT	3376	
Db	578	TGGTTCTCTCTTCAITTAATGCCATTAATCATAAAGGGTTTGATGAGCGCATGCATACAT	519	
Qy	3377	AGGTGGTATCTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTCCAAAAGCAATCAATA	3436	
Db	518	AGAGAGAAATGTTTGGGGCCGGATTTATTTTGTGTAAGAACTCTCTCAAAAAGCAACCAATA	459	
Qy	3437	TGTATATGGAATTTGGAGGAGGTAATCGGGGTCCAGTTTCAAAAAGACAGATCTTTGTTACAT	3496	
Db	458	TGTTTATGGAATTTGGAGGAGGAACAGGCTGCCCTACACACAAAGGACAGGTCATGCTATAT	399	
Qy	3497	TTGGCACAGGCACTGCTCTTTTGGCGGGTAAACCTTGGGNAAGTCTTCTCGCAGGTTGAG	3556	
Db	398	ATGTCAACAGCAAAATGCTCTTCTGTGAGTGAACCCCTTGGGAAATCTCTTCTGCAGTTTGA	339	
Qy	3557	TGCAATGMAAATGGCACATTTCTCCTCCAGGTCAATCACTCAGTCACTGGTAGGCCACAGTGT	3616	
Db	338	CACCAAGAAATGGCCCAACGGGCTCCAGGGCACCACTCACTGATTTGTTAGACCGAGCGT	279	
Qy	3617	AAATGGCCTAGCAATTAGCTGAATPATGTTATTTTACAGAGGAGAAACAGGCTTATCTCGAGTA	3676	
Db	278	CAATGGGCTGGCATATGCTGAATATGTGATCTTACAGAGAGAACAGGCATACCCAGAGTA	219	

Qy 3677 TTTAATTACTTACCAGATTATGAGGCCTGAAG 3708
| | | | | | | | | | | | | | | | | | | | | |
Db 218 TCTTATCACTTACCAGATCATGAGCCAGAAG 187

Search completed: December 18, 2006, 19:31:42
Job time : 762.887 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:21:00 ; Search time 139.536 Seconds
(without alignments)
3489.682 Million cell updates/sec

Title: US-10-616-101-3
Perfect score: 5585
Sequence: 1 GFGRKDVVEYLLQNGASVQA.....AMKMAHSPGHHSVTGRPSV 1065

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 8:*

- 1: geneseqp1980a:*
- 2: geneseqp1990a:*
- 3: geneseqp2000a:*
- 4: geneseqp2001s:*
- 5: geneseqp2002a:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005a:*
- 10: geneseqp2006a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5585	100.0	1065	9	ADY97761 Human tan
2	5585	100.0	1083	9	ADY97770 Human tan
3	5585	100.0	1084	6	ABG73736 Tankyrase
4	5585	100.0	1100	4	ADY97748 Human tan
5	5585	100.0	1100	6	ABG73732 Tankyrase
6	5585	100.0	1100	6	ABG73730 Tankyrase
7	5585	100.0	1100	7	ADH69405 Human tan
8	5585	100.0	1100	9	ADY97766 Human tan
9	5582	99.9	1166	4	ABG66295 Human tan
10	5582	99.9	1166	5	ABP69457 Human pol
11	5582	99.9	1166	8	ADR14792 Amino aci
12	5582	99.9	1169	4	ABG66288 Human tan
13	5582	99.9	1169	4	ABG66278 Human tan
14	5582	99.9	1240	4	ADY97749 Tankyrase
15	5582	99.9	1240	6	ABG73731 Tankyrase
16	5582	99.9	1240	7	ADH69406 Human tan
17	5582	99.9	1240	9	ADY97762 Human tan
18	5582	99.9	1262	4	ABG66290 Human tan
19	5582	99.9	1287	8	ADR66429 Human pro
20	5582	99.9	1287	8	ADR66087 Human tan
21	5582	99.9	1385	4	ABG66294 Human tan
22	5579	99.9	1100	6	ABG73735 Tankyrase
23	5579	99.9	1100	9	ADY97769 Human tan

24	5566	99.7	1166	3	AAB27211	Aab27211 Human tan
25	5533	99.1	1166	4	AAV72589	Aay72589 Human tan
26	5421	97.1	1074	2	AAV05734	Aay05734 Human Gpb
27	5017	89.8	1166	4	ABR47022	Aab47022 Human SPA
28	4974	89.1	1083	6	AAE35352	Aae35352 Human col
29	4748.5	85.0	1333	3	AAB27209	Aab27209 Human tan
30	4740.5	84.9	1327	3	AAV44402	Aay44402 Human tan
31	4740.5	84.9	1327	3	AAB27212	Aab27212 Human tan
32	4740.5	84.9	1327	4	ABG66279	Aab66279 Human tan
33	4740.5	84.9	1327	5	AAU79537	Aau79537 Human tan
34	4740.5	84.9	1327	8	ADR14791	Adr14791 Amino aci
35	4675	83.7	1431	3	AAB27210	Aab27210 Human tan
36	4523.5	81.0	991	4	ABR47023	Aab47023 Mouse SPA
37	4440.5	79.5	907	4	ABR48574	Aab48574 Human bre
38	3918	70.2	784	4	ABG66285	Aab66285 Human tan
39	3775	67.6	756	4	ABG66286	Aab66286 Human tan
40	3706.5	66.4	1181	4	ABG60894	Abb60894 Drosophil
41	3706.5	66.4	1181	4	ABG66297	Aab66297 Protein o
42	3412	61.1	802	5	AAO20512	Aao20512 Human tru
43	3093	55.4	949	3	AAV44404	Aay44404 Human tru
44	3093	55.4	949	5	AAU79539	Aau79539 Truncated
45	2916	52.2	583	9	ADY97768	Ady97768 Human tan

ALIGNMENTS

RESULT 1
ADY97761
ID ADY97761 standard; protein; 1065 AA.
XX AC ADY97761;
XX DT 16-JUN-2005 (first entry)
XX DE Human tankyrase homologue isotype 1 protein SEQ ID NO:3.
XX KW cell cycle; cancer; cytostatic; tankyrase homologue isotype 1.
XX OS Homo sapiens.
XX PN US2005074825-A1.
XX PD 07-APR-2005.
XX PF 08-JUL-2003; 2003US-00616101.
XX PR 25-OCT-1999; 99US-00427154.
XX PR 25-OCT-2000; 2000US-00696668.
XX PR 25-APR-2001; 2001US-00843159.
XX (LUOY/) LUO Y.
XX (CHAN/) CHAN E.
XX (XUX/) XU X.
XX (HUAN/) HUANG B.
XX (OSSO/) OSSOVSKAYA V.
XX PI Luo Y, Chan E, Xu X, Huang B, Ossovsckaya V;
XX WPI; 2005-294737/30.
XX N-PSDB; ADY97759.
XX Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase homolog, useful for screening its modulator.
XX Claim 21; SEQ ID NO 3; 75pp; English.
XX The invention relates to a recombinant polypeptide (I) such as cell cycle protein e.g. tankyrase homologue (Tah), comprising an amino acid sequence having 85% or more sequence identity to the 1065 amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also described: (I) diagnosing cancer, which involves determining the activity of (I) from a test sample of an individual and comparing the level with a

CC control with a control; (2) treating (M1) an individual with a cell cycle
 CC related disorder, which involves administering to the individual an
 CC inhibitor of tRaHo; (3) a recombinant nucleic acid (Ii) encoding (I),
 CC comprising a nucleic acid that hybridizes under high stringent conditions
 CC to a sequence complementary to the 3797 base pair sequence of ADY97759 or
 CC the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
 CC more sequence identity to ADY97759 or ADY97760; (4) an expression vector
 CC (Iii) comprising (Ii) operably linked to regulatory sequences recognized
 CC by a host cell (Iv) transformed with the nucleic acid; (5) a host cell
 CC specifically binds to (I); (6) producing (I); (7) a polypeptide that
 CC specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
 CC cell, involves contacting the tumor with a bioactive agent capable of
 CC inhibiting tRaHo activity. (I) is useful for screening a bioactive agent
 CC capable of modulating (I), or screening for agents capable of interfering
 CC with the binding of (I) and P21. (M1) is useful for treating an
 CC individual with a cell cycle related disorder. (M2) is useful for
 CC inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
 CC oligonucleotide. The present sequence represents the human tankyrase
 CC homologue isotype 1.
 XX
 SQ Sequence 1065 AA;

Query Match 100.0%; Score 5585; DB 9; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSPGHAEVNVNLLRHGADPNARDNNYNT 60
 DB 1 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSPGHAEVNVNLLRHGADPNARDNNYNT 60

QY 61 PLHEAAIKGKIDVCIVLQHGAEPIRTDGTALDADPSAKAVLTGEYKDELESAR 120
 DB 61 PLHEAAIKGKIDVCIVLQHGAEPIRTDGTALDADPSAKAVLTGEYKDELESAR 120

QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 180
 DB 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 180

QY 181 PLHNACSYGHYEVTELLVKHGACVNMADLWQPTPLHEAASKNRRVVCSSLISYGADPTLL 240
 DB 181 PLHNACSYGHYEVTELLVKHGACVNMADLWQPTPLHEAASKNRRVVCSSLISYGADPTLL 240

QY 241 NCHNKSALDAPTQPKERLAYEFKGHSLLQAREADVTRIKKHSLEWVNFKEHQTHET 300
 DB 241 NCHNKSALDAPTQPKERLAYEFKGHSLLQAREADVTRIKKHSLEWVNFKEHQTHET 300

QY 301 ALHCAAASPYPKRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVKEAKV 360
 DB 301 ALHCAAASPYPKRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVKEAKV 360

QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNITISLQGFALQMGNEVNVQQLQEGIS 420
 DB 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNITISLQGFALQMGNEVNVQQLQEGIS 420

QY 421 LGNSEADRLLEAAKAGADVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
 DB 421 LGNSEADRLLEAAKAGADVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480

QY 481 QHGADVHAKDGGVLPLHNACSYGHYEAELLVKHGAVNVNADLWKFTPLHEAAAKGKYE 540
 DB 481 QHGADVHAKDGGVLPLHNACSYGHYEAELLVKHGAVNVNADLWKFTPLHEAAAKGKYE 540

QY 541 ICKLLLQHGADPTKKNRGNTPLDLVKDGDITDQLLRGDAALLDAAKGCLARVKLLSS 600
 DB 541 ICKLLLQHGADPTKKNRGNTPLDLVKDGDITDQLLRGDAALLDAAKGCLARVKLLSS 600

QY 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
 DB 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660

QY 661 VAALLIKYNACVNATDKWAFPLHEAAKGRQTCALLAHGADPTLKNQEGTPTLDLVS 720
 DB 661 VAALLIKYNACVNATDKWAFPLHEAAKGRQTCALLAHGADPTLKNQEGTPTLDLVS 720

QY 721 ADDVSALLTAAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSSLSAASSLDNLG 780
 DB 721 ADDVSALLTAAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSSLSAASSLDNLG 780

QY 781 SFSELSVVSSSGTTEGASSLEKKEVGVDFISITQFVRNLGLEHLMDFIFEREQITLDVLE 840
 DB 781 SFSELSVVSSSGTTEGASSLEKKEVGVDFISITQFVRNLGLEHLMDFIFEREQITLDVLE 840

QY 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSTILLDLPDDKEFQ 900
 DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSTILLDLPDDKEFQ 900

QY 901 SVEEEMQSTVREHRODGGHAGGINRNYILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960
 DB 901 SVEEEMQSTVREHRODGGHAGGINRNYILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

QY 961 RMLFHGSPFVNAI IHKGFDERHAYIGCMFAGIYFAENSCKSNQYVYGGTGCPVHKD 1020
 DB 961 RMLFHGSPFVNAI IHKGFDERHAYIGCMFAGIYFAENSCKSNQYVYGGTGCPVHKD 1020

QY 1021 RSCYICHRQLLCFVRTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
 DB 1021 RSCYICHRQLLCFVRTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065

RESULT 2
 ADY97770
 ID ADY97770 standard; protein; 1083 AA.
 XX ADY97770;
 AC ADY97770;
 DT 16-JUN-2005 (first entry)
 DE Human tankyrase homologue isotype 1 mutant protein SEQ ID NO:12.
 KW cell cycle; cancer; cytostatic; tankyrase homologue isotype 1; mutain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2005074825-A1.
 PD 07-APR-2005.
 PF 08-JUL-2003; 2003US-00616101.
 PR 25-OCT-1999; 99US-00427154.
 PR 25-OCT-2000; 2000US-00696668.
 PR 25-APR-2001; 2001US-00843159.
 XX (LUOY/) LUO Y.
 PA (CHAN/) CHAN E.
 PA (XUXK/) XU X.
 PA (HUAN/) HUANG B.
 PA (OSSO/) OSSOVSKAYA V.
 XX
 PI Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
 XX WPI; 2005-294737/30.
 DR
 XX
 PT Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase
 PT homolog, useful for screening its modulator.
 XX
 PS Disclosure; SEQ ID NO 12; 75pp; English.
 XX
 CC The invention relates to a recombinant polypeptide (I) such as cell cycle
 CC protein e.g. tankyrase homologue (tRaHo), comprising an amino acid
 CC sequence having 85% or more sequence identity to the 1065 amino acid
 CC sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also
 CC described: (1) diagnosing cancer, which involves determining the activity
 CC of (I) from a test sample of an individual and comparing the level with a
 CC control with a control; (2) treating (M1) an individual with a cell cycle

CC related disorder, which involves administering to the individual an
CC inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I),
CC comprising a nucleic acid that hybridizes under high stringent conditions
CC to a sequence complementary to the 3797 base pair sequence of ADY97759 or
CC the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
CC more sequence identity to ADY97759 or ADY97760; (4) an expression vector
CC (III) comprising (II) operably linked to regulatory sequences recognized
CC by a host cell (IV) transformed with the nucleic acid; (5) a host cell
CC comprising (II) or (III); (6) producing (I); (7) a polypeptide that
CC specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
CC cell, involves contacting the tumor with a bioactive agent capable of
CC inhibiting TaHo activity. (I) is useful for screening a bioactive agent
CC capable of modulating (I), or screening for agents capable of interfering
CC with the binding of (I) and P21. (M1) is useful for treating an
CC individual with a cell cycle related disorder. (M2) is useful for
CC inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
CC oligonucleotide. The present sequence represents a human tankyrase
CC homologue isotype 1 mutant protein.
XX
SQ Sequence 1083 AA;

Query Match 100.0%; Score 5585; DB 9; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGKDVVEYLLQNGASVOARDGGGLPLHNACSGHAEVNNLLRHGADPNARDNNVYT 60
DB 1 GFGKDVVEYLLQNGASVOARDGGGLPLHNACSGHAEVNNLLRHGADPNARDNNVYT 60

QY 61 PLHEAAIKGIDVICVLLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKDELLESAR 120
DB 61 PLHEAAIKGIDVICVLLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKDELLESAR 120

QY 121 SGNEKMWALLTPNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDGLV 180
DB 121 SGNEKMWALLTPNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDGLV 180

QY 181 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSLISYGADPTLL 240
DB 181 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSLISYGADPTLL 240

QY 241 NCHNKSALDAPTPQLKRLAYEFKGHSLLQAREADVTRIKKHSLEMVNFKPQTHET 300
DB 241 NCHNKSALDAPTPQLKRLAYEFKGHSLLQAREADVTRIKKHSLEMVNFKPQTHET 300

QY 301 ALHCAAASPYPKRQICELLIRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHAKV 360
DB 301 ALHCAAASPYPKRQICELLIRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHAKV 360

QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDPNIISLQGTALQNGENVCOLLQEGIS 420
DB 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDPNIISLQGTALQNGENVCOLLQEGIS 420

QY 421 LGNSEADROLLEAAKAGDVETVKKLTCTQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB 421 LGNSEADROLLEAAKAGDVETVKKLTCTQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480

QY 481 QHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHEAAKAGKYE 540
DB 481 QHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHEAAKAGKYE 540

QY 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKLLSS 600
DB 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKLLSS 600

QY 601 PNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASGYHVD 660
DB 601 PNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASGYHVD 660

QY 661 VAALLIKYNACVNTDKWAFPLHEAAQKGRTOQLCALLLHAGADPTLKNQEQOTPLDLVS 720
DB 661 VAALLIKYNACVNTDKWAFPLHEAAQKGRTOQLCALLLHAGADPTLKNQEQOTPLDLVS 720

QY 721 ADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSPSSLSAASSLDNLSSG 780
DB 721 ADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSPSSLSAASSLDNLSSG 780

QY 781 SFSELSSVVSSSGTEGASSLEKKEVPGVDPSITQVRNLGLEHMDIFEREQITLDVLVE 840
DB 781 SFSELSSVVSSSGTEGASSLEKKEVPGVDPSITQVRNLGLEHMDIFEREQITLDVLVE 840

QY 841 MGHKELKEIGINAYGHRHKLKGVERLISGOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
DB 841 MGHKELKEIGINAYGHRHKLKGVERLISGOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900

QY 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQKVCNKKLWERYTHRRKEVSENNHANE 960
DB 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQKVCNKKLWERYTHRRKEVSENNHANE 960

QY 961 RMLFHGSPFVNAIHKGFDERHAYIGGFGAGIYFAENSSKSNQVYVYGGGTGCPVHKD 1020
DB 961 RMLFHGSPFVNAIHKGFDERHAYIGGFGAGIYFAENSSKSNQVYVYGGGTGCPVHKD 1020

QY 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065

RESULT 3
ABG73736
ID ABG73736 standard; protein; 1084 AA.
XX AC ABG73736;
XX DT 08-APR-2003 (first entry)
XX DE Tankyrase H isotype 1 TH-1 variant TaHo E/A dC.
XX KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TH-1; TaHo;
XX KW cytotstatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
XX KW cell cycle related disorder; poly ADP-ribose polymerase; PARP.
XX OS Synthetic.

Key Key Location/Qualifiers
Region 1..22 /label= Ankyrin_repeat_1
Region 24..55 /label= Ankyrin_repeat_2
Region 57..87 /label= Ankyrin_repeat_3
Region 89..113 /label= Ankyrin_repeat_4
Region 115..139 /label= Ankyrin_repeat_5
Misc-difference 127 /note= "TH1 start"
Region 147..176 /label= Ankyrin_repeat_6
Region 178..208 /label= Ankyrin_repeat_7
Region 210..241 /label= Ankyrin_repeat_8
Region 243..281 /label= Ankyrin_repeat_9
Region 283..332 /label= Ankyrin_repeat_10
Region 334..365 /label= Ankyrin_repeat_11
Region 367..398 /label= Ankyrin_repeat_12
Region 400..424 /label= Ankyrin_repeat_13
Region 426..458 /label= Ankyrin_repeat_14
Region 460..491 /label= Ankyrin_repeat_14

DT 06-AUG-2001 (first entry)
XX Tankyrase homologue isotype 1 protein sequence.
DE Tankyrase homologue isotype 1; TaHo-1; TaHo-2; cell proliferation;
KW cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
KW chromosome mapping; gene therapy; vaccine.
XX Unidentified.
XX WO2001130987-A2.
XX 03-MAY-2001.
XX 25-OCT-2000; 2000WO-US041528.
XX 25-OCT-1999; 99US-00427154.
XX (RIGE-) RIGEL PHARM INC.
XX Luo Y, Chan E, Xu X, Huang B;
XX WPI; 2001-300503/31.
XX N-PSDB; AAA91487.
XX Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing
PT or preventing cell proliferation in cells, and for diagnosing, treating
PT or preventing cell cycle associated disorders such as cancer.
XX Claim 22; Fig 3; 63pp; English.
XX This sequence is the Tankyrase homologue isotype 1 (TaHo-1) protein of
CC the invention. The invention also relates to the TaHo-2 protein. The TaHo
CC proteins are useful for inducing or preventing cell proliferation in
CC cells, and in the study or treatment of conditions mediated by the cell
CC cycle proteins, such as to diagnose, treat or prevent cell cycle
CC associated disorders, preferably cancer. The TaHo coding sequences are
CC useful as hybridisation probes, in chromosome and gene mapping and in the
CC generation of anti-sense DNA and RNA. The coding sequences are also
CC useful for the preparation of TaHo, for generating either transgenic
CC animals or knock out animals which, in turn, are useful in a development
CC and screening of therapeutically useful agents, in gene therapy, as
CC vaccine, and for construction of hybridisation probes for mapping the
CC gene which encodes TaHo and for the genetic analysis of individuals with
CC genetic disorders. The TaHo proteins, and their coding sequences are
CC useful in screening assays
XX
SQ Sequence 1100 AA;
Query Match 100.0%; Score 5585; DB 4; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFGKDVVEYLLQNGASVQARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNNYT 60
DB 1 GFGKDVVEYLLQNGASVQARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNNYT 60
QY 61 PLHEAAIKGIDVCIVLQHGAEPTIRNDGTALDADPSAKAVLTGEYKDELLESAR 120
DB 61 PLHEAAIKGIDVCIVLQHGAEPTIRNDGTALDADPSAKAVLTGEYKDELLESAR 120
QY 121 SGNEEKMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDKGLV 180
DB 121 SGNEEKMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDKGLV 180
QY 181 PLHNACSYGHYEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
DB 181 PLHNACSYGHYEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
QY 241 NCHNKSADLAPTPQKRLAYEFKGHSLLOAREADVTRIKKHLSELVNFKHPQTHET 300
DB 241 NCHNKSADLAPTPQKRLAYEFKGHSLLOAREADVTRIKKHLSELVNFKHPQTHET 300

QY 301 ALHCAAASPYPKRKQICELLRLKGANINEKTEFETPLHVASSEKAHNDVVEVVKHEAKV 360
DB 301 ALHCAAASPYPKRKQICELLRLKGANINEKTEFETPLHVASSEKAHNDVVEVVKHEAKV 360
QY 361 NALDNLGOTSILHRAAYCGHLOTCELLLSYGCDPNIIISLOGETALQMGNEVQOLLOEGIS 420
DB 361 NALDNLGOTSILHRAAYCGHLOTCELLLSYGCDPNIIISLOGETALQMGNEVQOLLOEGIS 420
QY 421 LGNSEADRLLEAAKAGDVETVKKICTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB 421 LGNSEADRLLEAAKAGDVETVKKICTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
QY 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VNVNADLWKFTPLHEAAAKGYE 540
DB 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VNVNADLWKFTPLHEAAAKGYE 540
QY 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLGRDAALLDAAKKGCLARVKLLSS 600
DB 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLGRDAALLDAAKKGCLARVKLLSS 600
QY 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
DB 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
QY 661 VAALLIKYNACVNATDKWAFPLHEAAQKRTQLCALLLAHGA DPTLKNQEGOTPLDLVS 720
DB 661 VAALLIKYNACVNATDKWAFPLHEAAQKRTQLCALLLAHGA DPTLKNQEGOTPLDLVS 720
QY 721 ADDVSALLTAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
DB 721 ADDVSALLTAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
QY 781 SFSSESSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHMDIFEREQITLDVLVE 840
DB 781 SFSSESSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHMDIFEREQITLDVLVE 840
QY 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTNTSGSGTILIDLSPDKKEFQ 900
DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTNTSGSGTILIDLSPDKKEFQ 900
QY 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLKIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
DB 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLKIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 961 RMLFHGSPFVNAIHKGFDERHAYIGGMFGAGIYPAENSSKSNQVYGGTGCPCVHKD 1020
DB 961 RMLFHGSPFVNAIHKGFDERHAYIGGMFGAGIYPAENSSKSNQVYGGTGCPCVHKD 1020
QY 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1065
RESULT 5
ABG73732
ID ABG73732 standard; protein; 1100 AA.
XX
AC ABG73732;
XX
DT 08-APR-2003 (first entry)
XX
DE Tankyrase H isotype 1 TH-1.
XX
KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TH-1; TaHo;
KW cytosstatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
KW cell cycle related disorder; poly ADP-ribose polymerase; PARP.
XX Unidentified.
XX
FH Key Location/Qualifiers
FT Region 1. .22
FT /label= Ankyrin_repeat_1
FT Region 24. .55

FT Region /label= Ankyrin_repeat_2
FT 57..87
FT /label= Ankyrin_repeat_3
FT 89..113
FT Region /label= Ankyrin_repeat_4
FT 115..139
FT /label= Ankyrin_repeat_5
FT 127
FT Misc-difference /note= "TH1 start"
FT 147..176
FT Region /label= Ankyrin_repeat_6
FT 178..208
FT Region /label= Ankyrin_repeat_7
FT 210..241
FT Region /label= Ankyrin_repeat_8
FT 243..281
FT Region /label= Ankyrin_repeat_9
FT 283..332
FT Region /label= Ankyrin_repeat_10
FT 334..365
FT Region /label= Ankyrin_repeat_11
FT 367..398
FT Region /label= Ankyrin_repeat_12
FT 400..424
FT Region /label= Ankyrin_repeat_13
FT 426..458
FT Region /label= Ankyrin_repeat_14
FT 460..491
FT Region /label= Ankyrin_repeat_15
FT 493..524
FT Region /label= Ankyrin_repeat_16
FT 526..557
FT Region /label= Ankyrin_repeat_17
FT 559..594
FT Region /label= Ankyrin_repeat_18
FT 596..644
FT Region /label= Ankyrin_repeat_19
FT 646..677
FT Region /label= Ankyrin_repeat_20
FT 679..710
FT Region /label= Ankyrin_repeat_21
FT 712..755
FT Region /label= Ankyrin_repeat_22
FT 757..793
FT Region /label= Ankyrin_repeat_23
FT 797..845
FT Domain /label= SAM_domain
FT 855..869
FT Region /note= "Unidentified region"
FT 956..1094
FT Domain /label= PARP_domain

XX WO200286170-A1.

XX 31-OCT-2002.

XX 25-APR-2002; 2002WO-US013185.

XX 25-APR-2001; 2001US-00843159.

XX (RIGE-) RIGEL PHARM INC.

XX Luo Y, Chan E, Xu X, Huang B, Ossovskeya V;

XX WPI; 2003-093158/08.

XX New recombinant nucleic acid encoding a cell cycle protein, useful for
XX diagnosing and treating a cell cycle related disorder, e.g. cancer.
XX Disclosure; Fig 16A-C; 90pp; English.

XX This invention describes a novel recombinant nucleic acid encoding the
XX cell cycle protein TaHo, a tankyrase H isoform. The products of the

CC invention have cytostatic and immunostimulant activity and can be used
CC for gene therapy and in vaccines. The cell cycle protein TaHo and the
CC nucleic acid encoding the protein are useful for diagnosing and treating
CC a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
CC tumour cell. The methods are useful for screening for a bioactive agent
CC capable of binding to a cell cycle protein tankyrase H, or a bioactive
CC agent capable of modulating a cell cycle protein tankyrase H or PARP
CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
CC inducing an immune response against the cell cycle proteins. This
CC sequence represents tankyrase H isoform 1, TH-1, described in the
CC disclosure of the invention

XX Sequence 1100 AA;

Query Match 100.0%; Score 5585; DB 6; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGRKDVVEYLLQNGASVQARDGGGLPLHNACSFQAEVNVNLLRHGADPNARDNNYIT 60
DB 1 GGRKDVVEYLLQNGASVQARDGGGLPLHNACSFQAEVNVNLLRHGADPNARDNNYIT 60
QY 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRITDLDADPSAKAVLTGEYKDELESAR 120
DB 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRITDLDADPSAKAVLTGEYKDELESAR 120
QY 121 SGNEEKOMALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADYHAKDGDV 180
DB 121 SGNEEKOMALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADYHAKDGDV 180
QY 181 PLHNACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
DB 181 PLHNACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
QY 241 NCHNSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKKLSLEWMVNFKHPQTHET 300
DB 241 NCHNSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKKLSLEWMVNFKHPQTHET 300
QY 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPHVASEKAHNDDVVEVVKHEAKV 360
DB 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPHVASEKAHNDDVVEVVKHEAKV 360
QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDNIIISLQGTALQMGNEVQQLQSGIS 420
DB 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDNIIISLQGTALQMGNEVQQLQSGIS 420
QY 421 LGNSEADROLLEAAKAGDVETVKKLCITVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 480
DB 421 LGNSEADROLLEAAKAGDVETVKKLCITVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 480
QY 481 QHGADYHAKDKGGLVPLHNACSYGHEVAEALLVKHGAVNVNADLWKFTPLHEAAKGYE 540
DB 481 QHGADYHAKDKGGLVPLHNACSYGHEVAEALLVKHGAVNVNADLWKFTPLHEAAKGYE 540
QY 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDTQDLLLRGDAALLDAKKGCLARVKLSS 600
DB 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDTQDLLLRGDAALLDAKKGCLARVKLSS 600
QY 601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
DB 601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
QY 661 VAALLIKYNACVNAWTKWAFTPLHEAAKQKRTQLCALLLAHGADPTLKNOEGQTPLDLVS 720
DB 661 VAALLIKYNACVNAWTKWAFTPLHEAAKQKRTQLCALLLAHGADPTLKNOEGQTPLDLVS 720
QY 721 ADDVSALLTAAMPSPSALPCYKPOVLNGVSPGATADALSSGPSSPSLSAASLNDLSG 780
DB 721 ADDVSALLTAAMPSPSALPCYKPOVLNGVSPGATADALSSGPSSPSLSAASLNDLSG 780
QY 781 SFSELSVSVSSSGTEGASSLEKKEVPGVDFPSITQFVRNLGLEHLMDFEREQITDLVLE 840
DB 781 SFSELSVSVSSSGTEGASSLEKKEVPGVDFPSITQFVRNLGLEHLMDFEREQITDLVLE 840

Qy 841 MGKELKEIGINAYGHRHKLKIGVERLISGOGLNPLYTLNTSGTLLIDLSPDKKEFQ 900
 Db 841 MGKELKEIGINAYGHRHKLKIGVERLISGOGLNPLYTLNTSGTLLIDLSPDKKEFQ 900
 Qy 901 SVEEMOSTVREHRDGGHAGGIFNRYNLTKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
 Db 901 SVEEMOSTVREHRDGGHAGGIFNRYNLTKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
 Qy 961 RMLFHGSPFVNAIIHKGFDERHAYIGMGFGAGIYFAENSCKSNQVYVIGGGTGPCVHKD 1020
 Db 961 RMLFHGSPFVNAIIHKGFDERHAYIGMGFGAGIYFAENSCKSNQVYVIGGGTGPCVHKD 1020
 Qy 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
 Db 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065

RESULT 6
 ID ABCG73730 standard; protein; 1100 AA.
 AC ABCG73730;
 XX
 DT 08-APR-2003 (first entry)
 XX
 DE Tankyrase H isotype 1 TaHo-1 from clone TH-1.
 KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-1;
 KW TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
 KW cell cycle related disorder; poly ADP-ribose polymerase; PARP.
 XX
 OS Unidentified.
 XX
 PN W0200286170-A1.
 XX
 PD 31-OCT-2002.
 XX
 PF 25-APR-2002; 2002WO-US013185.
 XX
 PR 25-APR-2001; 2001US-00843159.
 XX
 PA (RIGE-) RIGEL PHARM INC.
 XX
 PI Luo Y, Chan E, Xu X, Huang B, Ososovskaya V;
 XX
 DR WPI; 2003-093158/08.
 XX
 DR N-PSDB; ABQ77066.
 XX
 PT New recombinant nucleic acid encoding a cell cycle protein, useful for
 XX diagnosing and treating a cell cycle related disorder, e.g. cancer.
 PS Claim 14; Fig 3; 90pp; English.
 XX
 CC This invention describes a novel recombinant nucleic acid encoding the
 CC cell cycle protein TaHo, a tankyrase H isoform. The products of the
 CC invention have cytostatic and immunostimulant activity and can be used
 CC for gene therapy and in vaccines. The cell cycle protein TaHo and the
 CC nucleic acid encoding the protein are useful for diagnosing and treating
 CC a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
 CC tumour cell. The methods are useful for screening for a bioactive agent
 CC capable of binding to a cell cycle protein tankyrase H, or a bioactive
 CC agent capable of modulating a cell cycle protein tankyrase H or PARP
 CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
 CC inducing an immune response against the cell cycle proteins. This
 CC sequence represents the tankyrase H isoform 1, TaHo-1, isolated from
 CC clone TH-1 which is described in the disclosure of the invention
 XX
 SQ Sequence 1100 AA;

Query Match 100.0%; Score 5585; DB 6; Length 1100;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARDNNYT 60
 Db 1 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARDNNYT 60
 Qy 61 PLHAAI1KGKIDVICIVILQHGAEPTIRNTGRTALDLADPSAKAVLTGEYKDELLESAR 120
 Db 61 PLHAAI1KGKIDVICIVILQHGAEPTIRNTGRTALDLADPSAKAVLTGEYKDELLESAR 120
 Qy 121 SGNEKEMWALLTPLNVNCHASDGRKSTPLHAAAGVNRVKIIVOLLQHGADVHAKDGLV 180
 Db 121 SGNEKEMWALLTPLNVNCHASDGRKSTPLHAAAGVNRVKIIVOLLQHGADVHAKDGLV 180
 Qy 181 PLHNACSYGHEVTELLVKGHCACVNMADLMQFTPLHAAASKNRVEVCSLLSYGADPTLL 240
 Db 181 PLHNACSYGHEVTELLVKGHCACVNMADLMQFTPLHAAASKNRVEVCSLLSYGADPTLL 240
 Qy 241 NCHNSAIDLAPTQPKERLAYEPKSHSLLOAAREADVTRI1KXHLSELMVNFKHPQTHET 300
 Db 241 NCHNSAIDLAPTQPKERLAYEPKSHSLLOAAREADVTRI1KXHLSELMVNFKHPQTHET 300
 Qy 301 ALHCAASPYPKRKOICELLIRKGANINEKTEFLTPHVASEKAHNDVVEVVKHEAKV 360
 Db 301 ALHCAASPYPKRKOICELLIRKGANINEKTEFLTPHVASEKAHNDVVEVVKHEAKV 360
 Qy 361 NALDNLGOTSLHRAAYCGHLQTCRLLLSYCGDPNIISLQGFALTQMGNNVQQLLQEGIS 420
 Db 361 NALDNLGOTSLHRAAYCGHLQTCRLLLSYCGDPNIISLQGFALTQMGNNVQQLLQEGIS 420
 Qy 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
 Db 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
 Qy 481 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCACVNMADLMQFTPLHAAASKNRVE 540
 Db 481 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCACVNMADLMQFTPLHAAASKNRVE 540
 Qy 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDITDIOQLRGLDAAALLDAKKGCLARVKLSS 600
 Db 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDITDIOQLRGLDAAALLDAKKGCLARVKLSS 600
 Qy 601 PDVNCRDTOGRHSTPLHAAAGYNRVSVVEYLLQHGADVNAODXGGLIPLHNAASYGHVD 660
 Db 601 PDVNCRDTOGRHSTPLHAAAGYNRVSVVEYLLQHGADVNAODXGGLIPLHNAASYGHVD 660
 Qy 661 VAALLIKYNACVNAATDKWAFPLHAAAKGRTQJCALLLAHAGADPTLKNQSGQTPDLVS 720
 Db 661 VAALLIKYNACVNAATDKWAFPLHAAAKGRTQJCALLLAHAGADPTLKNQSGQTPDLVS 720
 Qy 721 ADDVSALLTAAMPSPALPCYKQVINGVRSPGATADALSSGSPSPSSLSAASSLDNLSSG 780
 Db 721 ADDVSALLTAAMPSPALPCYKQVINGVRSPGATADALSSGSPSPSSLSAASSLDNLSSG 780
 Qy 781 SFSLSVSSSSGTEGASSLEKKEVPVDFSIQFVRNLGLEHMDIPERQITLDVLVE 840
 Db 781 SFSLSVSSSSGTEGASSLEKKEVPVDFSIQFVRNLGLEHMDIPERQITLDVLVE 840
 Qy 841 MGKELKEIGINAYGHRHKLKIGVERLISGOGLNPLYTLNTSGTLLIDLSPDKKEFQ 900
 Db 841 MGKELKEIGINAYGHRHKLKIGVERLISGOGLNPLYTLNTSGTLLIDLSPDKKEFQ 900
 Qy 901 SVEEMOSTVREHRDGGHAGGIFNRYNLTKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
 Db 901 SVEEMOSTVREHRDGGHAGGIFNRYNLTKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
 Qy 961 RMLFHGSPFVNAIIHKGFDERHAYIGMGFGAGIYFAENSCKSNQVYVIGGGTGPCVHKD 1020
 Db 961 RMLFHGSPFVNAIIHKGFDERHAYIGMGFGAGIYFAENSCKSNQVYVIGGGTGPCVHKD 1020
 Qy 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
 Db 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065

25-OCT-2000; 2000US-00696668.
25-APR-2001; 2001US-00843159.
(LUOY/) LUO Y.
(CHAN/) CHAN E.
(XUXX/) XU X.
(HUAN/) HUANG B.
(OSSO/) OSSOVSKAYA V.
Luo Y, Chan E, Xu X, Huang B, Ossovsckaya V;
WPI; 2005-294737/30.
Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase
homolog, useful for screening its modulator.
Disclosure; SEQ ID NO 8; 75pp; English.
The invention relates to a recombinant polypeptide (I) such as cell cycle
protein e.g. tankyrase homologue (Tah), comprising an amino acid
sequence having 85% or more sequence identity to the 1065 amino acid
sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also
described: (1) diagnosing cancer, which involves determining the activity
of (I) from a test sample of an individual and comparing the level with a
control with a control; (2) treating (M1) an individual with a cell cycle
related disorder, which involves administering to the individual an
inhibitor of Tah; (3) a recombinant nucleic acid (II) encoding (I),
comprising a nucleic acid that hybridizes under high stringent conditions
to a sequence complementary to the 3797 base pair sequence of ADY97759 or
the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
more sequence identity to ADY97759 or ADY97760; (4) an expression vector
(III) comprising (II) operably linked to regulatory sequences recognized
by a host cell (IV) transformed with the nucleic acid; (5) a host cell
comprising (II) or (III); (6) producing (I); (7) a polypeptide that
specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
cell, involves contacting the tumor with a bioactive agent capable of
inhibiting Tah activity. (I) is useful for screening a bioactive agent
capable of modulating (I), or screening for agents capable of interfering
with the binding of (I) and P21. (M1) is useful for treating an
individual with a cell cycle related disorder. (M2) is useful for
inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
oligonucleotide. The present sequence represents the human tankyrase
homologue isotype 1.
Sequence 1100 AA;
Query Match 100.0%; Score 5585; DB 9; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFGKDVVEYLLONGASVQARDGGLIPLHNACSGHAENVNLLRHGADPNARDNNYNT 60
DB 1 GFGKDVVEYLLONGASVQARDGGLIPLHNACSGHAENVNLLRHGADPNARDNNYNT 60
QY 61 PLHEAAIKGKIDVCIVLLOHGAEPTRINTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
DB 61 PLHEAAIKGKIDVCIVLLOHGAEPTRINTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
QY 121 SGNEKMMALLPPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDGLV 180
DB 121 SGNEKMMALLPPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDGLV 180
QY 181 PLHNACSGHYEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
DB 181 PLHNACSGHYEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
QY 241 NCHNKSADIDLAPTPOLKELAYEFKGHSLLOAREADVTIRIKHLSLEWVNFKPHQTHET 300
DB 241 NCHNKSADIDLAPTPOLKELAYEFKGHSLLOAREADVTIRIKHLSLEWVNFKPHQTHET 300
QY 301 ALHCAAAAPYPRKQICELLFRKGANINEKTEFTPLHVAASEKAHNDVVEVVVHEAKV 360
DB 301 ALHCAAAAPYPRKQICELLFRKGANINEKTEFTPLHVAASEKAHNDVVEVVVHEAKV 360

QY 361 NALDNLGOTSILHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQMGNNVQQLLEGIS 420
DB 361 NALDNLGOTSILHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQMGNNVQQLLEGIS 420
QY 421 LGNSEADRLLEAAKAGADVETVKKLCVTQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB 421 LGNSEADRLLEAAKAGADVETVKKLCVTQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
QY 481 OHGADVHAKDKKGLVPLHNACSGHYEVAEVLVKGHGVNVDLWKFTPLHEAAAKGYE 540
DB 481 OHGADVHAKDKKGLVPLHNACSGHYEVAEVLVKGHGVNVDLWKFTPLHEAAAKGYE 540
QY 541 ICKLLQHGADPTKKNRDGNTPLDIVKDGDTDIQDLRGDAALLDAKKGCLARVKLSS 600
DB 541 ICKLLQHGADPTKKNRDGNTPLDIVKDGDTDIQDLRGDAALLDAKKGCLARVKLSS 600
QY 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
DB 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
QY 661 VAAALLIKYNACVNATDKWAFPLHEAAOKGRTQLCALLLAHAGADPTLKNQEGTPLDLVS 720
DB 661 VAAALLIKYNACVNATDKWAFPLHEAAOKGRTQLCALLLAHAGADPTLKNQEGTPLDLVS 720
QY 721 ADDVSALLTAAMPSPSALPCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
DB 721 ADDVSALLTAAMPSPSALPCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
QY 781 SFSBELSSVSSSGTEGASSLEKKEVPGVDFSTQFVRNLGLEHMDIFERQITLDVLVE 840
DB 781 SFSBELSSVSSSGTEGASSLEKKEVPGVDFSTQFVRNLGLEHMDIFERQITLDVLVE 840
QY 841 MGHEKELKEIGINAYCHRRHKLKGVRELISGOGLNPYLTNTSGSTLIDLSPPDKERFQ 900
DB 841 MGHEKELKEIGINAYCHRRHKLKGVRELISGOGLNPYLTNTSGSTLIDLSPPDKERFQ 900
QY 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
DB 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSKSNQYVYGGGTGCPVHKD 1020
DB 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSKSNQYVYGGGTGCPVHKD 1020
QY 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV 1065
RESULT 9
AAB66295
ID AAB66295 standard; protein; 1166 AA.
XX AAB66295;
XX AC AAB66295;
XX DT 05-APR-2001 (first entry)
XX DE Human tankyrase2 TANK2-SHORT SEQ ID NO: 135.
XX KW Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasia; aging;
XX KW inflammatory disorder.
XX OS Homo sapiens.
XX PN WO200100849-A1.
XX PD 04-JAN-2001.
XX PF 28-JUN-2000; 2000WO-US017827.
XX PR 29-JUN-1999; 99US-0141582P.
XX XX

PA (ICOS-) ICOS CORP.
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
PI WPI; 2001-102896/11.
XX N-PSDB; AAF63953.
DR
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX
XX Claim 3; Page 200-203; 242pp; English.
XX
XX The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
XX
SQ Sequence 1166 AA;

Query Match 99.9%; Score 5582; DB 4; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
DB 67 GFGRKDVVEYLLONGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 126

QY 61 PLHEAAIKGIDVICVILLOHGAETPIRTDGRALDADPSAKAVLTGEYKDELLSAR 120
DB 127 PLHEAAIKGIDVICVILLOHGAETPIRTDGRALDADPSAKAVLTGEYKDELLSAR 186

QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLOHGDVHAKGDLV 180
DB 187 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLOHGDVHAKGDLV 246

QY 181 PLHNACSYGHEVTELLVKGACVNDLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
DB 247 PLHNACSYGHEVTELLVKGACVNDLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 306

QY 241 NCHNKAIDLAPTQPKERLAYEFKSHLSLQAAREADVTRIKHLSLEMVNFKHPQTHET 300
DB 307 NCHNKAIDLAPTQPKERLAYEFKSHLSLQAAREADVTRIKHLSLEMVNFKHPQTHET 366

QY 301 ALHCAASAPYKPKOICELLIRKGANINEKTKFELTPLHVASEKANDVVEVVKHEAV 360
DB 367 ALHCAASAPYKPKOICELLIRKGANINEKTKFELTPLHVASEKANDVVEVVKHEAV 426

QY 361 NALDNLGQTSLHRAAYCCHLTQCRLLLSYGCDPNIISLQGFALTQMGNNVQQLQEGIS 420
DB 427 NALDNLGQTSLHRAAYCCHLTQCRLLLSYGCDPNIISLQGFALTQMGNNVQQLQEGIS 486

QY 421 LGNSEADRLQLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB 487 LGNSEADRLQLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546

QY 481 QHGADVHAKDGGVPLHNACSYGHEVAELLVKGAVNVNADLWKETPLHEAAKGYE 540
DB 547 QHGADVHAKDGGVPLHNACSYGHEVAELLVKGAVNVNADLWKETPLHEAAKGYE 606

QY 541 ICKLLLOHGDPTKKNRDNTPDLVKDGDPTDIQDLRGDAALDAAKGGCLARVKLSS 600
DB 607 ICKLLLOHGDPTKKNRDNTPDLVKDGDPTDIQDLRGDAALDAAKGGCLARVKLSS 666

QY 601 PDNVNCRDTPQGRHSTPLHAAAGYNVLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
DB 667 PDNVNCRDTPQGRHSTPLHAAAGYNVLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 726

QY 661 VAALLIKYNACVNATDKWAFPLHEAAKQKRTQICALLLAHAGADPTLKQEGQTPDLIVS 720

DB 727 VAALLIKYNACVNATDKWAFPLHEAAKQKRTQICALLLAHAGADPTLKQEGQTPDLIVS 786
QY 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSPSLSAASSLDNLG 780
DB 787 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSPSLSAASSLDNLG 846
QY 781 SFSELSVSSSGTEGASSLEKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVIVE 840
DB 847 SFSELSVSSSGTEGASSLEKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVIVE 906
QY 841 MGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTNTSGSTILDLSPDDKEFQ 900
DB 907 MGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTNTSGSTILDLSPDDKEFQ 966
QY 901 SVEEEMQSTVREHRDGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEENHNANE 960
DB 967 SVEEEMQSTVREHRDGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEENHNANE 1026
QY 961 RMLFHGSPFVNAILHKGDFDERHAYIGCMFGAGIYFAENSCKSNQYVYIGGGTGCPVHKD 1020
DB 1027 RMLFHGSPFVNAILHKGDFDERHAYIGCMFGAGIYFAENSCKSNQYVYIGGGTGCPVHKD 1086
QY 1021 RSCVICHROLLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1065
DB 1087 RSCVICHROLLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1131

RESULT 10
ABP69457
ID ABP69457 standard; protein; 1166 AA.
XX ABP69457;
XX AC
XX DT 20-JAN-2003 (first entry)
XX Human polypeptide SEQ ID NO 1504.
XX
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; neutropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
XX Homo sapiens.
XX WO200270539-A2.
XX PD 12-SEP-2002.
XX 05-MAR-2002; 2002WO-US005095.
XX 05-MAR-2001; 2001US-00799451.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
XX WPI; 2002-759812/82.
XX N-PSDB; ABZ11674.
XX
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative, or platelet
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or coagulation disorders.
XX
XX Claim 9; SEQ ID NO 1504; 1012pp + Sequence Listing; English.
XX

CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (AB211119-
CC AB212066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP69802-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burn, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 1166 AA;

Query Match 99.9%; Score 5582; DB 5; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFGKRVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYNT 60
Db 67 GFGKRVVEYLLQNGANVOARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYNT 126
Qy 61 PLHEAAIKGKIDVCIVLQHGAEPIRTNDGRTALDLPSPAKAVLTGEYKDELLESAR 120
Db 127 PLHEAAIKGKIDVCIVLQHGAEPIRTNDGRTALDLPSPAKAVLTGEYKDELLESAR 186
Qy 121 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGNVRVKIQLLQHGADVHAKDGLV 180
Db 187 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGNVRVKIQLLQHGADVHAKDGLV 246
Qy 181 PLHNACSYGHEVTELLVKGHCANVMDLQWFTPLHEAASKNRVEVCSLLSYGADPTLL 240
Db 247 PLHNACSYGHEVTELLVKGHCANVMDLQWFTPLHEAASKNRVEVCSLLSYGADPTLL 306
Qy 241 NCHNKAIDLAPTOLKRLAYEPKGLSHLQAAAREADVTRIKGHLSEMVNFKPQTHET 300
Db 307 NCHNKAIDLAPTOLKRLAYEPKGLSHLQAAAREADVTRIKGHLSEMVNFKPQTHET 366
Qy 301 ALHCAAASPYPKRKQICELLRKGANINEKTEFLTLPHVASEKAHNDVVEVVKHAKV 360
Db 367 ALHCAAASPYPKRKQICELLRKGANINEKTEFLTLPHVASEKAHNDVVEVVKHAKV 426
Qy 361 NALDNLGQTSLHRAAYCGHLOTCELLLSYGCDDPNIISLQGTALQMGNNVQQLQEGIS 420
Db 427 NALDNLGQTSLHRAAYCGHLOTCELLLSYGCDDPNIISLQGTALQMGNNVQQLQEGIS 486
Qy 421 LGNSEADRLQLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVYELL 480
Db 487 LGNSEADRLQLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVYELL 546
Qy 481 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCANVMDLQWFTPLHEAASKNRVEV 540
Db 547 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCANVMDLQWFTPLHEAASKNRVEV 606
Qy 541 ICKLLQHGADPTCKNRDGNTPDLVKGDDTDIDQLLRGDAALLDAKKGCLARVKLLSS 600
Db 607 ICKLLQHGADPTCKNRDGNTPDLVKGDDTDIDQLLRGDAALLDAKKGCLARVKLLSS 666
Qy 601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 667 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 726
Qy 661 VAAALIKYNACVNTDQWAFPLHEAAKGRTOCLCALLLAGADPTLKNQSGQTPDLVLS 720
Db 727 VAAALIKYNACVNTDQWAFPLHEAAKGRTOCLCALLLAGADPTLKNQSGQTPDLVLS 786
Qy 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSQSPSSLSAASSLDNLISG 780

Db 787 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSQSPSSLSAASSLDNLISG 846
Qy 781 SFSLSLSSVSSSGTEGASSLEKKEVPGVDFSIITOPVRNLGLEHLMDFERQITLDVLVE 840
Db 847 SFSLSLSSVSSSGTEGASSLEKKEVPGVDFSIITOPVRNLGLEHLMDFERQITLDVLVE 906
Qy 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPNYLTNTSGSGTILIDLSPDDKEFQ 900
Db 907 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPNYLTNTSGSGTILIDLSPDDKEFQ 966
Qy 901 SVEEMOSTVREHRDGGHAGGIFNRYNLIKQVKNKLMWERYTHRRKEVSEENHNHANE 960
Db 967 SVEEMOSTVREHRDGGHAGGIFNRYNLIKQVKNKLMWERYTHRRKEVSEENHNHANE 1026
Qy 961 RMLFHGSPFVNAILHKGDFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCPCVHKD 1020
Db 1027 RMLFHGSPFVNAILHKGDFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCPCVHKD 1086
Qy 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGHHSVTCRPSV 1065
Db 1087 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGHHSVTCRPSV 1131
RESULT 11
ADRL14792
ID ADRL14792 standard; protein; 1166 AA.
XX
AC ADRL14792;
XX
DT 04-NOV-2004 (first entry)
XX
DE Amino acid sequence of human MAPCAX orthologue #24.
XX
KW adenomatous polyposis coli protein; APC; axin pathway;
KW modifier of APC and axin; MAPCAX; cancer; human.
XX
OS Homo sapiens.
XX
PN WO2004066948-A2.
XX
PD 12-AUG-2004.
XX
PF 28-JAN-2004; 2004WO-US002338.
XX
PR 29-JAN-2003; 2003US-0443484P.
PR 11-FEB-2003; 2003US-0447358P.
PR 10-APR-2003; 2003US-0461789P.
PR 14-MAY-2003; 2003US-0470684P.
PR 19-JUN-2003; 2003US-0479650P.
XX
PA (EXEL-) EXELIXIS INC.
XX
XX Gendreau SB, Morablanco EL, Lickteig K, Zhang H;
PI WPI; 2004-580849/56.
XX N-PSDB; ADRL14766.
DR
DR
XX
XX
PT Identifying a candidate adenomatous polyposis coli protein (APC) and axin
PT pathways modulating agent for treating cancer by contacting an assay
PT system comprising a modifier of APC and axin polypeptide or nucleic acid
PT with a test agent.
XX
XX Example 1; SEQ ID NO 50; 199pp; English.
PS
XX
XX The specification describes a method for identifying a candidate
XX adenomatous polyposis coli protein (APC) and axin pathways modulating
CC agents. The method comprises providing an assay system comprising a
CC modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting
CC the assay system with a test agent under conditions where, except for the
CC presence of the test agent, the system provides a reference activity, and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate APC and axin pathways

CC modulating agent. The method is useful in identifying a candidate
CC adenomatous polyposis coli protein (APC) and a pathways modulating agent,
CC which are useful for preparing a composition for diagnosing or treating
CC cancer. The present sequence represents a human orthologue of a
CC Caenorhabditis elegans MAPCAX polypeptide. The sequence was identified
CC using BLAST analysis.

XX
SQ Sequence 1166 AA;

Query Match 99.9%; Score 5582; DB 8; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GFGRKDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYNT	60
Db	67	GFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYNT	126
Qy	61	PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALDADPSAKAVLTGEYKDELLESAR	120
Db	127	PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALDADPSAKAVLTGEYKDELLESAR	186
Qy	121	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGLV	180
Db	187	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGLV	246
Qy	181	PLHNACSYGHEVTELLVKGACVAMDLQWFTPLHEAAKSNRVEVCSSLLSYGADPTLL	240
Db	247	PLHNACSYGHEVTELLVKGACVAMDLQWFTPLHEAAKSNRVEVCSSLLSYGADPTLL	306
Qy	241	NCHNKAIDAPTPQKERLAYEFKGSLLQAAREADVTRIKKHLSEMNFHQPOTHT	300
Db	307	NCHNKAIDAPTPQKERLAYEFKGSLLQAAREADVTRIKKHLSEMNFHQPOTHT	366
Qy	301	ALHCAAAAPYPRKQICELLRLRGANINEKTKEFLTPLHVASEKAHNDVVEVVVKEAKV	360
Db	367	ALHCAAAAPYPRKQICELLRLRGANINEKTKEFLTPLHVASEKAHNDVVEVVVKEAKV	426
Qy	361	NALDNLGQTSLHRAAYCGHLOTRCLLSYGCDDNIISLOFTALQWGNENVOQLLEGIS	420
Db	427	NALDNLGQTSLHRAAYCGHLOTRCLLSYGCDDNIISLOFTALQWGNENVOQLLEGIS	486
Qy	421	LGNSEADRLLEAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL	480
Db	487	LGNSEADRLLEAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL	546
Qy	481	QHGAADVHAKDKGLVPLHNACSYGHEVTELLVKGAVNVNADLWKFTPLHEAAAKGYE	540
Db	547	QHGAADVHAKDKGLVPLHNACSYGHEVTELLVKGAVNVNADLWKFTPLHEAAAKGYE	606
Qy	541	ICKLLQHGADPTKQNRDGNTPDLVKDGTDLQDLRGDAALLDAKKGCLARVKLSS	600
Db	607	ICKLLQHGADPTKQNRDGNTPDLVKDGTDLQDLRGDAALLDAKKGCLARVKLSS	666
Qy	601	PDNVNCRDITQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGHVD	660
Db	667	PDNVNCRDITQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGHVD	726
Qy	661	VAALLIKYNACVNATDKWFTPLHEAAKQRTQCALLAHGADPTLKNQEGQTPDLVLS	720
Db	727	VAALLIKYNACVNATDKWFTPLHEAAKQRTQCALLAHGADPTLKNQEGQTPDLVLS	786
Qy	721	ADVDSALLTAAMPSPALPSCKYQVNLGNVRSPGATADALSSGSPSSLSAASLNLGS	780
Db	787	ADVDSALLTAAMPSPALPSCKYQVNLGNVRSPGATADALSSGSPSSLSAASLNLGS	846
Qy	781	SFSELSVSSSGTEGASSLEKEVEPCVDFSIQFVRNLGLEHLMIDIFEREQITLDVLVE	840
Db	847	SFSELSVSSSGTEGASSLEKEVEPCVDFSIQFVRNLGLEHLMIDIFEREQITLDVLVE	906
Qy	841	MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLTNTSGSGTILDLSPDDKEFQ	900
Db	907	MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLTNTSGSGTILDLSPDDKEFQ	966

Qy	901	SVEEEMQSTVREHRDGGHAGGIENRYNLIKQVCNKKLWERYTHRRKEYSEENHNHANE	960
Db	967	SVEEEMQSTVREHRDGGHAGGIENRYNLIKQVCNKKLWERYTHRRKEYSEENHNHANE	1026
Qy	961	RMLFHGSPFFVNAIIHKGFDRHAYIGGMFGAGIYFAENSCKSNQYVYGIGGTCPCVHKD	1020
Db	1027	RMLFHGSPFFVNAIIHKGFDRHAYIGGMFGAGIYFAENSCKSNQYVYGIGGTCPCVHKD	1086
Qy	1021	RSYIYCHROQLLCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV	1065
Db	1087	RSYIYCHROQLLCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV	1131

RESULT 12
AAB66288
ID AAB66288 standard; protein; 1169 AA.

XX	AAB66288;
XX	AC
XX	05-APR-2001 (first entry)
XX	Human tankyrase2 clone consensus protein SEQ ID NO: 101.
XX	Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
XX	inflammatory disorder.
XX	Homo sapiens.
XX	WO200100849-A1.
XX	04-JAN-2001.
XX	28-JUN-2000; 2000WO-US017827.
XX	29-JUN-1999; 99US-0141582P.
XX	(ICOS-) ICOS CORP.
XX	Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
XX	WPI; 2001-102896/11.
XX	N-PSDB; AAF63926.
XX	New tankyrase2 polypeptides, useful for treating conditions mediated by
XX	poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
XX	inflammatory and autoimmune disorders.
XX	Example 1; Page 162-1665; 242pp; English.

The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-riboseylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders

SQ Sequence 1169 AA;

Query Match 99.9%; Score 5582; DB 4; Length 1169;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GFGRKDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYNT	60
Db	70	GFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYNT	129
Qy	61	PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALDADPSAKAVLTGEYKDELLESAR	120
Db	130	PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALDADPSAKAVLTGEYKDELLESAR	189
Qy	121	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGLV	180

Db 130 SCNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 249
Qy 181 PLHNACSYGHEVTELLVKGHCACVNDLWQFTPLHGAASKNRVEVCSSLLSYGADPTLL 240
Db 250 PLHNACSYGHEVTELLVKGHCACVNDLWQFTPLHGAASKNRVEVCSSLLSYGADPTLL 309
Qy 241 NCHNKAIDLAFTPOLKERLAYEFKHSLLQAAREADVTRIKKHLSEMVNFKHPQTHET 300
Db 310 NCHNKAIDLAFTPOLKERLAYEFKHSLLQAAREADVTRIKKHLSEMVNFKHPQTHET 369
Qy 301 ALHCAASPYPRKQICELLIRKGANINEKTEFLTPHVAASEKANDVVEVVVKEAKV 360
Db 370 ALHCAASPYPRKQICELLIRKGANINEKTEFLTPHVAASEKANDVVEVVVKEAKV 429
Qy 361 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGTALQMGNEVQOLLQEGIS 420
Db 430 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGTALQMGNEVQOLLQEGIS 489
Qy 421 LGNSEADQLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 490 LGNSEADQLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 549
Qy 481 QHGADVHAKDKGLVPLHNACSYGHEVAELLVKGVVNVADLWKFTPLHGAAGKYE 540
Db 550 QHGADVHAKDKGLVPLHNACSYGHEVAELLVKGVVNVADLWKFTPLHGAAGKYE 609
Qy 541 ICKLLQHGADPTKVRDGTPLDLVKQDGTIDQLLRGDAALLDAKKGCLARVKLSS 600
Db 610 ICKLLQHGADPTKVRDGTPLDLVKQDGTIDQLLRGDAALLDAKKGCLARVKLSS 669
Qy 601 PDNVNCRDTQGRHSHTPLHAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 670 PDNVNCRDTQGRHSHTPLHAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 729
Qy 661 VAALLIKYNACVNATDKWAFTPLHGAAGKRTQLCALLAHGADPTLKNQEGQTPDLVLS 720
Db 730 VAALLIKYNACVNATDKWAFTPLHGAAGKRTQLCALLAHGADPTLKNQEGQTPDLVLS 789
Qy 721 ADDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 780
Db 790 ADDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 849
Qy 781 SFSELSVVSSSGTGASLEKKEVGVDFSTQFVRNIGLEHMDIFEREQITLDVLVE 840
Db 850 SFSELSVVSSSGTGASLEKKEVGVDFSTQFVRNIGLEHMDIFEREQITLDVLVE 909
Qy 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQQLNPYLTLNTSGSTILIDLSPDDKEFQ 900
Db 910 MGHKELKEIGINAYGHRHKLKGVVERLISGQQLNPYLTLNTSGSTILIDLSPDDKEFQ 969
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVNCNKKLWERYTHRRKEVSEENINHANE 960
Db 970 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVNCNKKLWERYTHRRKEVSEENINHANE 1029
Qy 961 RMLFHGSPPVNAIHKGPDERHAYTGMFGAGIYFAENSNNQVYVGGTGCPVHKD 1020
Db 1030 RMLFHGSPPVNAIHKGPDERHAYTGMFGAGIYFAENSNNQVYVGGTGCPVHKD 1089
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTRGPSV 1065
Db 1090 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTRGPSV 1134

RESULT 13

AAB66278

ID AAB66278 standard; protein; 1169 AA.

XX

AC AAB66278;

XX

DT 05-APR-2001 (first entry)

XX

DE Human tankyrase2 related protein sequence SEQ ID NO: 2.

XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasia; aging;
KW inflammatory disorder.
XX Homo sapiens.
OS WO200100849-A1.
PN 04-JAN-2001.
PD 28-JUN-2000; 2000WO-US017827.
PF 29-JUN-1999; 99US-0141582P.
PR (ICOS-) ICOS CORP.
PI Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
XX WPI; 2001-102896/11.
DR N-PSDB; AAF63837.
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX Disclosure; Page 109-113; 242pp; English.
XX The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
SQ Sequence 1169 AA;
Query Match 99.9%; Score 5582; DB 4; Length 1169;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFGKRDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
Db 70 GFGKRDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 129
Qy 61 PLHEAAIKGKIDVICVILVQHGAEPTIRNTDGRDLDADPSAKAVLTGEYKDELLESAR 120
Db 130 PLHEAAIKGKIDVICVILVQHGAEPTIRNTDGRDLDADPSAKAVLTGEYKDELLESAR 189
Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 180
Db 190 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 249
Qy 181 PLHNACSYGHEVTELLVKGHCACVNDLWQFTPLHGAASKNRVEVCSSLLSYGADPTLL 240
Db 250 PLHNACSYGHEVTELLVKGHCACVNDLWQFTPLHGAASKNRVEVCSSLLSYGADPTLL 309
Qy 241 NCHNKAIDLAFTPOLKERLAYEFKHSLLQAAREADVTRIKKHLSEMVNFKHPQTHET 300
Db 310 NCHNKAIDLAFTPOLKERLAYEFKHSLLQAAREADVTRIKKHLSEMVNFKHPQTHET 369
Qy 301 ALHCAASPYPRKQICELLIRKGANINEKTEFLTPHVAASEKANDVVEVVVKEAKV 360
Db 370 ALHCAASPYPRKQICELLIRKGANINEKTEFLTPHVAASEKANDVVEVVVKEAKV 429
Qy 361 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGTALQMGNEVQOLLQEGIS 420
Db 430 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGTALQMGNEVQOLLQEGIS 489
Qy 421 LGNSEADQLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 490 LGNSEADQLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 549

QY 481 QHGADVHAKDKGGLVPLPHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGKYE 540
Db 550 QHGADVHAKDKGGLVPLPHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGKYE 609
QY 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDI QDLLRGDAALLDAAKKGCLARVKKLSS 600
Db 610 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDI QDLLRGDAALLDAAKKGCLARVKKLSS 669
QY 601 PDVNCRDQTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 670 PDVNCRDQTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 729
QY 661 VAALLIKYNACVNAATDKWAFPLHEAAQKRTQLCALLAHGADPTLKNQEGTPLDLVS 720
Db 730 VAALLIKYNACVNAATDKWAFPLHEAAQKRTQLCALLAHGADPTLKNQEGTPLDLVS 789
QY 721 ADDVSALLTAAMPSPALPSCYKQVINGVRSFGATADALSSGSPSSLSAASSLDNLGG 780
Db 790 ADDVSALLTAAMPSPALPSCYKQVINGVRSFGATADALSSGSPSSLSAASSLDNLGG 849
QY 781 SFSELSSVSSSGTEGASSLEKKEKVPDGSITQFVRNLGLEHLMDFEREQITLIDLVE 840
Db 850 SFSELSSVSSSGTEGASSLEKKEKVPDGSITQFVRNLGLEHLMDFEREQITLIDLVE 909
QY 841 MGHKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTLNTSGSTLIDLSPDDKEPQ 900
Db 910 MGHKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTLNTSGSTLIDLSPDDKEPQ 969
QY 901 SVEEBMQSTVREHROGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 970 SVEEBMQSTVREHROGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNHANE 1029
QY 961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQVYVIGGTCGCPVHKD 1020
Db 1030 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQVYVIGGTCGCPVHKD 1089
QY 1021 RSCYIChRQLLFCRVTLGKSFLOFSAMKWAHSPPGHSHSVTGRPSV 1065
Db 1090 RSCYIChRQLLFCRVTLGKSFLOFSAMKWAHSPPGHSHSVTGRPSV 1134

RESULT 14
AA97749
ID AAY97749 standard; protein; 1240 AA.

AC AAY97749;
DT 06-AUG-2001 (first entry)
DE Tankyrase homologue isotype 2 protein sequence.
DX Tankyrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation;
KW cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
KW chromosome mapping; gene therapy; vaccine.

OS Unidentified.
PN WO200130987-A2.
XX 03-MAY-2001.
XX 25-OCT-2000; 2000WO-US041528.
PF 25-OCT-1999; 99US-00427154.
PR (RIGE-) RIGEL PHARM INC.
PA Luo Y, Chan E, Xu X, Huang B;

PI WPI; 2001-300503/31.
XX N-PSDB; AAA91488.
DR
XX

PT Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing
PT or preventing cell proliferation in cells, and for diagnosing, treating
PT or preventing cell cycle associated disorders such as cancer.
XX Claim 22; Fig 4; 63pp; English.

XX This sequence is the Tankyrase homologue isotype 2 (TaHo-2) protein of
CC the invention. The invention also relates to the TaHo-2 protein. The TaHo
CC proteins are useful for inducing or preventing cell proliferation in
CC cells, and in the study or treatment of conditions mediated by the cell
CC cycle proteins, such as to diagnose, treat or prevent cell cycle
CC associated disorders, preferably cancer. The TaHo coding sequences are
CC useful as hybridisation probes, in chromosome and gene mapping and in the
CC generation of anti-sense DNA and RNA. The coding sequences are also
CC useful for the preparation of TaHo, for generating either transgenic
CC animals or knock out animals which, in turn, are useful in a development
CC and screening of therapeutically useful agents, in gene therapy, as
CC vaccine, and for construction of hybridisation probes for mapping the
CC gene which encodes TaHo and for the genetic analysis of individuals with
CC genetic disorders. The TaHo proteins, and their coding sequences are
CC useful in screening assays

XX Sequence 1240 AA;

Query Match 99.9%; Score 5582; DB 4; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1084; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGKRDVVEYLLQNGASVQARDGGIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 60
Db 141 GFGKRDVVEYLLQNGAVQARDGGIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 200
QY 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRTPALDLADPSAKAVLTGEYKDELLSAR 120
Db 201 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRTPALDLADPSAKAVLTGEYKDELLSAR 260
QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 180
Db 261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 320
QY 181 PLHNACSYGHEVTELLVKGACVNAWDLWQFTPLHEAAAKNRVEVCSLLSYGADPTLL 240
Db 321 PLHNACSYGHEVTELLVKGACVNAWDLWQFTPLHEAAAKNRVEVCSLLSYGADPTLL 380
QY 241 NCHNSAIDLAPTPQLKERLAYEFKGHSLLOAAREADVTRIKHLSLEMYNFKHPQTHET 300
Db 381 NCHNSAIDLAPTPQLKERLAYEFKGHSLLOAAREADVTRIKHLSLEMYNFKHPQTHET 440
QY 301 ALHCAAASPYPKRKQICELLRRKANINEKTEFLTPLHVASEKAHNDVVEVVVKEAKV 360
Db 441 ALHCAAASPYPKRKQICELLRRKANINEKTEFLTPLHVASEKAHNDVVEVVVKEAKV 500
QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFTALQMGNNVQQLQEGIS 420
Db 501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFTALQMGNNVQQLQEGIS 560
QY 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGNVRVSVYELL 480
Db 561 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGNVRVSVYELL 620
QY 481 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGKYE 540
Db 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGKYE 680
QY 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDI QDLLRGDAALLDAAKKGCLARVKKLSS 600
Db 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDI QDLLRGDAALLDAAKKGCLARVKKLSS 740
QY 601 PDVNCRDQTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 741 PDVNCRDQTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800
QY 661 VAALLIKYNACVNAATDKWAFPLHEAAQKRTQLCALLAHGADPTLKNQEGTPLDLVS 720

801 VAAALLIKYNACVNTDKWAFTPLHEAAQKGRTOCALLAHGADPTLKNQEGOTPLDLVS 860
 721 ADDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSSLSAASSLDNLSS 780
 861 ADDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSSLSAASSLDNLSS 920
 781 SPSSESSVSSSGTEGASLEKKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDLVE 840
 921 SPSSESSVSSSGTEGASLEKKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDLVE 980
 841 MGHEKELKEGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSTILIDLSPDKEFQ 900
 981 MGHEKELKEGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSTILIDLSPDKEFQ 1040
 901 SVEEEMQSTVREHRDGHAGGIFNRNIIKIQKVCNKKLWERYTHRRKEVSEENHNANE 960
 1041 SVEEEMQSTVREHRDGHAGGIFNRNIIKIQKVCNKKLWERYTHRRKEVSEENHNANE 1100
 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFCAGIYFAENSSKNQVYVIGGTCGCPVHKD 1020
 1101 RMLFHGSPFNVAIIHKGFDERHAYIGMFCAGIYFAENSSKNQVYVIGGTCGCPVHKD 1160
 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205

RESULT 15

ABG73731
 ID ABG73731 standard; protein; 1240 AA.
 AC ABG73731;
 DT 08-APR-2003 (first entry)
 DE Tankyrase H isotype 2 TaHo-2 fragment from clone K23.
 KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2;
 KW TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
 KW cell cycle related disorder; poly ADP-ribose polymerase; PARP.
 OS Unidentified.
 PN WO200286170-A1.
 PD 31-OCT-2002.
 PF 25-APR-2002; 2002WO-US013185.
 PR 25-APR-2001; 2001US-00843159.
 PA (RIGE-) RIGEL PHARM INC.
 PI Luo Y, Chan E, Xu X, Huang B, Ososovskaya V;
 XX WPI; 2003-093158/08.
 DR N-PSDB; ABQ77067.
 PT New recombinant nucleic acid encoding a cell cycle protein, useful for
 XX diagnosing and treating a cell cycle related disorder, e.g. cancer.

Claim 14; Fig 4; 90pp; English.

This invention describes a novel recombinant nucleic acid encoding the cell cycle protein TaHo, a tankyrase H isoform. The products of the invention have cytostatic and immunostimulant activity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a tumour cell. The methods are useful for screening for a bioactive agent capable of binding to a cell cycle protein tankyrase H, or a bioactive agent capable of modulating a cell cycle protein tankyrase H or PARP

CC (poly ADP-ribose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence represents the tankyrase H isoform 2, TaHo-2, isolated from clone K23 which is described in the disclosure of the invention
 XX Sequence 1240 AA;
 SQ
 Query Match 99.9%; Score 5582; DB 6; Length 1240;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNWT 60
 DB 141 GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNWT 200
 QY 61 PLHEAAIKGKIDVCIVLLOHGAEPTRINTDGTALDPSAKAVLTGEYKDELESAR 120
 DB 201 PLHEAAIKGKIDVCIVLLOHGAEPTRINTDGTALDPSAKAVLTGEYKDELESAR 260
 QY 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKI VOLLLOHGADVHAKDKGDLV 180
 DB 261 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKI VOLLLOHGADVHAKDKGDLV 320
 QY 181 PLHNACSYGHEVTELLVKGACVNMADLWQPTPLHEAASKNRVVCVSLLSYGADPTLL 240
 DB 321 PLHNACSYGHEVTELLVKGACVNMADLWQPTPLHEAASKNRVVCVSLLSYGADPTLL 380
 QY 241 NCHNKSADLAPTPOKLERLAYEFKSHLSLQNAAREADVTRIKKHSLEMVNFKHPQTHET 300
 DB 381 NCHNKSADLAPTPOKLERLAYEFKSHLSLQNAAREADVTRIKKHSLEMVNFKHPQTHET 440
 QY 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFTPLHVASEKAHNDVVEVVHAEKV 360
 DB 441 ALHCAAAAPYPRKQICELLRLKGANINEKTEFTPLHVASEKAHNDVVEVVHAEKV 500
 QY 361 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDPNIIISLQGFALQMGNNVQOLLQEGIS 420
 DB 501 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDPNIIISLQGFALQMGNNVQOLLQEGIS 560
 QY 421 LGNSADQLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 480
 DB 561 LGNSADQLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 620
 QY 481 QHGDVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540
 DB 621 QHGDVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 680
 QY 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDITDIQDLRGDAALLDAKKGCLARVKLSS 600
 DB 681 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDITDIQDLRGDAALLDAKKGCLARVKLSS 740
 QY 601 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLLOHGADVNAQDKGLIPLHNAASVGHVD 660
 DB 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLLOHGADVNAQDKGLIPLHNAASVGHVD 800
 QY 661 VAAALLIKYNACVNTDKWAFTPLHEAAQKGRTOCALLAHGADPTLKNQEGOTPLDLVS 720
 DB 801 VAAALLIKYNACVNTDKWAFTPLHEAAQKGRTOCALLAHGADPTLKNQEGOTPLDLVS 860
 QY 721 ADDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSSLSAASSLDNLSS 780
 DB 861 ADDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSSLSAASSLDNLSS 920
 QY 781 SPSSESSVSSSGTEGASLEKKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDLVE 840
 DB 921 SPSSESSVSSSGTEGASLEKKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDLVE 980
 QY 841 MGHEKELKEGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSTILIDLSPDKEFQ 900
 DB 981 MGHEKELKEGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSTILIDLSPDKEFQ 1040
 QY 901 SVEEEMQSTVREHRDGHAGGIFNRNIIKIQKVCNKKLWERYTHRRKEVSEENHNANE 960

Db 1041 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 1100
Qy 961 RMLFHGSPFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTCCPVHKD 1020
Db 1101 RMLFHGSPFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTCCPVHKD 1160
Qy 1021 RSCYICHRQLLCRVTLGKSLQFSAMKMAHSPFGHHSVTGRPSV 1065
Db 1161 RSCYICHRQLLCRVTLGKSLQFSAMKMAHSPFGHHSVTGRPSV 1205

Search completed: December 18, 2006, 17:26:52
Job time : 142.536 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:51:56 ; Search time 132.143 Seconds
(without alignments)
3733.253 Million cell updates/sec

Title: US-10-616-101-3
Perfect score: 5585
Sequence: 1 GFRKDVVEYLLONGASVQA.....AMKMAHSPGHHSVTGRPSV 1065

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Print out

Result No.	Score	Query Match	Length	DB ID	Description
1	5585	100.0	1065	5	US-10-616-101-3
2	5585	100.0	1083	5	US-10-616-101-12
3	5585	100.0	1100	5	US-10-616-101-8
4	5582	99.9	1166	4	US-09-972-115A-6
5	5582	99.9	1166	4	US-10-163-587A-15
6	5582	99.9	1166	4	US-10-199-937-135
7	5582	99.9	1169	4	US-10-199-937-2
8	5582	99.9	1169	4	US-10-199-937-101
9	5582	99.9	1240	5	US-10-616-101-4
10	5582	99.9	1262	4	US-10-199-937-107
11	5582	99.9	1385	4	US-10-199-937-133
12	5579	99.9	1100	5	US-10-616-101-11
13	5421	97.1	1074	3	US-09-509-196A-2
14	5363.5	96.0	1227	3	US-09-849-602-26
15	4740.5	84.9	1327	3	US-09-841-835-2
16	4740.5	84.9	1327	3	US-09-972-115A-8
17	4740.5	84.9	1327	3	US-10-199-937-4
18	4739.5	84.9	1333	3	US-09-972-115A-2
19	4663	83.5	1267	3	US-09-972-115A-4
20	3918	70.2	784	4	US-10-199-937-89
21	3775	67.6	756	4	US-10-199-937-91
22	3706.5	66.4	1181	4	US-10-199-937-139
23	3706.5	66.4	1181	6	US-11-097-143-9474
24	3412	61.1	802	3	US-09-964-899-41
25	3412	61.1	802	5	US-10-975-523-41
26	3093	55.4	949	3	US-09-841-835-10
27	2916	52.2	583	5	US-10-616-101-10

28	2367	42.4	522	4	US-10-199-937-99	Sequence 99, Appl
29	2165	38.8	415	4	US-10-276-774-1690	Sequence 1690, Ap
30	1918.5	34.4	673	3	US-09-841-835-8	Sequence 8, Appli
31	1895	33.9	362	4	US-10-199-937-160	Sequence 160, App
32	1869.5	33.5	1099	4	US-10-199-937-178	Sequence 178, App
33	1038	18.6	338	5	US-10-616-101-9	Sequence 9, Appli
34	877.5	15.7	1765	5	US-10-055-877-140	Sequence 140, App
35	875.5	15.7	4274	5	US-10-450-763-31331	Sequence 31331, A
36	875.5	15.7	4377	5	US-10-756-149-4917	Sequence 4917, Ap
37	875.5	15.7	4384	5	US-10-821-234-1120	Sequence 1120, Ap
38	875.5	15.7	4386	5	US-10-450-763-37734	Sequence 37734, A
39	871.5	15.6	1940	5	US-10-055-877-141	Sequence 141, App
40	863.5	15.5	1762	4	US-10-205-194-117	Sequence 117, App
41	860.5	15.4	1330	4	US-10-108-260A-3237	Sequence 3237, Ap
42	852.5	15.3	4397	5	US-10-450-763-52303	Sequence 52303, A
43	836	15.0	1549	6	US-11-097-143-1776	Sequence 1776, Ap
44	836	15.0	1549	6	US-11-097-143-29028	Sequence 29028, A
45	820	14.7	1159	5	US-10-055-877-139	Sequence 139, App

ALIGNMENTS

RESULT 1

US-10-616-101-3
; Sequence 3, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: Tankrase H, Compositions Involved in the Cell Cycle and Methods c
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1065
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-101-3

Query Match	100.0%	Score	5585;	DB	5;	Length	1065;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1065;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	GFRKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVWVNLRLRHGADPNARDNWT	60				
Db	1	GFRKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVWVNLRLRHGADPNARDNWT	60				
QY	61	PLHEAAIKGIDVCIIVLLOHGAETIRNTDGTALDLDADPSAKAVLTGEYKKDELLESAR	120				
Db	61	PLHEAAIKGIDVCIIVLLOHGAETIRNTDGTALDLDADPSAKAVLTGEYKKDELLESAR	120				
QY	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGVNRVKIVQLLLOHGAHVHAKDKGDLV	180				
Db	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGVNRVKIVQLLLOHGAHVHAKDKGDLV	180				
QY	181	PLHNACSYGHVEVTELLVKGACVNVMDLWQFTPLHEAASKNRVVCVCSLLLSYGADPTLL	240				
Db	181	PLHNACSYGHVEVTELLVKGACVNVMDLWQFTPLHEAASKNRVVCVCSLLLSYGADPTLL	240				
QY	241	NCHNKAIDLAFTPOLKERLAYEFKXGHSLLQAAAREADVTRIKKHLSEMVNFKPQTHT	300				

Db 241 NCHNKAIDLAPTPQKRLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKHPOTHET 300
Qy 301 ALHCAASPPYKKEKQICELLRRKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKV 360
Db 301 ALHCAASPPYKKEKQICELLRRKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKV 360
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVQQLQEGIS 420
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVQQLQEGIS 420
Qy 421 LGNSEADROLLEAAKAGDVETVKKCTVQSVNCRDIEGROSTPLHFAAGVNRVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKKCTVQSVNCRDIEGROSTPLHFAAGVNRVSVVEYLL 480
Qy 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VNVADLWKFTPLHFAAAGKGYE 540
Db 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VNVADLWKFTPLHFAAAGKGYE 540
Qy 541 ICKLLQHAGADPTKQRDGNTPDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLS 600
Db 541 ICKLLQHAGADPTKQRDGNTPDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLS 600
Qy 601 PDNVNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGYHD 660
Db 601 PDNVNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGYHD 660
Qy 661 VAALLIKYNACVNAATDKWAFTPLHAAQKGRTOQLCALLAHGADPTLKQEGOTPLDLVS 720
Db 661 VAALLIKYNACVNAATDKWAFTPLHAAQKGRTOQLCALLAHGADPTLKQEGOTPLDLVS 720
Qy 721 ADDVSALLTAAMPSPALPCYKQVNLGVNSPGATADALSSGSPSSLSAASLDNLG 780
Db 721 ADDVSALLTAAMPSPALPCYKQVNLGVNSPGATADALSSGSPSSLSAASLDNLG 780
Qy 781 SFSELSVSSVSSGTEGASSLEKEVPGVDFSIITQFVNRNGLHLMDFEREQITLDVLVE 840
Db 781 SFSELSVSSVSSGTEGASSLEKEVPGVDFSIITQFVNRNGLHLMDFEREQITLDVLVE 840
Qy 841 MGHKELKEIGINAYGHRHKLIKGVERLISQOQGLNPYLTINTSGSGTILIDLSPDDKEFQ 900
Db 841 MGHKELKEIGINAYGHRHKLIKGVERLISQOQGLNPYLTINTSGSGTILIDLSPDDKEFQ 900
Qy 901 SVEEENQSTVREHDCGHAGGIFNRRNLIKIQVCNKKLWERTHRKKEVSEENHNHANE 960
Db 901 SVEEENQSTVREHDCGHAGGIFNRRNLIKIQVCNKKLWERTHRKKEVSEENHNHANE 960
Qy 961 RMLFHGSPFNALIIHKGFDERHAYIGMFGAGIYFAENSCKSNQYVYGGGTGCPVHKD 1020
Db 961 RMLFHGSPFNALIIHKGFDERHAYIGMFGAGIYFAENSCKSNQYVYGGGTGCPVHKD 1020
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065

RESULT 2
US-10-616-101-12
; Sequence 12, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossoskava, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-10-616-101-12

Query Match 100.0%; Score 5585; DB 5; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKRDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYTT 60
Db 1 GFGKRDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYTT 60
Qy 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRTPALDADPSAKAVLTGEYKKDELLSAR 120
Db 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRTPALDADPSAKAVLTGEYKKDELLSAR 120
Qy 121 SGNEEKWALLTPLVNCHASDGRKSTPLHLAGYNRVKIVOLLQHGADVHAKDKGDLV 180
Db 121 SGNEEKWALLTPLVNCHASDGRKSTPLHLAGYNRVKIVOLLQHGADVHAKDKGDLV 180
Qy 181 PLHNACSYGHYEYVELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSSLISYGADPTLL 240
Db 181 PLHNACSYGHYEYVELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSSLISYGADPTLL 240
Qy 241 NCHNKAIDLAPTPQKRLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKHPOTHET 300
Db 241 NCHNKAIDLAPTPQKRLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKHPOTHET 300
Qy 301 ALHCAASPPYKKEKQICELLRRKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKV 360
Db 301 ALHCAASPPYKKEKQICELLRRKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKV 360
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVQQLQEGIS 420
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVQQLQEGIS 420
Qy 421 LGNSEADROLLEAAKAGDVETVKKCTVQSVNCRDIEGROSTPLHFAAGVNRVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKKCTVQSVNCRDIEGROSTPLHFAAGVNRVSVVEYLL 480
Qy 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VNVADLWKFTPLHFAAAGKGYE 540
Db 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VNVADLWKFTPLHFAAAGKGYE 540
Qy 541 ICKLLQHAGADPTKQRDGNTPDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLS 600
Db 541 ICKLLQHAGADPTKQRDGNTPDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLS 600
Qy 601 PDNVNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGYHD 660
Db 601 PDNVNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGYHD 660
Qy 661 VAALLIKYNACVNAATDKWAFTPLHAAQKGRTOQLCALLAHGADPTLKQEGOTPLDLVS 720
Db 661 VAALLIKYNACVNAATDKWAFTPLHAAQKGRTOQLCALLAHGADPTLKQEGOTPLDLVS 720
Qy 721 ADDVSALLTAAMPSPALPCYKQVNLGVNSPGATADALSSGSPSSLSAASLDNLG 780
Db 721 ADDVSALLTAAMPSPALPCYKQVNLGVNSPGATADALSSGSPSSLSAASLDNLG 780
Qy 781 SFSELSVSSVSSGTEGASSLEKEVPGVDFSIITQFVNRNGLHLMDFEREQITLDVLVE 840
Db 781 SFSELSVSSVSSGTEGASSLEKEVPGVDFSIITQFVNRNGLHLMDFEREQITLDVLVE 840
Qy 841 MGHKELKEIGINAYGHRHKLIKGVERLISQOQGLNPYLTINTSGSGTILIDLSPDDKEFQ 900

Db	841	MGHKLKEIGINAYGHRHKLKGVVERLISGQGLNPLYLTNTSGSGTTLIDLSPDDKEFQ	900
Qy	901	SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE	960
Db	901	SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE	960
Qy	961	RMLFHGSPFNVAI IHKGFDERHAYIGCMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD	1020
Db	961	RMLFHGSPFNVAI IHKGFDERHAYIGCMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD	1020
Qy	1021	RSYCHIRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV	1065
Db	1021	RSYCHIRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV	1065
RESULT 3			
US-10-616-101-8			
; Sequence 8, Application US/10616101			
; Publication No. US20050074825A1			
GENERAL INFORMATION:			
; APPLICANT: Luo, Ying			
; APPLICANT: Chan, Eva			
; APPLICANT: Xu, Xiang			
; APPLICANT: Huang, Betty			
; APPLICANT: Ossovskaya, Valeria			
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods			
; FILE REFERENCE: RIGL-010CIP3			
; CURRENT APPLICATION NUMBER: US/10/616,101			
; PRIOR FILING DATE: 2003-07-08			
; PRIOR APPLICATION NUMBER: US 09/843,159			
; PRIOR FILING DATE: 2001-04-25			
; PRIOR APPLICATION NUMBER: US 09/596,668			
; PRIOR FILING DATE: 2000-10-25			
; PRIOR APPLICATION NUMBER: US 09/427,154			
; PRIOR FILING DATE: 1999-10-25			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 8			
; LENGTH: 1100			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-616-101-8			
Query Match 100.0%; Score 5585; DB 5; Length 1100;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GFGKRDVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARDNNYTT	60
Db	1	GFGKRDVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARDNNYTT	60
Qy	61	PLHEAAIKGKIDVCIVLLOHGAEPITRNDGTALDADPSAKAVLTGEYKDELLESAR	120
Db	61	PLHEAAIKGKIDVCIVLLOHGAEPITRNDGTALDADPSAKAVLTGEYKDELLESAR	120
Qy	121	SGNEKMMALLTPLNVNCHASGRKSTPLHLAAGNRYKIVOLLLOHGAHVAKDKGLV	180
Db	121	SGNEKMMALLTPLNVNCHASGRKSTPLHLAAGNRYKIVOLLLOHGAHVAKDKGLV	180
Qy	181	PLHNACSYGHVEVTELLVKGHCACVAMDLWQFTPLHEAASKRVEVCILLISYGDPTLL	240
Db	181	PLHNACSYGHVEVTELLVKGHCACVAMDLWQFTPLHEAASKRVEVCILLISYGDPTLL	240
Qy	241	NCHNKAISDALPTPOLKERLAYEFKGHLSLQAAAREADVTRIKKHSLEWVNFKHPQTHET	300
Db	241	NCHNKAISDALPTPOLKERLAYEFKGHLSLQAAAREADVTRIKKHSLEWVNFKHPQTHET	300
Qy	301	ALHCAASPYKPKQKICELLKKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV	360
Db	301	ALHCAASPYKPKQKICELLKKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV	360
Qy	361	NALDNLGQTSLHRAAYCGHLOTCELLLSYGCDDPNIIISLQGFALQMGNENVOQLLEQGIS	420

Db	361	NALDNLGQTSLHRAAYCGHLOTCELLLSYGCDDPNIIISLQGFALQMGNENVOQLLEQGIS	420
Qy	421	LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVEYLL	480
Db	421	LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVEYLL	480
Qy	481	QHGAADVHAQDKGGLVPLHNACSYGHYEAELLVKHGA VNVNADLWKFTPLHEAAAKGYE	540
Db	481	QHGAADVHAQDKGGLVPLHNACSYGHYEAELLVKHGA VNVNADLWKFTPLHEAAAKGYE	540
Qy	541	ICKLLOHGAADPTKKNRDGNTPLDLVKDGDTDIOQLLRGDAALLDAKKGCLARVKKLSS	600
Db	541	ICKLLOHGAADPTKKNRDGNTPLDLVKDGDTDIOQLLRGDAALLDAKKGCLARVKKLSS	600
Qy	601	PDVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNADQKGLIPLHNAASYGHVD	660
Db	601	PDVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNADQKGLIPLHNAASYGHVD	660
Qy	661	VAALLIKYNACVNATDKWAFPLHEAAQKGTQCALILLAHGADPTLKNQEGOTPLDLVS	720
Db	661	VAALLIKYNACVNATDKWAFPLHEAAQKGTQCALILLAHGADPTLKNQEGOTPLDLVS	720
Qy	721	ADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSPSSLSAASSLONLSG	780
Db	721	ADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSPSSLSAASSLONLSG	780
Qy	781	SFSELSSVSSSGTEGASSLEKKEVPGVDFITQFVRNLGLEHLMDFEREQITLDLVE	840
Db	781	SFSELSSVSSSGTEGASSLEKKEVPGVDFITQFVRNLGLEHLMDFEREQITLDLVE	840
Qy	841	MGHKLKEIGINAYGHRHKLKGVVERLISGQGLNPLYLTNTSGSGTTLIDLSPDDKEFQ	900
Db	841	MGHKLKEIGINAYGHRHKLKGVVERLISGQGLNPLYLTNTSGSGTTLIDLSPDDKEFQ	900
Qy	901	SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE	960
Db	901	SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE	960
Qy	961	RMLFHGSPFNVAI IHKGFDERHAYIGCMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD	1020
Db	961	RMLFHGSPFNVAI IHKGFDERHAYIGCMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD	1020
Qy	1021	RSYCHIRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV	1065
Db	1021	RSYCHIRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV	1065

RESULT 4

US-09-972-115A-6
; Sequence 6, Application US/09972115A
; Publication No. US20030032769A1

GENERAL INFORMATION:

; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-6

already issued
has issued result No.4

Query Match									
Best Local Similarity 99.9%; Score 5582; DB 3; Length 1166;									
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GFGKDVVEYLLQNGASVQARDGGLPLHNACSF	GHAENVNLLRHGADPNARDNNYT	60					
Db	67	GFGKDVVEYLLQNGANVQARDGGLPLHNACSF	GHAENVNLLRHGADPNARDNNYT	126					
Qy	61	PLHEAAIKGIDVICIVLLQHGAEPTIRNTDGR	TALDLPDSAKAVLTGEYKOBELLESAR	120					
Db	127	PLHEAAIKGIDVICIVLLQHGAEPTIRNTDGR	TALDLPDSAKAVLTGEYKOBELLESAR	186					
Qy	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLA	AGYNRVKIVQLLQHGADVHAKDGDIV	180					
Db	187	SGNEEKWALLTPLNVNCHASDGRKSTPLHLA	AGYNRVKIVQLLQHGADVHAKDGDIV	246					
Qy	181	PLHNACSYGHYEVTELLVKGACVNMQLWQFT	PLHEAASKNRVEVCSLLSYGADPTLL	240					
Db	247	PLHNACSYGHYEVTELLVKGACVNMQLWQFT	PLHEAASKNRVEVCSLLSYGADPTLL	306					
Qy	241	NCHNKAIDLAPTLPQKERLAYEFKSHLSLQA	AREADVTRIKKHLSEMNVFKHPQTHET	300					
Db	307	NCHNKAIDLAPTLPQKERLAYEFKSHLSLQA	AREADVTRIKKHLSEMNVFKHPQTHET	366					
Qy	301	ALHCAAAAPYPRKQICELLRKGANINEKTK	EFLTPLHVASEKAHNDVVEVVVKEAKV	360					
Db	367	ALHCAAAAPYPRKQICELLRKGANINEKTK	EFLTPLHVASEKAHNDVVEVVVKEAKV	426					
Qy	361	NALNGLQTSLHRAAYCGHLQTCRLLLSYGC	DPNIIISLQGTALQMGNEVQQLQEGIS	420					
Db	427	NALNGLQTSLHRAAYCGHLQTCRLLLSYGC	DPNIIISLQGTALQMGNEVQQLQEGIS	486					
Qy	421	LGNSEADQLLEAAKAGDVETVKKLCTVQSV	NCRDIEGRQSTPLHFAAGYNRVSVVEYLL	480					
Db	487	LGNSEADQLLEAAKAGDVETVKKLCTVQSV	NCRDIEGRQSTPLHFAAGYNRVSVVEYLL	546					
Qy	481	QHGADVHAKDGGGLVPLHNACSYGHYEVA	ELLVKHGAVNVADLWKFTPLHEAAAKGYE	540					
Db	547	QHGADVHAKDGGGLVPLHNACSYGHYEVA	ELLVKHGAVNVADLWKFTPLHEAAAKGYE	606					
Qy	541	ICKLLQHGADPTKKNRDGNTPLDLVKDGD	TDIQDLLRGDAALLDAAKGCCLARVKKLS	600					
Db	607	ICKLLQHGADPTKKNRDGNTPLDLVKDGD	TDIQDLLRGDAALLDAAKGCCLARVKKLS	666					
Qy	601	PDVNCRDTCGRHSTPLHLAAGYNNLEVA	EYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660					
Db	667	PDVNCRDTCGRHSTPLHLAAGYNNLEVA	EYLLQHGADVNAQDKGGLIPLHNAASYGHVD	726					
Qy	661	VAALLIKYNACVNAATDKWAFPLHEAAQK	GRTOCALLLAHGADPTLKNQEGOTPLDIVS	720					
Db	727	VAALLIKYNACVNAATDKWAFPLHEAAQK	GRTOCALLLAHGADPTLKNQEGOTPLDIVS	786					
Qy	721	ADDVSALLTAAMPSPALPSCYKPVQVNG	VRSPGATADALSSGSPSSPSLSAASLNDLSG	780					
Db	787	ADDVSALLTAAMPSPALPSCYKPVQVNG	VRSPGATADALSSGSPSSPSLSAASLNDLSG	846					
Qy	781	SFSELSSVSSSGTEGASSLEKKEVPVDF	SITQFVRNLGLEHLMIDIFEREQITLDLVE	840					
Db	847	SFSELSSVSSSGTEGASSLEKKEVPVDF	SITQFVRNLGLEHLMIDIFEREQITLDLVE	906					
Qy	841	MGHKELKEIGINAYGHRHKLTKGVERLI	SGOQGLNPYLTLNTSGSGTILLDLSDDKEFQ	900					
Db	907	MGHKELKEIGINAYGHRHKLTKGVERLI	SGOQGLNPYLTLNTSGSGTILLDLSDDKEFQ	966					
Qy	901	SVEEMOSTVREHDDGGHAGGIFNRYNIL	KIQKCNKKLWERYTHRKEVSEENHNANE	960					
Db	967	SVEEMOSTVREHDDGGHAGGIFNRYNIL	KIQKCNKKLWERYTHRKEVSEENHNANE	1026					
Qy	961	RMLFHGSPFVNAIIHKGFDERHAYIGGM	FGAGIYFAENSCKSNQYVYIGGGTCGPVHKD	1020					
Db	1027	RMLFHGSPFVNAIIHKGFDERHAYIGGM	FGAGIYFAENSCKSNQYVYIGGGTCGPVHKD	1086					
Qy	1021	RSCYICHRQLLFCRVTLGKSLQFSAMKMA	HSPPGHHSVTGRPSV 1065						

Db	1087	RSCYICHRQLLFCRVTLGKSLQFSAMKMA	HSPPGHHSVTGRPSV 1131						
RESULT 5									
US-10-163-587A-15									
; Sequence 15, Application US/10163587A									
; Publication No. US20030096263A1									
; GENERAL INFORMATION:									
; APPLICANT: Oliveira, Marcos									
; TITLE OF INVENTION: SELECTING PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING I									
; FILE REFERENCE: 50229-306									
; CURRENT APPLICATION NUMBER: US/10/163,587A									
; CURRENT FILING DATE: 2003-01-10									
; PRIOR APPLICATION NUMBER: 60/296,110									
; PRIOR FILING DATE: 2001-06-07									
; NUMBER OF SEQ ID NOS: 40									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 15									
; LENGTH: 1166									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-163-587A-15									
Query Match									
Best Local Similarity 99.9%; Score 5582; DB 4; Length 1166;									
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GFGKDVVEYLLQNGASVQARDGGLPLHNACSF	GHAENVNLLRHGADPNARDNNYT	60					
Db	67	GFGKDVVEYLLQNGANVQARDGGLPLHNACSF	GHAENVNLLRHGADPNARDNNYT	126					
Qy	61	PLHEAAIKGIDVICIVLLQHGAEPTIRNTDGR	TALDLPDSAKAVLTGEYKOBELLESAR	120					
Db	127	PLHEAAIKGIDVICIVLLQHGAEPTIRNTDGR	TALDLPDSAKAVLTGEYKOBELLESAR	186					
Qy	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLA	AGYNRVKIVQLLQHGADVHAKDGDIV	180					
Db	187	SGNEEKWALLTPLNVNCHASDGRKSTPLHLA	AGYNRVKIVQLLQHGADVHAKDGDIV	246					
Qy	181	PLHNACSYGHYEVTELLVKGACVNMQLWQFT	PLHEAASKNRVEVCSLLSYGADPTLL	240					
Db	247	PLHNACSYGHYEVTELLVKGACVNMQLWQFT	PLHEAASKNRVEVCSLLSYGADPTLL	306					
Qy	241	NCHNKAIDLAPTLPQKERLAYEFKSHLSLQA	AREADVTRIKKHLSEMNVFKHPQTHET	300					
Db	307	NCHNKAIDLAPTLPQKERLAYEFKSHLSLQA	AREADVTRIKKHLSEMNVFKHPQTHET	366					
Qy	301	ALHCAAAAPYPRKQICELLRKGANINEKTK	EFLTPLHVASEKAHNDVVEVVVKEAKV	360					
Db	367	ALHCAAAAPYPRKQICELLRKGANINEKTK	EFLTPLHVASEKAHNDVVEVVVKEAKV	426					
Qy	361	NALNGLQTSLHRAAYCGHLQTCRLLLSYGC	DPNIIISLQGTALQMGNEVQQLQEGIS	420					
Db	427	NALNGLQTSLHRAAYCGHLQTCRLLLSYGC	DPNIIISLQGTALQMGNEVQQLQEGIS	486					
Qy	421	LGNSEADQLLEAAKAGDVETVKKLCTVQSV	NCRDIEGRQSTPLHFAAGYNRVSVVEYLL	480					
Db	487	LGNSEADQLLEAAKAGDVETVKKLCTVQSV	NCRDIEGRQSTPLHFAAGYNRVSVVEYLL	546					
Qy	481	QHGADVHAKDGGGLVPLHNACSYGHYEVA	ELLVKHGAVNVADLWKFTPLHEAAAKGYE	540					
Db	547	QHGADVHAKDGGGLVPLHNACSYGHYEVA	ELLVKHGAVNVADLWKFTPLHEAAAKGYE	606					
Qy	541	ICKLLQHGADPTKKNRDGNTPLDLVKDGD	TDIQDLLRGDAALLDAAKGCCLARVKKLS	600					
Db	607	ICKLLQHGADPTKKNRDGNTPLDLVKDGD	TDIQDLLRGDAALLDAAKGCCLARVKKLS	666					
Qy	601	PDVNCRDTCGRHSTPLHLAAGYNNLEVA	EYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660					
Db	667	PDVNCRDTCGRHSTPLHLAAGYNNLEVA	EYLLQHGADVNAQDKGGLIPLHNAASYGHVD	726					
Qy	661	VAALLIKYNACVNAATDKWAFPLHEAAQK	GRTOCALLLAHGADPTLKNQEGOTPLDIVS	720					
Db	727	VAALLIKYNACVNAATDKWAFPLHEAAQK	GRTOCALLLAHGADPTLKNQEGOTPLDIVS	786					
Qy	721	ADDVSALLTAAMPSPALPSCYKPVQVNG	VRSPGATADALSSGSPSSPSLSAASLNDLSG	780					
Db	787	ADDVSALLTAAMPSPALPSCYKPVQVNG	VRSPGATADALSSGSPSSPSLSAASLNDLSG	846					
Qy	781	SFSELSSVSSSGTEGASSLEKKEVPVDF	SITQFVRNLGLEHLMIDIFEREQITLDLVE	840					
Db	847	SFSELSSVSSSGTEGASSLEKKEVPVDF	SITQFVRNLGLEHLMIDIFEREQITLDLVE	906					
Qy	841	MGHKELKEIGINAYGHRHKLTKGVERLI	SGOQGLNPYLTLNTSGSGTILLDLSDDKEFQ	900					
Db	907	MGHKELKEIGINAYGHRHKLTKGVERLI	SGOQGLNPYLTLNTSGSGTILLDLSDDKEFQ	966					
Qy	901	SVEEMOSTVREHDDGGHAGGIFNRYNIL	KIQKCNKKLWERYTHRKEVSEENHNANE	960					
Db	967	SVEEMOSTVREHDDGGHAGGIFNRYNIL	KIQKCNKKLWERYTHRKEVSEENHNANE	1026					
Qy	961	RMLFHGSPFVNAIIHKGFDERHAYIGGM	FGAGIYFAENSCKSNQYVYIGGGTCGPVHKD	1020					
Db	1027	RMLFHGSPFVNAIIHKGFDERHAYIGGM	FGAGIYFAENSCKSNQYVYIGGGTCGPVHKD	1086					
Qy	1021	RSCYICHRQLLFCRVTLGKSLQFSAMKMA	HSPPGHHSVTGRPSV 1065						

Db 727 VAAALLIKYNACVATDKWAFPLHEAAQKGRTOCALLAHGADPTLKNQEGQTPDLVLS 786
Qy 721 ADDVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 780
Db 787 ADDVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 846
Qy 781 SFSELSVVSSSGTGASLEKKEVPGVDFTSQFVRLNGLHLMDFEREQITLDVLVE 840
Db 847 SFSELSVVSSSGTGASLEKKEVPGVDFTSQFVRLNGLHLMDFEREQITLDVLVE 906
Qy 841 MGHEKKEIGINAYGHRHKLKGVRLISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
Db 907 MGHEKKEIGINAYGHRHKLKGVRLISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 967 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 1026
Qy 961 RMLFHGSPFVNAILHKGDFERHAYIGMGFAGIYFAENSSKSNQVYVYGGTGCPVHKD 1020
Db 1027 RMLFHGSPFVNAILHKGDFERHAYIGMGFAGIYFAENSSKSNQVYVYGGTGCPVHKD 1086
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1087 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1131
RESULT 6
US-10-199-937-135
; Sequence 135, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-135
Query Match 99.9%; Score 5582; DB 4; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFGRKDVVYLLQNGASVQARDGGLIPLHNACSFHAEVNVLLRHGADPNARDNNVT 60
Db 67 GFGRKDVVYLLQNGASVQARDGGLIPLHNACSFHAEVNVLLRHGADPNARDNNVT 126
Qy 61 PLHEAAKIDVICVILLOHGAEPTRINTDGTALDPSAKAVLTGEYKDELLESAR 120
Db 127 PLHEAAKIDVICVILLOHGAEPTRINTDGTALDPSAKAVLTGEYKDELLESAR 186
Qy 121 SGNEEKOMALLPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGDIV 180
Db 187 SGNEEKOMALLPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGDIV 246
Qy 181 PLHNACSYGHEVTELLVHKGACVNAWDLQWFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 247 PLHNACSYGHEVTELLVHKGACVNAWDLQWFTPLHEAASKNRVEVCSLLLSYGADPTLL 306

Qy 241 NCHNKSALDAPTQPKERLAYEFKSHLSLOAAREADVTRIKKHLSEMMVNFKIPQTHET 300
Db 307 NCHNKSALDAPTQPKERLAYEFKSHLSLOAAREADVTRIKKHLSEMMVNFKIPQTHET 366
Qy 301 ALHCAASAPYPRKQICELLRLKGANINEKTEFLPLHVASEKANDVDVVEVVKHEAKV 360
Db 367 ALHCAASAPYPRKQICELLRLKGANINEKTEFLPLHVASEKANDVDVVEVVKHEAKV 426
Qy 361 NALNIGQTSLHRAAYCGHLOTCRLLLSYGDNPNIISLOGFTALQMGNNVQQLLOEGIS 420
Db 427 NALNIGQTSLHRAAYCGHLOTCRLLLSYGDNPNIISLOGFTALQMGNNVQQLLOEGIS 486
Qy 421 LGNEADQRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 487 LGNEADQRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546
Qy 481 QHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHEAAKAGYE 540
Db 547 QHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHEAAKAGYE 606
Qy 541 ICKLLHQHAGDPTTKNRDGNTPDLVKDGDITDIODLLRGDAALLDAKKGCLARVKKLSS 600
Db 607 ICKLLHQHAGDPTTKNRDGNTPDLVKDGDITDIODLLRGDAALLDAKKGCLARVKKLSS 666
Qy 601 PDVNCRDTCGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 667 PDVNCRDTCGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 726
Qy 661 VAAALLIKYNACVATDKWAFPLHEAAQKGRTOCALLAHGADPTLKNQEGQTPDLVLS 720
Db 727 VAAALLIKYNACVATDKWAFPLHEAAQKGRTOCALLAHGADPTLKNQEGQTPDLVLS 786
Qy 721 ADDVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 780
Db 787 ADDVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 846
Qy 781 SFSELSVVSSSGTGASLEKKEVPGVDFTSQFVRLNGLHLMDFEREQITLDVLVE 840
Db 847 SFSELSVVSSSGTGASLEKKEVPGVDFTSQFVRLNGLHLMDFEREQITLDVLVE 906
Qy 841 MGHEKKEIGINAYGHRHKLKGVRLISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
Db 907 MGHEKKEIGINAYGHRHKLKGVRLISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 967 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 1026
Qy 961 RMLFHGSPFVNAILHKGDFERHAYIGMGFAGIYFAENSSKSNQVYVYGGTGCPVHKD 1020
Db 1027 RMLFHGSPFVNAILHKGDFERHAYIGMGFAGIYFAENSSKSNQVYVYGGTGCPVHKD 1086
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1087 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1131
RESULT 7
US-10-199-937-2
; Sequence 2, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582

;; PRIOR FILING DATE: 1999-06-29
;; NUMBER OF SEQ ID NOS: 178
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 1169
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-199-937-2

Query Match 99.9%; Score 5582; DB 4; Length 1169;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 60
Db 70 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 129
Qy 61 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLSAR 120
Db 130 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLSAR 189
Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGDV 180
Db 190 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGDV 249
Qy 181 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
Db 250 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 309
Qy 241 NCHNKAIDLAPTQKRLAYEFKSHLSLQAAREADVTRIKKHLSEMNFKHPQTHET 300
Db 310 NCHNKAIDLAPTQKRLAYEFKSHLSLQAAREADVTRIKKHLSEMNFKHPQTHET 369
Qy 301 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPLVHASEKAHNDVVEVVKHEAKV 360
Db 370 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPLVHASEKAHNDVVEVVKHEAKV 429
Qy 361 NALNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQMGNEVQQLQEGIS 420
Db 430 NALNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQMGNEVQQLQEGIS 489
Qy 421 LGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 490 LGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 549
Qy 481 QHGADVHAKDGGVPLHNACSYGHEVVAELLVKGAVNVNADLWKFTPLHEAAAKGYE 540
Db 550 QHGADVHAKDGGVPLHNACSYGHEVVAELLVKGAVNVNADLWKFTPLHEAAAKGYE 609
Qy 541 ICKLLQHGADPTKKNRGNTPLDLVKDGDITDQLLRGDAALLDAAKKGCLARVKLSS 600
Db 610 ICKLLQHGADPTKKNRGNTPLDLVKDGDITDQLLRGDAALLDAAKKGCLARVKLSS 669
Qy 601 PDNVCNCRDTQGRHSTPLHLAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 670 PDNVCNCRDTQGRHSTPLHLAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 729
Qy 661 VAALLIKYCNVATDKWAFPLHEAAQKGTQCLALLAHGADPTLKNQSGQPTDLVS 720
Db 730 VAALLIKYCNVATDKWAFPLHEAAQKGTQCLALLAHGADPTLKNQSGQPTDLVS 789
Qy 721 ADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSSLSAASLDNLISG 780
Db 790 ADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSSLSAASLDNLISG 849
Qy 781 SFSELSSVSSSGTEGASSLEKKEVPGVDFISITQFVNLGHEHLMDFEREQITDLVIVE 840
Db 850 SFSELSSVSSSGTEGASSLEKKEVPGVDFISITQFVNLGHEHLMDFEREQITDLVIVE 909
Qy 841 MGHKELKEIGINAYCHRRHKLIGVERLISGQOGLNPLYTLNTSGSGTILIDLSPPDKFEQ 900
Db 910 MGHKELKEIGINAYCHRRHKLIGVERLISGQOGLNPLYTLNTSGSGTILIDLSPPDKFEQ 969

Qy 901 SVEEEMOSTVREHRDGGHAGGIENRYNLIKQKCNKWLWERYTHRRKEYSEENHNHANE 960
Db 970 SVEEEMOSTVREHRDGGHAGGIENRYNLIKQKCNKWLWERYTHRRKEYSEENHNHANE 1029
Qy 961 RMLFHGSPFVNAIHHKGFDERHAYIGMFCGAGYFAENSCKSNQYVYIGGGTCCPVHKD 1020
Db 1030 RMLFHGSPFVNAIHHKGFDERHAYIGMFCGAGYFAENSCKSNQYVYIGGGTCCPVHKD 1089
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHSHSVTGRPSV 1065
Db 1090 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHSHSVTGRPSV 1134

RESULT 8

US-10-199-937-101
; Sequence 101, Application US/10199937
; Publication No. US20070190739A1

GENERAL INFORMATION:

; APPLICANT: Christenson, Erik
; APPLICANT: Demaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 101

; LENGTH: 1169

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-199-937-101

Query Match 99.9%; Score 5582; DB 4; Length 1169;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 60
Db 70 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 129
Qy 61 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLSAR 120
Db 130 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLSAR 189
Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGDV 180
Db 190 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGDV 249
Qy 181 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
Db 250 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 309
Qy 241 NCHNKAIDLAPTQKRLAYEFKSHLSLQAAREADVTRIKKHLSEMNFKHPQTHET 300
Db 310 NCHNKAIDLAPTQKRLAYEFKSHLSLQAAREADVTRIKKHLSEMNFKHPQTHET 369
Qy 301 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPLVHASEKAHNDVVEVVKHEAKV 360
Db 370 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPLVHASEKAHNDVVEVVKHEAKV 429
Qy 361 NALNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQMGNEVQQLQEGIS 420
Db 430 NALNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQMGNEVQQLQEGIS 489
Qy 421 LGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 490 LGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 549

QY 481 QHGDVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
DB 550 QHGDVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 609
QY 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKLSS 600
DB 610 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKLSS 669
QY 601 PDVNCRTDQGRHSTPLHNAAGYNVLAELVQHGADVNAQDKGLIPLHNAASYGHVD 660
DB 670 PDVNCRTDQGRHSTPLHNAAGYNVLAELVQHGADVNAQDKGLIPLHNAASYGHVD 729
QY 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLHAGADPTLKNQEGOTPLDLVS 720
DB 730 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLHAGADPTLKNQEGOTPLDLVS 789
QY 721 ADDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
DB 790 ADDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 849
QY 781 SFSELSVVSSSGTGASLEKEVPVDFSTQFVRNLGLEHLMDFEREQITLDLVE 840
DB 850 SFSELSVVSSSGTGASLEKEVPVDFSTQFVRNLGLEHLMDFEREQITLDLVE 909
QY 841 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTNTSGSGTILIDLSPDKBFQ 900
DB 910 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTNTSGSGTILIDLSPDKBFQ 969
QY 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
DB 970 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 1029
QY 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGPCVHKD 1020
DB 1030 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGPCVHKD 1089
QY 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1090 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1134

RESULT 9

US-10-616-101-4
; Sequence 4, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; PRIORITY FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-101-4

Query Match 99.9%; Score 5582; DB 5; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVVNLLLRHGADPNARDNNYNT 60
DB 141 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVVNLLLRHGADPNARDNNYNT 200
QY 61 PLHBAAIKGIKIDVICVILVQHGABPTIRNTDQRTALDLADPSAKAVLTGEYKDELLESAR 120
DB 201 PLHBAAIKGIKIDVICVILVQHGABPTIRNTDQRTALDLADPSAKAVLTGEYKDELLESAR 260
QY 121 SGNEKEMALLTPLNVNCHASDGRKSTPLHNAAGYNVRVKI VOLLQHGADVHAKDKGLV 180
DB 261 SGNEKEMALLTPLNVNCHASDGRKSTPLHNAAGYNVRVKI VOLLQHGADVHAKDKGLV 320
QY 181 PLHNACSYGHEVTELLVKGHCACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYGDPTLL 240
DB 321 PLHNACSYGHEVTELLVKGHCACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYGDPTLL 380
QY 241 NCHNKAIDLAPTQKLERLAYEPKSHSLLOAAREADVTRIKKHLLEMVNPKHPQTHET 300
DB 381 NCHNKAIDLAPTQKLERLAYEPKSHSLLOAAREADVTRIKKHLLEMVNPKHPQTHET 440
QY 301 ALHCAAAAPYKPKROI CELLLRKGANINEKTEPLTPLHVASEKAHNDVVEVVVKEAKV 360
DB 441 ALHCAAAAPYKPKROI CELLLRKGANINEKTEPLTPLHVASEKAHNDVVEVVVKEAKV 500
QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYCGDPNI ISLQGFALTQMGNNVQOLLQEGIS 420
DB 501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYCGDPNI ISLQGFALTQMGNNVQOLLQEGIS 560
QY 421 LGNSEADQRLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB 561 LGNSEADQRLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
QY 481 QHGDVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
DB 621 QHGDVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 680
QY 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKLSS 600
DB 681 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKLSS 740
QY 601 PDVNCRTDQGRHSTPLHNAAGYNVLAELVQHGADVNAQDKGLIPLHNAASYGHVD 660
DB 741 PDVNCRTDQGRHSTPLHNAAGYNVLAELVQHGADVNAQDKGLIPLHNAASYGHVD 800
QY 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLHAGADPTLKNQEGOTPLDLVS 720
DB 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLHAGADPTLKNQEGOTPLDLVS 860
QY 721 ADDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
DB 861 ADDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 920
QY 781 SFSELSVVSSSGTGASLEKEVPVDFSTQFVRNLGLEHLMDFEREQITLDLVE 840
DB 921 SFSELSVVSSSGTGASLEKEVPVDFSTQFVRNLGLEHLMDFEREQITLDLVE 980
QY 841 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTNTSGSGTILIDLSPDKBFQ 900
DB 981 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTNTSGSGTILIDLSPDKBFQ 1040
QY 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
DB 1041 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 1100
QY 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGPCVHKD 1020
DB 1101 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGPCVHKD 1160
QY 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1161 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1205


```
RESULT 10
; Sequence 107, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 1262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-107

Query Match 99.9%; Score 5582; DB 4; Length 1262;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFRKDVVYLLQNGASVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARNWNNT 60
DB 163 GFRKDVVYLLQNGANVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARNWNNT 222
QY 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDADPSKAVLTGEYKDELLESAR 120
DB 223 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDADPSKAVLTGEYKDELLESAR 282
QY 121 SGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 180
DB 283 SGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 342
QY 181 PLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHVAEKAHNDVVEVVKHEAKV 240
DB 343 PLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHVAEKAHNDVVEVVKHEAKV 402
QY 241 NCHNKSALDAPTPOLKERLAYEFKHSLLQAREADVTRIKKHSLEWVNFKEPQTHET 300
DB 403 NCHNKSALDAPTPOLKERLAYEFKHSLLQAREADVTRIKKHSLEWVNFKEPQTHET 462
QY 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLHVAEKAHNDVVEVVKHEAKV 360
DB 463 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLHVAEKAHNDVVEVVKHEAKV 522
QY 361 NALDNLGTSLHRAAYCCHLQTCRLLLSYCGDPNIIISLQFTALQNGENVQQLQEGIS 420
DB 523 NALDNLGTSLHRAAYCCHLQTCRLLLSYCGDPNIIISLQFTALQNGENVQQLQEGIS 582
QY 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
DB 583 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 642
QY 481 QHGADVHAKDGGGLVPLHNACSYGHVEVAELLVKRGAVNVNADLWKFTPLHEAAAKGYE 540
DB 643 QHGADVHAKDGGGLVPLHNACSYGHVEVAELLVKRGAVNVNADLWKFTPLHEAAAKGYE 702
QY 541 ICKLLQHGADPTKKNRGNTPLDLVKDGDTDIQLLRGDAALLDAAKKGCILARVKLSS 600
DB 703 ICKLLQHGADPTKKNRGNTPLDLVKDGDTDIQLLRGDAALLDAAKKGCILARVKLSS 762
QY 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
DB 763 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 822

RESULT 11
US-10-199-937-133
; Sequence 133, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-133

Query Match 99.9%; Score 5582; DB 4; Length 1385;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFRKDVVYLLQNGASVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARNWNNT 60
DB 286 GFRKDVVYLLQNGANVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARNWNNT 345
QY 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDADPSKAVLTGEYKDELLESAR 120
DB 346 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDADPSKAVLTGEYKDELLESAR 405
QY 121 SGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 180
DB 406 SGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 465
QY 181 PLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHVAEKAHNDVVEVVKHEAKV 240
DB 763 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 822
```

Db 466 PLHNACSYGHEVTELLVKGHCACVNDMLWQFTPLHEAASKNRVVCVCSLLSYGADPTLL 525
Qy 241 NCHNKSALDAPTPOLKERLAYEFKSHLSLQAREADVTRIKKHLSEVMVNFQHPQTHET 300
Db 526 NCHNKSALDAPTPOLKERLAYEFKSHLSLQAREADVTRIKKHLSEVMVNFQHPQTHET 585
Qy 301 ALHCAAAAPYPRKQICELLRKGANINEKTEFTPLHVAASEKANDVVEVVVKEAKV 360
Db 586 ALHCAAAAPYPRKQICELLRKGANINEKTEFTPLHVAASEKANDVVEVVVKEAKV 645
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISQGTALQMGNEVQOQLQEGIS 420
Db 646 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISQGTALQMGNEVQOQLQEGIS 705
Qy 421 LGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 706 LGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 765
Qy 481 QHGADVHAADKGGVLPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
Db 766 QHGADVHAADKGGVLPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 825
Qy 541 ICKLLQHGADPTKQNRGNTPLDVLKQDGTDIQDLRGDAALLDAKKGCLARVKKLSS 600
Db 826 ICKLLQHGADPTKQNRGNTPLDVLKQDGTDIQDLRGDAALLDAKKGCLARVKKLSS 885
Qy 601 PDVNCNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLPLHNAASYGHVD 660
Db 886 PDVNCNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLPLHNAASYGHVD 945
Qy 661 VAALLIKYNACVNAATDKWFTPLHEAAQKGTQLCALLAHGADPTLKNQEGQTPDLVLS 720
Db 946 VAALLIKYNACVNAATDKWFTPLHEAAQKGTQLCALLAHGADPTLKNQEGQTPDLVLS 1005
Qy 721 ADDVSALLTAAMPSPALPSYKQVINGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Db 1006 ADDVSALLTAAMPSPALPSYKQVINGVRSPGATADALSSGSPSSLSAASSLDNLSSG 1065
Qy 781 SFSSELSSVVSSSGTGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDVLVE 840
Db 1066 SFSSELSSVVSSSGTGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDVLVE 1125
Qy 841 MGHKELKEIGNAYGHRHKLKGVERLJSGQOGLNPYLTANTSGGTLIDLSPDKQEFQ 900
Db 1126 MGHKELKEIGNAYGHRHKLKGVERLJSGQOGLNPYLTANTSGGTLIDLSPDKQEFQ 1185
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLMERYTHRRKEVSEENHNHANE 960
Db 1186 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLMERYTHRRKEVSEENHNHANE 1245
Qy 961 RMLFHGSPVNAI IHKGFDERHAYIGMFGAGIYFAENSSKNQVYGGIGGTGCPVHKD 1020
Db 1246 RMLFHGSPVNAI IHKGFDERHAYIGMFGAGIYFAENSSKNQVYGGIGGTGCPVHKD 1305
Qy 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGCHHSVTGRPSV 1065
Db 1306 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGCHHSVTGRPSV 1350

RESULT 12

US-10-616-101-11
; Sequence 11, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossoskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08

; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-10-616-101-11

Query Match 99.9%; Score 5579; DB 5; Length 1100;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GFGKRDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARNWNT 60
Db 1 GFGKRDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARNWNT 60
Qy 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKDELESAR 120
Db 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKDELESAR 120
Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHAAAGYNNRVKIVQLLLOHGADVNAQDKGLV 180
Db 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHAAAGYNNRVKIVQLLLOHGADVNAQDKGLV 180
Qy 181 PLHNACSYGHEVTELLVKGHCACVNDMLWQFTPLHEAASKNRVVCVCSLLSYGADPTLL 240
Db 181 PLHNACSYGHEVTELLVKGHCACVNDMLWQFTPLHEAASKNRVVCVCSLLSYGADPTLL 240
Qy 241 NCHNKSALDAPTPOLKERLAYEFKSHLSLQAREADVTRIKKHLSEVMVNFQHPQTHET 300
Db 241 NCHNKSALDAPTPOLKERLAYEFKSHLSLQAREADVTRIKKHLSEVMVNFQHPQTHET 300
Qy 301 ALHCAAAAPYPRKQICELLRKGANINEKTEFTPLHVAASEKANDVVEVVVKEAKV 360
Db 301 ALHCAAAAPYPRKQICELLRKGANINEKTEFTPLHVAASEKANDVVEVVVKEAKV 360
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISQGTALQMGNEVQOQLQEGIS 420
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISQGTALQMGNEVQOQLQEGIS 420
Qy 421 LGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 421 LGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Qy 481 QHGADVHAADKGGVLPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
Db 481 QHGADVHAADKGGVLPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
Qy 541 ICKLLQHGADPTKQNRGNTPLDVLKQDGTDIQDLRGDAALLDAKKGCLARVKKLSS 600
Db 541 ICKLLQHGADPTKQNRGNTPLDVLKQDGTDIQDLRGDAALLDAKKGCLARVKKLSS 600
Qy 601 PDVNCNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLPLHNAASYGHVD 660
Db 601 PDVNCNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLPLHNAASYGHVD 660
Qy 661 VAALLIKYNACVNAATDKWFTPLHEAAQKGTQLCALLAHGADPTLKNQEGQTPDLVLS 720
Db 661 VAALLIKYNACVNAATDKWFTPLHEAAQKGTQLCALLAHGADPTLKNQEGQTPDLVLS 720
Qy 721 ADDVSALLTAAMPSPALPSYKQVINGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Db 721 ADDVSALLTAAMPSPALPSYKQVINGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Qy 781 SFSSELSSVVSSSGTGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDVLVE 840

Db 781 SFSLSVSSGTEGASSLEKVPVDFRISITQFVNLGLHLMDFEREQITLDLVE 840
Qy 841 MGKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLTNTSGSTLIDLSDDKEFQ 900
Db 841 MGKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLTNTSGSTLIDLSDDKEFQ 900
Qy 901 SVEBEMOSTVREHRDGGHAGGIFRNYNLIKQVCKNKKLMERYTHRRKEVSEENHNHANE 960
Db 901 SVEBEMOSTVREHRDGGHAGGIFRNYNLIKQVCKNKKLMERYTHRRKEVSEENHNHANE 960
Qy 961 RMLFHGSPFNVAIITHKGDERHAYIGMGFGAGIYFAENSSKNQVYVIGGGTCCPVHKD 1020
Db 961 RMLFHGSPFNVAIITHKGDERHAYIGMGFGAGIYLAENSSKNQVYVIGGGTCCPVHKD 1020
Qy 1021 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHSHTVGRPSV 1065
Db 1021 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHSHTVGRPSV 1065
RESULT 13
US-09-509-196A-2
; Sequence 2, Application US/09509196A
; Patent No. US20020037582A1
; GENERAL INFORMATION:
; APPLICANT: DALY, Roger J.
; APPLICANT: SUTHERLAND, Robert L.
; TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 1871-129
; CURRENT APPLICATION NUMBER: US/09/509.196A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: P09388
; PRIOR FILING DATE: 1997-09-23
; PRIOR APPLICATION NUMBER: PCT AU98/00795
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 2
; LENGTH: 1074
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-509-196A-2
Query Match 97.1%; Score 5421; DB 3; Length 1074;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1034; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 27 IPLHNACSFHAEVNVNLLRHGADPNARDNNYTPLHEAAIKGKIDYCVILLOHGASPTI 86
Db 1 IPLHNACSFHAEVNVNLLRHGADPNARDNNYTPLHEAAIKGKIDYCVILLOHGASPTI 60
Qy 87 RNTDGRALDADPSAKAVLTGEYKOBELLESARGNEEKWALLTPLNVNCHASDGRKS 146
Db 61 RNTDGRALDADPSAKAVLTGEYKOBELLESARGNEEKWALLTPLNVNCHASDGRKS 120
Qy 147 TPLHLAGYNRVKIVQLLQHGADVHAKDGDVPLHNACSYGHEVTELLVKGACVNA 206
Db 121 TPLHLAGYNRVKIVQLLQHGADVHAKDGDVPLHNACSYGHEVTELLVKGACVNA 180
Qy 207 MDLWQFTPLHEAASKRVEVCSLLSYGADPTLNCNKSAIDAPTQPKERLAYBFGK 266
Db 181 MDLWQFTPLHEAASKRVEVCSLLSYGADPTLNCNKSAIDAPTQPKERLAYBFGK 240
Qy 267 HSLLOQAREADVTRIKHLSLEWNVFKPQTHETALHCAASPYPKRQICELLRLKGAN 326
Db 241 HSLLOQAREADVTRIKHLSLEWNVFKPQTHETALHCAASPYPKRQICELLRLKGAN 300
Qy 327 INEKTKEPLTPLHVASEKAHNDVEVVVHAKVNALDNLGQTSLHRAAYCGHLQTCRLL 386
Db 301 INEKTKEPLTPLHVASEKAHNDVEVVVHAKVNALDNLGQTSLHRAAYCGHLQTCRLL 360
Qy 387 LSYGCDPNIISLQGFALQMGNEVQQLQEGISLGNSEADQRLLEAAKAGDVETVKLC 446

Db 361 LSYGCDPNIISLQGFALQMGNEVQQLQEGISLGNSEADQRLLEAAKAGDVETVKLC 420
Qy 447 TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYLLQHGADVHAKDGGVPLHNACSYGHY 506
Db 421 TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYLLQHGADVHAKDGGVPLHNACSYGHY 480
Qy 507 EVAELLYKHGAVNVADLWKFTPLHEAAKAGYKYEICKLLQHGADPTKKRDGNTPLDLV 566
Db 481 EVAELLYKHGAVNVADLWKFTPLHEAAKAGYKYEICKLLQHGADPTKKRDGNTPLDLV 540
Qy 567 KDGDTDIQDLRLGDAALLDAKKGCLARVKLSSPDVNCNCRDQGRHSTPLHLAAGYNNL 626
Db 541 KDGDTDIQDLRLGDAALLDAKKGCLARVKLSSPDVNCNCRDQGRHSTPLHLAAGYNNL 600
Qy 627 EVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAPTPLHEA 686
Db 601 EVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNASLNTADKWAPTPLHEA 660
Qy 687 AQKRTQLCALLAHGADPTLKNQEGQTPLDLVSAADDVSALLTAAMPSPALPSCYKQVVL 746
Db 661 AQKRTQLCALLAHGADPTLKNQEGQTPLDLVSAADDVSALLTAAMPSPALPSCYKQVVL 720
Qy 747 NGVRSPGATADALSSGSPSSLSAASSLNLGSGFSELSVSVSSSGTEGASSLEKKEVP 806
Db 721 NGVRSPGATADALSSGSPSSLSAASSLNLGSGFSELSVSVSSSGTEGASSLEKKEVP 780
Qy 807 GVDFSITQFVRNLGLEHLMDFEREQITLDLVEMGHKELKEIGINAYGHRHKLKIGVER 866
Db 781 GVDFSITQFVRNLGLEHLMDFEREQITLDLVEMGHKELKEIGINAYGHRHKLKIGVER 840
Qy 867 LISGQGLNPLYTLTNTSGSTLIDLSDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRY 926
Db 841 LISGQGLNPLYTLTNTSGSTLIDLSDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRY 900
Qy 927 NILKIQKCNKWLERYTHRRKEVSEENHNHNERMLFHGSPFNVAIITHKGDFDERHAYIG 986
Db 901 NILKIQKCNKWLERYTHRRKEVSEENHNHNERMLFHGSPFNVAIITHKGDFDERHAYIG 960
Qy 987 GMFGAGIYFAENSSKNQVYVIGGGTCCPVHKDRSCYIHRQLLFCRVTLGKSPLOFSA 1046
Db 961 GMFGAGIYFAENSSKNQVYVIGGGTCCPVHKDRSCYIHRQLLFCRVTLGKSPLOFSA 1020
Qy 1047 MKMAHSPGHSHTVGRPSV 1065
Db 1021 MKMAHSPGHSHTVGRPSV 1039
RESULT 14
US-09-849-602-26
; Sequence 26, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849.602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 26
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-26
Query Match 96.0%; Score 5363.5; DB 3; Length 1227;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1035; Conservative 3; Mismatches 25; Indels 3; Gaps 2;

Qy 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
Db 129 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 188
Qy 61 PLHEAAIKGKIDVCIVLLOHGAETPIRNTDGTALDADPSAKAVLTGEYKDELLESAR 120
Db 189 PLHEAAIKGKIDVCIVLLOHGAETPIRNTDGTALDADPSAKAVLTGEYKDELLESAR 248
Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKI VOLLQHGADVHAKDKGLV 180
Db 249 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKI VOLLQHGADVHAKDKGLV 308
Qy 181 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 309 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 368
Qy 241 NCHNKSALDAPTOLKERLAYEFKHSLLQAREADVTRIKKHLSELMVNFKHPQTHET 300
Db 369 NCHNKSALDAPTOLKERLAYEFKHSLLQAREADVTRIKKHLSELMVNFKHPQTHET 428
Qy 301 ALHCAAAAPYPRKQICELLIRKGANINEKTEFLTPLHVAASEKAHNDVVEVVKHEAKV 360
Db 429 ALHCAAAAPYPRKQICELLIRKGANINEKTEFLTPLHVAASEKAHNDVVEVVKHEAKV 488
Qy 361 NALDNLGOTSLHRAAYCCHLOTCTRLLSYGCDPNIIISLQGFALQMGNEVQOLLQEGIS 420
Db 489 NALDNLGOTSLHRAAYCCHLOTCTRLLSYGCDPNIIISLQGFALQMGNEVQOLLQEGIS 548
Qy 421 LGSNADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 549 LGSNADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 608
Qy 481 QHGADVHAKDKGLVPLHNAACSYGHEVVAELLVKHGAVNVNADLWKFTPLHEAAKAGYE 540
Db 609 QHGADVHAKDKGLVPLHNAACSYGHEVVAELLVKHGAVNVNADLWKFTPLHEAAKAGYE 668
Qy 541 ICKLLQHGADPTKKNRGDPTDLVKDGDITDIQDLRGDAALDAAKGGCLARVKLSS 600
Db 669 ICKLLQHGADPTKKNRGDPTDLVKDGDITDIQDLRGDAALDAAKGGCLARVKLSS 728
Qy 601 PDNVNCRDTQGRHSTPLHLAAGYNNRVVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 729 PDNVNCRDTQGRHSTPLHLAAGYNNRVVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 788
Qy 661 VAAALLIKYNACVNAATDKWFTPLHEAAKQRTQLCALLAHGADPTLANOGSTPLDLVS 720
Db 789 VAAALLIKYNACVNAATDKWFTPLHEAAKQRTQLCALLAHGADPTLANOGSTPLDLVS 848
Qy 721 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGPPSPSSLSAASSLDNLSSG 780
Db 849 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGPPSPSSLSAASSLDNLSSG 908
Qy 781 SFSELSSVSSSGTSGASLEKKEVPGVDFSIQFVRNLGLEHLMIDIFEREQITLDVLVE 840
Db 909 SFSELSSVSSSGTSGASLEKKEVPGVDFSIQFVRNLGLEHLMIDIFEREQITLDVLVE 968
Qy 841 MGHKELKEIGINAYGHRKLIKGVERRLISGOQGLNPYLTLNTSGSTLIDLSPDKQEFQ 900
Db 969 MGHKELKEIGINAYGHRKLIKGVERRLISGOQGLNPYLTLNTSGSTLIDLSPDKQEFQ 1028
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLTIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 1029 SVEEMQSTVREHRDGGHAGGIFNRYNLTIKQVCNKKLWERYTHRRKEVSEENHNHANE 1088
Qy 961 RMLFHGSPFVNAI IHKGFDERHAYIGGMFGAGIYFAENSSKSNQVYVIGGGTGCPVHK- 1019
Db 1089 RMLFHGSPFVNAI IHKGFDERHAYIGGMFGAGIYFAENSSKSNQVYVIGGGTGCPVHK- 1148
Qy 1020 DRSCYIQRQLLFCRVTLGKFLQPSAMKAHSPGHHSVTGRPSV 1065
Db 1149 DLVTFATAALL--PGNLGRFPVAVQCENGTSPFGHHSVTGRPSV 1192

RESULT 15
US-09-841-835-2
; Sequence 2, Application US/09841835
; Patent No. US20020076795A1
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRP1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841.835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-09-841-835-2
Query Match 84.9%; Score 4740.5; DB 3; Length 1327;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 882; Conservative 97; Mismatches 79; Indels 9; Gaps 2;
Qy 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
Db 225 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 284
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Db 285 PLHEAAIKGKIDVCIVLLOHGAETPIRNTDGTALDADPSAKAVLTGEYKDELLESAR 344
Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKI VOLLQHGADVHAKDKGLV 180
Db 345 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKI VOLLQHGADVHAKDKGLV 404
Qy 181 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 405 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 464
Qy 241 NCHNKSALDAPTOLKERLAYEFKHSLLQAREADVTRIKKHLSELMVNFKHPQTHET 300
Db 465 NCHNKSALDAPTOLKERLAYEFKHSLLQAREADVTRIKKHLSELMVNFKHPQTHET 524
Qy 301 ALHCAAAAPYPRKQICELLIRKGANINEKTEFLTPLHVAASEKAHNDVVEVVKHEAKV 360

Db 525 ALHCASVSLHPKXQVTELLRLKGANVNEKNQDMPFPLHVAERAHNDVMEVLHKGAKM 584
Qy 361 NALDNLGQTSLSHRAAYCGHLOTCLRLLSYCDPNIISLQGTALQMGNEVQQLQEGIS 420
Db 585 NALDNLGQTSLSHRAALAGHLOTCLRLLSYSDPSIISLQGTAAQMGNEAVQOILSESTP 644
Qy 421 LGHSEADROLLEAKAGDVETVKLCTVQSVNCRDTEGROSTPLHFAAGYNRVSVVEYLL 480
Db 645 IRTSDVDYRLLEASKAGDLETVQLCSSQVNCNCRDLEGRHSTPLHFAAGYNRVSVVEYLL 704
Qy 481 QHGADVHAKDKGGLVPLHNAACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
Db 705 HGGADVHAKDKGGLVPLHNAACSYGHEVAELLVPHGASVNVADLWKFTPLHEAAAKGYE 764
Qy 541 ICKLLQHGADPTKKNRDGNTPLDLVKGDPTDIQDLLRGDAALLDAAKCGCLARVKKLS 600
Db 765 ICKLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLLKGDAALLDAAKCGCLARVQKLC 824
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 825 PENINCRDTCGRNSTPLHLAAGYNNLEVAEYLLHGGADVNAQDKGGLIPLHNAASYGHVD 884
Qy 661 VAALLIKYNACVATDKWFTPLHEAAKQKRTOLCALLAHGADPTLKNQEGOTPLDLVS 720
Db 885 IALLIKYNTCVATDKWFTPLHEAAKQKRTOLCALLAHGADPTKNQEGOTPLDLAT 944
Qy 721 ADDVSALLTAAMPPSALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASSLONLSG 780
Db 945 ADDIRALLIDAMPEALPTCFKQAT-----VVSASLISPASTPSCLSAASSIDNLG 997
Qy 781 SFSELSVSVSSGTEGASSLEKK--EVPQVDFSTQFVRNLGLEHLMDFEREQITLDVL 838
Db 998 PLAEVAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSLGLEHLRDIPEFETQITLDVL 1057
Qy 839 VEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTNTSGSGTILIDLSPDDKE 898
Db 1058 ADMGHEELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTTHCVNQGTILLDLAPEDKE 1117
Qy 899 FQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHHA 958
Db 1118 YQSVVEEMQSTIREHRDGGNAGGIFNRYNVIRIQKVVNKKLRERFCHROKEVSEENHH 1177
Qy 959 NERMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPVH 1018
Db 1178 NERMLFHGSPFINAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPVH 1237
Qy 1019 KDRSCYICHRQLFCRVTLGKSLQFSAMKWAHSPGHHSVTGRPSV 1065
Db 1238 KDRSCYICHRQMLFCRVTLGKSLQFSMTKWAHAPPGHHSVIGRPSV 1284

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:34:55 ; Search time 35.577 Seconds
(without alignments)
2620.235 Million cell updates/sec

Title: US-10-616-101-3
Perfect score: 5585
Sequence: 1 GFRKDVVEYLQNGASVQA.....AMKVAHSPGHHSVTGRDSV 1065

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents_AA:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.psp:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.psp:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.psp:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCRUS_COMB.psp:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.psp:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.psp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pair (✓)

Result No.	Score	Query Match	Length	ID	Description
1	5585	100.0	1083	2	US-09-843-1598-10
2	5585	100.0	1100	2	US-09-696-668-3
3	5585	100.0	1100	2	US-09-843-1598-3
4	5582	99.9	1166	2	US-09-972-115A-6
5	5582	99.9	1240	2	US-09-696-668-4
6	5582	99.9	1240	2	US-09-843-1598-4
7	5579	99.9	1100	2	US-09-843-1598-9
8	5542.5	99.2	1100	2	US-09-427-154-2
9	5533	99.1	1166	2	US-09-350-982C-5
10	5363.5	96.0	1227	2	US-09-849-602-26
11	4740.5	84.9	1327	2	US-09-196-387-2
12	4740.5	84.9	1327	2	US-09-841-835-2
13	4740.5	84.9	1327	2	US-09-972-115A-8
14	4739.5	84.9	1333	2	US-09-972-115A-2
15	4663	83.5	1267	2	US-09-972-115A-4
16	3412	61.1	802	2	US-09-964-899-41
17	3093	55.4	949	2	US-09-196-387-10
18	3093	55.4	949	2	US-09-841-835-10
19	2916	52.2	583	2	US-09-843-1598-8
20	1918.5	34.4	673	2	US-09-196-387-8
21	1918.5	34.4	673	2	US-09-841-835-8
22	875.5	15.7	4377	2	US-09-949-016-6978
23	860.5	15.4	1839	1	US-09-172-977-4
24	860.5	15.4	1839	2	US-09-404-108-4
25	860.5	15.4	3924	2	US-09-538-092-1246
26	842	15.1	1719	2	US-09-949-016-6966

27	842	15.1	1856	2	US-09-949-016-6964	Sequence 6964, Ap
28	842	15.1	1880	2	US-09-949-016-5876	Sequence 5876, Ap
29	842	15.1	1881	2	US-09-949-016-6965	Sequence 6965, Ap
30	842	15.1	1883	2	US-09-949-016-9010	Sequence 9010, Ap
31	842	15.1	1883	2	US-09-949-016-9011	Sequence 9011, Ap
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34	842	15.1	1883	2	US-09-949-016-9014	Sequence 9014, Ap
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36	842	15.1	1883	2	US-09-949-016-9016	Sequence 9016, Ap
37	842	15.1	1883	2	US-09-949-016-9017	Sequence 9017, Ap
38	841.5	15.1	843	1	US-09-172-977-3	Sequence 3, Appl
39	841.5	15.1	843	1	US-09-404-108-3	Sequence 3, Appl
40	821	14.7	1745	1	US-09-031-485-33	Sequence 33, Appl
41	821	14.7	1745	1	US-08-847-429A-33	Sequence 33, Appl
42	821	14.7	1745	2	US-09-065-474-33	Sequence 33, Appl
43	821	14.7	1745	2	US-09-557-034-33	Sequence 33, Appl
44	799	14.3	2753	2	US-09-949-016-7659	Sequence 7659, Ap
45	799	14.3	2753	2	US-09-949-016-7660	Sequence 7660, Ap

ALIGNMENTS

RESULT 1
US-09-843-1598-10
; Sequence 10, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H. Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68252-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-09-843-1598-10

Query Match	100.0%	Score 5585;	DB 2;	Length 1083;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1065;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	GFRKDVVEYLQNGASVQARDGGLIPLHNACSFGEAEVNNLLRHGADPNARDNWT	60	
Db	1	GFRKDVVEYLQNGASVQARDGGLIPLHNACSFGEAEVNNLLRHGADPNARDNWT	60	
QY	61	PLHEAAIKGIDVCIVLLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKKDELLESAR	120	
Db	61	PLHEAAIKGIDVCIVLLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKKDELLESAR	120	
QY	121	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKGDLV	180	
Db	121	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKGDLV	180	
QY	181	PLHNACSYGHEVTELLVKHGACVNMADLWQPTPLHEAASKNRVVCSSLISYGDPTLL	240	
Db	181	PLHNACSYGHEVTELLVKHGACVNMADLWQPTPLHEAASKNRVVCSSLISYGDPTLL	240	
QY	241	NCHNKSALDAPTPOKLERLAYEFKXGHSLLQAREADVTRIKKHLSEMVNFKPQTHET	300	
Db	241	NCHNKSALDAPTPOKLERLAYEFKXGHSLLQAREADVTRIKKHLSEMVNFKPQTHET	300	

Db 241 NCHNSAIDLAPTOLKERLAYEPKHSLLQAAREADVTRIKKHSLSLEWVNFKHPQTHET 300
Qy 301 ALHCAAASPYPRKQICELLIRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 360
Db 301 ALHCAAASPYPRKQICELLIRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 360
Qy 361 NALDNLGOTSILHRAAYCGHLCOTCRLLLSYGCDPNIIISLQGFALOMGNENVOQLLOEGIS 420
Db 361 NALDNLGOTSILHRAAYCGHLCOTCRLLLSYGCDPNIIISLQGFALOMGNENVOQLLOEGIS 420
Qy 421 LGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Qy 481 QHGADVHAADKGGVLPLHNACSYGHYEAELLVKGAVVNVADLWKFTPLHEAAAKGYE 540
Db 481 QHGADVHAADKGGVLPLHNACSYGHYEAELLVKGAVVNVADLWKFTPLHEAAAKGYE 540
Qy 541 ICKLLLOHGADPTKQNRDGNTPDLVKDGDTDIQLLRGDAALLDAAKKGCLARVKKLSS 600
Db 541 ICKLLLOHGADPTKQNRDGNTPDLVKDGDTDIQLLRGDAALLDAAKKGCLARVKKLSS 600
Qy 601 PDVNCRDTOGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 601 PDVNCRDTOGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Qy 661 VAALLIKYNACVNATDKWAFPLHFAAQKGRQTOLCALLAHGADPTLKNQEGOTPLDLVS 720
Db 661 VAALLIKYNACVNATDKWAFPLHFAAQKGRQTOLCALLAHGADPTLKNQEGOTPLDLVS 720
Qy 721 ADDVSALLTAAMPSPSALPCYKQVINGVRSPGATADALSPPSSPSLSAASLDNLSG 780
Db 721 ADDVSALLTAAMPSPSALPCYKQVINGVRSPGATADALSPPSSPSLSAASLDNLSG 780
Qy 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSTQFVRNLGLEHLMDIPIEREQITLDVLVE 840
Db 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSTQFVRNLGLEHLMDIPIEREQITLDVLVE 840
Qy 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQOGLNPYLTLNTSGSTILIDLSPDDKEFQ 900
Db 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQOGLNPYLTLNTSGSTILIDLSPDDKEFQ 900
Qy 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960

RESULT 2
US-09-696-668-3
; Sequence 3, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chen, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-696-668-3

Query Match 100.0%; Score 5585; DB 2; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKDDVYLLQNGASVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYTT 60
Db 1 GFGKDDVYLLQNGASVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYTT 60
Qy 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRTPALDADPSAKAVLTGEYKDBELLESAR 120
Db 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRTPALDADPSAKAVLTGEYKDBELLESAR 120
Qy 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLLOHGADVHAADKGDV 180
Db 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLLOHGADVHAADKGDV 180
Qy 181 PLHNACSYGHYETELLVKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 181 PLHNACSYGHYETELLVKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Qy 241 NCHNSAIDLAPTOLKERLAYEFKHSLLQAAREADVTRIKKHSLSLEWVNFKHPQTHET 300
Db 241 NCHNSAIDLAPTOLKERLAYEFKHSLLQAAREADVTRIKKHSLSLEWVNFKHPQTHET 300
Qy 301 ALHCAAASPYPRKQICELLIRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 360
Db 301 ALHCAAASPYPRKQICELLIRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 360
Qy 361 NALDNLGOTSILHRAAYCGHLCOTCRLLLSYGCDPNIIISLQGFALOMGNENVOQLLOEGIS 420
Db 361 NALDNLGOTSILHRAAYCGHLCOTCRLLLSYGCDPNIIISLQGFALOMGNENVOQLLOEGIS 420
Qy 421 LGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Qy 481 QHGADVHAADKGGVLPLHNACSYGHYEAELLVKGAVVNVADLWKFTPLHEAAAKGYE 540
Db 481 QHGADVHAADKGGVLPLHNACSYGHYEAELLVKGAVVNVADLWKFTPLHEAAAKGYE 540
Qy 541 ICKLLLOHGADPTKQNRDGNTPDLVKDGDTDIQLLRGDAALLDAAKKGCLARVKKLSS 600
Db 541 ICKLLLOHGADPTKQNRDGNTPDLVKDGDTDIQLLRGDAALLDAAKKGCLARVKKLSS 600
Qy 601 PDVNCRDTOGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 601 PDVNCRDTOGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Qy 661 VAALLIKYNACVNATDKWAFPLHFAAQKGRQTOLCALLAHGADPTLKNQEGOTPLDLVS 720
Db 661 VAALLIKYNACVNATDKWAFPLHFAAQKGRQTOLCALLAHGADPTLKNQEGOTPLDLVS 720
Qy 721 ADDVSALLTAAMPSPSALPCYKQVINGVRSPGATADALSPPSSPSLSAASLDNLSG 780
Db 721 ADDVSALLTAAMPSPSALPCYKQVINGVRSPGATADALSPPSSPSLSAASLDNLSG 780
Qy 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSTQFVRNLGLEHLMDIPIEREQITLDVLVE 840
Db 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSTQFVRNLGLEHLMDIPIEREQITLDVLVE 840
Qy 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQOGLNPYLTLNTSGSTILIDLSPDDKEFQ 900
Db 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQOGLNPYLTLNTSGSTILIDLSPDDKEFQ 900
Qy 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960

QY 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYIGGTCGPVHKD 1020
DB 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYIGGTCGPVHKD 1020
QY 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
RESULT 3
US-09-843-159B-3
; Sequence 3, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-159B-3
Query Match 100.0%; Score 5585; DB 2; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHGAHVNNLLRHGADPNARDNNYNT 60
DB 1 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHGAHVNNLLRHGADPNARDNNYNT 60
QY 61 PLHEAAIKGIDVCIVLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLESAR 120
DB 61 PLHEAAIKGIDVCIVLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLESAR 120
QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVIQVLLQHGADVHAKDKGLV 180
DB 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVIQVLLQHGADVHAKDKGLV 180
QY 181 PLHNACSYGHYVTELLVKGACVNMADLWQPTPLHEAASKNRVEVCSLLSYGADPTLL 240
DB 181 PLHNACSYGHYVTELLVKGACVNMADLWQPTPLHEAASKNRVEVCSLLSYGADPTLL 240
QY 241 NCHNKSATDLAFTPOLKRLAYEPFKGHSLLQAREADVTRIKKHSLEWVNFKPHQTHET 300
DB 241 NCHNKSATDLAFTPOLKRLAYEPFKGHSLLQAREADVTRIKKHSLEWVNFKPHQTHET 300
QY 301 ALHCAAASYPKPKOICELLKRGANINEKTEFTPLHVASEKAHNDVVEVVKHEAKV 360
DB 301 ALHCAAASYPKPKOICELLKRGANINEKTEFTPLHVASEKAHNDVVEVVKHEAKV 360
QY 361 NALDNLGQTSLHRAAYCGHLOTICRLLSYGCDPNIIISLQGFALQMNENVOQLLOEGIS 420
DB 361 NALDNLGQTSLHRAAYCGHLOTICRLLSYGCDPNIIISLQGFALQMNENVOQLLOEGIS 420
QY 421 LGNSEADROLLEAAKAGDVETVKLTCTVQSVNCRDIEGQSTPLHFAAGYNNRVSVVEYLL 480
DB 421 LGNSEADROLLEAAKAGDVETVKLTCTVQSVNCRDIEGQSTPLHFAAGYNNRVSVVEYLL 480
QY 481 OHGADVHAKDKGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540

DB 481 OHGADVHAKDKGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
QY 541 ICKLLQHGADPTTKNRDGNTPDLVKDGDTDIQLLRGDAALLDAAKGGCLARVKLLSS 600
DB 541 ICKLLQHGADPTTKNRDGNTPDLVKDGDTDIQLLRGDAALLDAAKGGCLARVKLLSS 600
QY 601 PDVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
DB 601 PDVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
QY 661 VAALLIKYNACVNATDKWAFPTPLHAAQKGTOLCALLAHGADPTLKNQEGOTPLDLVS 720
DB 661 VAALLIKYNACVNATDKWAFPTPLHAAQKGTOLCALLAHGADPTLKNQEGOTPLDLVS 720
QY 721 ADDVSALLTAAMPPSALPSCYKQVNLGVNRPFGATADALSSGSPSSLSAASSLDNLSS 780
DB 721 ADDVSALLTAAMPPSALPSCYKQVNLGVNRPFGATADALSSGSPSSLSAASSLDNLSS 780
QY 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE 840
DB 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE 840
QY 841 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTNTSGSTLIDLSPPDKKEFQ 900
DB 841 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTNTSGSTLIDLSPPDKKEFQ 900
QY 901 SVEBEMOSTVREHRRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNANE 960
DB 901 SVEBEMOSTVREHRRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNANE 960
QY 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYIGGTCGPVHKD 1020
DB 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYIGGTCGPVHKD 1020
QY 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
RESULT 4
US-09-972-115A-6
; Sequence 6, Application US/09972115A
; Patent No. 6593228
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-6
Query Match 99.9%; Score 5582; DB 2; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHGAHVNNLLRHGADPNARDNNYNT 60
DB 67 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHGAHVNNLLRHGADPNARDNNYNT 126
QY 61 PLHEAAIKGIDVCIVLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLESAR 120

||||| 127 PLHEAAIKGIDVICIVLQHGAEPTIRNTDGR TALDLADPSAKAVLTGEYKDELLSAR 186
QY ||||| 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 180
Db ||||| 187 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 246
QY ||||| 181 PLHNACSYGHEVTELLVKGACVNA MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db ||||| 247 PLHNACSYGHEVTELLVKGACVNA MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 306
QY ||||| 241 NCHNKSALDAPTQPKERLAYEPKHLSLQAAREADVTRIKHLSLEMVNFHQPQTHET 300
Db ||||| 307 NCHNKSALDAPTQPKERLAYEPKHLSLQAAREADVTRIKHLSLEMVNFHQPQTHET 366
QY ||||| 301 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPHLVASEKANDVVEVVVKHEAKV 360
Db ||||| 367 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPHLVASEKANDVVEVVVKHEAKV 426
QY ||||| 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVVOQLLQEGIS 420
Db ||||| 427 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVVOQLLQEGIS 486
QY ||||| 421 LGNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db ||||| 487 LGNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546
QY ||||| 481 QHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVVNAVDLWKFTPLHEAAGKGYE 540
Db ||||| 547 QHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVVNAVDLWKFTPLHEAAGKGYE 606
QY ||||| 541 ICKLLQHGADPTKKNRDNTPDLVKDGTDIQDLRLGDAALLDAKKGCLARVKKLS 600
Db ||||| 607 ICKLLQHGADPTKKNRDNTPDLVKDGTDIQDLRLGDAALLDAKKGCLARVKKLS 666
QY ||||| 601 PDVNCNCRDTQGRHSTPLHLAAGYNRVVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db ||||| 667 PDVNCNCRDTQGRHSTPLHLAAGYNRVVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 726
QY ||||| 661 VAALLIKYNACVNA TDKWAFTPLHEAAQKGRTOCALLAHGADPTLKNQEGQTPDLVLS 720
Db ||||| 727 VAALLIKYNACVNA TDKWAFTPLHEAAQKGRTOCALLAHGADPTLKNQEGQTPDLVLS 786
QY ||||| 721 ADDVSALLTAAMPSPALPSCVKPQVINGVRSPGATADALSSGSPSSSLSAASLDNLG 780
Db ||||| 787 ADDVSALLTAAMPSPALPSCVKPQVINGVRSPGATADALSSGSPSSSLSAASLDNLG 846
QY ||||| 781 SFSELSSVSSSGTEGASSLEKKEVPVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 840
Db ||||| 847 SFSELSSVSSSGTEGASSLEKKEVPVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 906
QY ||||| 841 MGHKELKEIGINAYGHRHKLTKGVERLISGOQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
Db ||||| 907 MGHKELKEIGINAYGHRHKLTKGVERLISGOQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966
QY ||||| 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNANE 960
Db ||||| 967 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNANE 1026
QY ||||| 961 RMLPHGSPFFVNAIITHKGFDEHAYIGMFGAGIYFAENSSKNQYVYIGGTCGPVHKD 1020
Db ||||| 1027 RMLPHGSPFFVNAIITHKGFDEHAYIGMFGAGIYFAENSSKNQYVYIGGTCGPVHKD 1086
QY ||||| 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
Db ||||| 1087 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1131

RESULT 5
US-09-696-668-4
; Sequence 4, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:

; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Osovskaaya, Valeria
; TITLE OF INVENTION: TANKVRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS C
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-696-668-4

Query Match 99.9%; Score 5582; DB 2; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGRKQDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
Db 141 GGRKQDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 200
QY 61 PLHEAAIKGIDVICIVLQHGAEPTIRNTDGR TALDLADPSAKAVLTGEYKDELLSAR 120
Db 201 PLHEAAIKGIDVICIVLQHGAEPTIRNTDGR TALDLADPSAKAVLTGEYKDELLSAR 260
QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 180
Db 261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 320
QY 181 PLHNACSYGHEVTELLVKGACVNA MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 321 PLHNACSYGHEVTELLVKGACVNA MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 380
QY 241 NCHNKSALDAPTQPKERLAYEPKHLSLQAAREADVTRIKHLSLEMVNFHQPQTHET 300
Db 381 NCHNKSALDAPTQPKERLAYEPKHLSLQAAREADVTRIKHLSLEMVNFHQPQTHET 440
QY 301 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPHLVASEKANDVVEVVVKHEAKV 360
Db 441 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPHLVASEKANDVVEVVVKHEAKV 500
QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVVOQLLQEGIS 420
Db 501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVVOQLLQEGIS 560
QY 421 LGNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 561 LGNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
QY 481 QHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVVNAVDLWKFTPLHEAAGKGYE 540
Db 621 QHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVVNAVDLWKFTPLHEAAGKGYE 680
QY 541 ICKLLQHGADPTKKNRDNTPDLVKDGTDIQDLRLGDAALLDAKKGCLARVKKLS 600
Db 681 ICKLLQHGADPTKKNRDNTPDLVKDGTDIQDLRLGDAALLDAKKGCLARVKKLS 740
QY 601 PDVNCNCRDTQGRHSTPLHLAAGYNRVVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 741 PDVNCNCRDTQGRHSTPLHLAAGYNRVVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
QY 661 VAALLIKYNACVNA TDKWAFTPLHEAAQKGRTOCALLAHGADPTLKNQEGQTPDLVLS 720
Db 801 VAALLIKYNACVNA TDKWAFTPLHEAAQKGRTOCALLAHGADPTLKNQEGQTPDLVLS 860
QY 721 ADDVSALLTAAMPSPALPSCVKPQVINGVRSPGATADALSSGSPSSSLSAASLDNLG 780

Db 861 ADDVSALLTAAMPSPALPSCYKQVINGVRSPCATADALLSGPSSLSAASSLDNLG 920
Qy 781 SFSELSVVSSSGTSGASLEKKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 840
Db 921 SFSELSVVSSSGTSGASLEKKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 980
Qy 841 MGKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTLNTSGSGTILIDLSPDKBQFQ 900
Db 981 MGKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTLNTSGSGTILIDLSPDKBQFQ 1040
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 1041 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 1100
Qy 961 RMLFHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVGGTGCPCVHKD 1020
Db 1101 RMLFHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVGGTGCPCVHKD 1160
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205

RESULT 6
US-09-843-159B-4
; Sequence 4, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-159B-4

Query Match 99.9%; Score 5582; DB 2; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGRKDVVEYLLQNGASVQARDGGIPLPHNACSFGHAEVNVNLLRHGADPNARDNWNVT 60
Db 141 GFGRKDVVEYLLQNGANVQARDGGIPLPHNACSFGHAEVNVNLLRHGADPNARDNWNVT 200
Qy 61 PLHEAAIKGKIDVICVILLQHGAEPTIRNTDGTALDLPDSAKAVLTGEYKDELLSAR 120
Db 201 PLHEAAIKGKIDVICVILLQHGAEPTIRNTDGTALDLPDSAKAVLTGEYKDELLSAR 260
Qy 121 SGNEEKWALLPPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDGLV 180
Db 261 SGNEEKWALLPPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDGLV 320
Qy 181 PLHNACSYGHEVTELLVKGACVNAWDLQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
Db 321 PLHNACSYGHEVTELLVKGACVNAWDLQFTPLHEAASKNRVEVCSLLSYGADPTLL 380
Qy 241 NCHNKSADLATPQLKERLAYEFKHSLLQAREADVTIRIKHLSLEWVNFKHQTHET 300
Db 381 NCHNKSADLATPQLKERLAYEFKHSLLQAREADVTIRIKHLSLEWVNFKHQTHET 440
Qy 301 ALHCAASPYPKRKQICELLRLKGANINEKTEFTPLHVASEKAHNDVVEVVVHKAHV 360

Db 441 ALHCAASPYPKRKQICELLRLKGANINEKTEFTPLHVASEKAHNDVVEVVVHKAHV 500
Qy 361 NALDNLGQTSLHRAAYCGHLOTCHLLLSYGCDPNIIISLOGFTALQMGNNVQOOLQEGIS 420
Db 501 NALDNLGQTSLHRAAYCGHLOTCHLLLSYGCDPNIIISLOGFTALQMGNNVQOOLQEGIS 560
Qy 421 LGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 561 LGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 620
Qy 481 QHGADVHAKDGGVPLHNACSYGHEVVAELLVKHGA VNVNADLWKFTPLHEAAAKGYE 540
Db 621 QHGADVHAKDGGVPLHNACSYGHEVVAELLVKHGA VNVNADLWKFTPLHEAAAKGYE 680
Qy 541 ICKLLQHGADPTKQRDGNTPDLVKDGDTDIQLLGRDAALLDAKKGCLARVKLSS 600
Db 681 ICKLLQHGADPTKQRDGNTPDLVKDGDTDIQLLGRDAALLDAKKGCLARVKLSS 740
Qy 601 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800
Qy 661 VAALLIKYNACVNAATDKWAFPLHEAAQKGRTOCALLLAHAGADPTLKNQEGOTPLDLVS 720
Db 801 VAALLIKYNACVNAATDKWAFPLHEAAQKGRTOCALLLAHAGADPTLKNQEGOTPLDLVS 860
Qy 721 ADDVSALLTAAMPSPALPSCYKQVINGVRSPCATADALLSGPSSLSAASSLDNLG 780
Db 861 ADDVSALLTAAMPSPALPSCYKQVINGVRSPCATADALLSGPSSLSAASSLDNLG 920
Qy 781 SFSELSVVSSSGTSGASLEKKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 840
Db 921 SFSELSVVSSSGTSGASLEKKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 980
Qy 841 MGKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTLNTSGSGTILIDLSPDKBQFQ 900
Db 981 MGKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTLNTSGSGTILIDLSPDKBQFQ 1040
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 1041 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 1100
Qy 961 RMLFHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVGGTGCPCVHKD 1020
Db 1101 RMLFHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVGGTGCPCVHKD 1160
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205

RESULT 7

US-09-843-159B-9

; Sequence 9, Application US/09843159B

; Patent No. 6887675

; GENERAL INFORMATION:

; APPLICANT: Luo, Yin

; APPLICANT: Chan, Evan

; APPLICANT: Xu, Xiang

; APPLICANT: Huang, Betty

; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods

; FILE REFERENCE: A-68292-2/RMS/DHR

; CURRENT APPLICATION NUMBER: US/09/843,159B

; CURRENT FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: US 09/696,668

; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 09/427,154

; PRIOR FILING DATE: 1999-10-25

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 1100

; TYPE: PRT									
; ORGANISM: Artificial sequence									
; FEATURE:									
; OTHER INFORMATION: synthetic mutant									
US-09-843-159B-9									
Query Match									
Best Local Similarity 99.9%; Score 5579; DB 2; Length 1100;									
Matches 1064; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	1	GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT	60						
Db	1	GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT	60						
Qy	61	PLHEAAIKGIDVCI VLLQHGAEPTIRNTDGR TALDPSAKAVLTGEYKDELLSAR	120						
Db	61	PLHEAAIKGIDVCI VLLQHGAEPTIRNTDGR TALDPSAKAVLTGEYKDELLSAR	120						
Qy	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGDV	180						
Db	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGDV	180						
Qy	181	PLHNACSYGHEVTELLVKGACVNMQLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL	240						
Db	181	PLHNACSYGHEVTELLVKGACVNMQLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL	240						
Qy	241	NCHNKSALDAPTLPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKHPQTHET	300						
Db	241	NCHNKSALDAPTLPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKHPQTHET	300						
Qy	301	ALHCAAAASPYPKPKQICELLRKGANINEKTEFTPLHVASEKAHNDVVEVVVYKHEAV	360						
Db	301	ALHCAAAASPYPKPKQICELLRKGANINEKTEFTPLHVASEKAHNDVVEVVVYKHEAV	360						
Qy	361	NALDNLGQTSLHRAAYCGHLQTCRLLSYSGCDPNIISLQGF TALQMGNEVQQLQEGIS	420						
Db	361	NALDNLGQTSLHRAAYCGHLQTCRLLSYSGCDPNIISLQGF TALQMGNEVQQLQEGIS	420						
Qy	421	LGNEADRQLLEAAKAGDVETVKKLCVQSYNCRDIEGRQSTPLHFAAGYNRVSVVEYLL	480						
Db	421	LGNEADRQLLEAAKAGDVETVKKLCVQSYNCRDIEGRQSTPLHFAAGYNRVSVVEYLL	480						
Qy	481	QHGAADVHAKDGGVLPVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE	540						
Db	481	QHGAADVHAKDGGVLPVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE	540						
Qy	541	ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS	600						
Db	541	ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS	600						
Qy	601	PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660						
Db	601	PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660						
Qy	661	VAALLIKYNACVNATDKWAFPLHEAAKQKGTQICALLLAHGA DPTLKNQEGQTPDLVS	720						
Db	661	VAALLIKYNACVNATDKWAFPLHEAAKQKGTQICALLLAHGA DPTLKNQEGQTPDLVS	720						
Qy	721	ADDVSALLTAAMPSPALPSCYKPVQVNGVRSPGATADALS SPSSPSLSAASLDNLSG	780						
Db	721	ADDVSALLTAAMPSPALPSCYKPVQVNGVRSPGATADALS SPSSPSLSAASLDNLSG	780						
Qy	781	SFSELSVSVSSSGTEGASSLEKKEVPVDFSIQFVRNLGLEHLMDFPEREQITLDVLVE	840						
Db	781	SFSELSVSVSSSGTEGASSLEKKEVPVDFSIQFVRNLGLEHLMDFPEREQITLDVLVE	840						
Qy	841	MGHKELKEIGINAYCHRRKLIKGVRLISGQOGLNPYLTNTSGSGITLIDLSPDDKEFQ	900						
Db	841	MGHKELKEIGINAYCHRRKLIKGVRLISGQOGLNPYLTNTSGSGITLIDLSPDDKEFQ	900						
Qy	901	SVEBEMQSTVREHRDGGHAGGIFNRYNTLKIQVCNKKLWERYTHRRKEVSEENHNANE	960						
Db	901	SVEBEMQSTVREHRDGGHAGGIFNRYNTLKIQVCNKKLWERYTHRRKEVSEENHNANE	960						
RESULT 8									
US-09-427-154-2									
; Sequence 2, Application US/09427154									
; Patent No. 6589725									
; GENERAL INFORMATION:									
; APPLICANT: Luo, Ying									
; APPLICANT: Chan, Eva									
; APPLICANT: Xu, Xiang									
; APPLICANT: Huang, Betty									
; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND									
; TITLE OF INVENTION: METHODS OF USE									
; FILE REFERENCE: A-68292-DJB/RMS/DAV									
; CURRENT APPLICATION NUMBER: US/09/427,154									
; CURRENT FILING DATE: 1999-10-25									
; NUMBER OF SEQ ID NOS: 9									
; SOFTWARE: Patentin Ver. 2.1									
; SEQ ID NO 2									
; LENGTH: 1100									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-427-154-2									
Query Match									
Best Local Similarity 99.2%; Score 5542.5; DB 2; Length 1100;									
Matches 1059; Conservative 2; Mismatches 3; Indels 1; Gaps 1;									
Qy	1	GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT	60						
Db	1	GFRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT	60						
Qy	61	PLHEAAIKGIDVCI VLLQHGAEPTIRNTDGR TALDPSAKAVLTGEYKDELLSAR	120						
Db	61	PLHEAAIKGIDVCI VLLQHGAEPTILNTDGR TALDPSAKAVLTGEYKDELLSAR	120						
Qy	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGDV	180						
Db	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDGDV	180						
Qy	181	PLHNACSYGHEVTELLVKGACVNMQLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL	240						
Db	181	PLHNACSYGHEVTELLVKGACVNMQLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL	240						
Qy	241	NCHNKSALDAPTLPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKHPQTHET	300						
Db	241	NCHNKSALDAPTLPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKHPQTHET	300						
Qy	301	ALHCAAAASPYPKPKQICELLRKGANINEKTEFTPLHVASEKAHNDVVEVVVYKHEAV	360						
Db	301	ALHCAAAASPYPKPKQICELLRKGANINEKTEFTPLHVASEKAHNDVVEVVVYKHEAV	360						
Qy	361	NALDNLGQTSLHRAAYCGHLQTCRLLSYSGCDPNIISLQGF TALQMGNEVQQLQEGIS	420						
Db	361	NALDNLGQTSLHRAAYCGHLQTCRLLSYSGCDPNIISLQGF TALQMGNEVQQLQEGIS	420						
Qy	421	LGNEADRQLLEAAKAGDVETVKKLCVQSYNCRDIEGRQSTPLHFAAGYNRVSVVEYLL	480						
Db	421	LGNEADRQLLEAAKAGDVETVKKLCVQSYNCRDIEGRQSTPLHFAAGYNRVSVVEYLL	480						
Qy	481	QHGAADVHAKDGGVLPVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE	540						
Db	481	QHGAADVHAKDGGVLPVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE	540						
Qy	541	ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS	600						
Db	541	ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS	600						
Qy	601	PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660						
Db	601	PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660						
Qy	661	VAALLIKYNACVNATDKWAFPLHEAAKQKGTQICALLLAHGA DPTLKNQEGQTPDLVS	720						
Db	661	VAALLIKYNACVNATDKWAFPLHEAAKQKGTQICALLLAHGA DPTLKNQEGQTPDLVS	720						
Qy	721	ADDVSALLTAAMPSPALPSCYKPVQVNGVRSPGATADALS SPSSPSLSAASLDNLSG	780						
Db	721	ADDVSALLTAAMPSPALPSCYKPVQVNGVRSPGATADALS SPSSPSLSAASLDNLSG	780						
Qy	781	SFSELSVSVSSSGTEGASSLEKKEVPVDFSIQFVRNLGLEHLMDFPEREQITLDVLVE	840						
Db	781	SFSELSVSVSSSGTEGASSLEKKEVPVDFSIQFVRNLGLEHLMDFPEREQITLDVLVE	840						
Qy	841	MGHKELKEIGINAYCHRRKLIKGVRLISGQOGLNPYLTNTSGSGITLIDLSPDDKEFQ	900						
Db	841	MGHKELKEIGINAYCHRRKLIKGVRLISGQOGLNPYLTNTSGSGITLIDLSPDDKEFQ	900						
Qy	901	SVEBEMQSTVREHRDGGHAGGIFNRYNTLKIQVCNKKLWERYTHRRKEVSEENHNANE	960						
Db	901	SVEBEMQSTVREHRDGGHAGGIFNRYNTLKIQVCNKKLWERYTHRRKEVSEENHNANE	960						

Db 541 ICKLLHQHGDPTKQKRDGNTPLDLVKDGDTHVLLRGDAALLDAAKGGLARVKCLSS 600
Qy 601 PDVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLHNAASYGVD 660
Db 601 PDVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLHNAASYGVD 660
Qy 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 720
Db 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 720
Qy 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLNLSSG 780
Db 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLNLSSG 780
Qy 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSTQFVRNIGLHLMDFEREQITLDLVE 840
Db 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSTQFVRNIGLHLMDFEREQITLDLVE 840
Qy 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGGTILIDLSPDDKEFQ 900
Db 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGGTILIDLSPDDKEFQ 900
Qy 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNHANE 960
Qy 961 RMLFHGSPFNVAIHKGFDERHAYIGMGFAGIYFAENSSKSNQVYGGTGCPCVHKD 1020
Db 961 RMLFHGSPFNVAIHKGFDERHAYIGMGFAGIYFAENSSKSNQVYGGTGCPCVHKD 1020
Qy 1021 RSCYICHRQLLCFRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1065
Db 1021 RSCYICHRQLLCFRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1064

RESULT 9
US-09-350-982C-5
Sequence 5, Application US/09350982C
Patent No. 6452590
GENERAL INFORMATION:
APPLICANT: Berthelsen, Jens
APPLICANT: Toma, Salvatore
APPLICANT: Isacchi, Antonella
TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Rel
TITLE OF INVENTION: Same
FILE REFERENCE: PHRM-0043
CURRENT APPLICATION NUMBER: US/09/350,982C
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 1166
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (1102)..(1102)
OTHER INFORMATION: n is any nucleic acid
NAME/KEY: misc_feature
LOCATION: (2650)..(2650)
OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-5

Query Match 99.1%; Score 5533; DB 2; Length 1166;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1056; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GFGKRDVVEYLLQNGASVQARDGGGLPLHNAACSFHAEVFNLLLRHGGADPNARDNNYNT 60
Db 67 GFGKRDVVEYLLQNGANVQARDGGGLPLHNAACSFHAEVFNLLLRHGGADPNARDNNYNT 126

Qy 61 PLHEAAIKGIDVCIIVLLOHGAEPTRINTDGRALTDLADPSAKAVLTGEYKKDELLESAR 120
Db 127 PLHEAAIKGIDVCIIVLLOHGAEPTRINTDGRALTDLADPSAKAVLTGEYKKDELLESAR 186
Qy 121 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIKIVOLLQHGADVNAQDKGLV 180
Db 187 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIKIVOLLQHGADVNAQDKGLV 246
Qy 181 PLHNACSYGHEVTELLVKGACVNAQDKGLVPLHEAAKSNRVEVCILLISYGDPTLL 240
Db 247 PLHNACSYGHEVTELLVKGACVNAQDKGLVPLHEAAKSNRVEVCILLISYGDPTLL 306
Qy 241 NCHNKSALDAPTQKLERLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db 307 NCHNKSALDAPTQKLERLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKHPQTHET 366
Qy 301 ALHCAAAAPYPRKQICELLERKGANINEKTEFELTPLHVASEKANDVVEVVVHEAKV 360
Db 367 AXHCAAAAPYPRKQICELLERKGANINEKTEFELTPLHVASEKANDVVEVVVHEAKV 426
Qy 361 NALDNLGQTSLHRAAYCGHLOTCLLLISYGCDDNIIISLOGETALOMGNENVOQLLOEGIS 420
Db 427 NALDNLGQTSLHRAAYCGHLOTCLLLISYGCDDNIIISLOGETALOMGNENVOQLLOEGIS 486
Qy 421 LGNSEADRLLEAAKAGDVETVKCLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 487 LGNSEADRLLEAAKAGDVETVKCLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 546
Qy 481 QHGADVNAQDKGLVPLHNACSYGHEVVAELLVKHGA VNVNADLWKFTPLHEAAAKGYE 540
Db 547 QHGADVNAQDKGLVPLHNACSYGHEVVAELLVKHGA VNVNADLWKFTPLHEAAAKGYE 606
Qy 541 ICKLLHQHGDPTKQKRDGNTPLDLVKDGDTHVLLRGDAALLDAAKGGLARVKCLSS 600
Db 607 ICKLLHQHGDPTKQKRDGNTPLDLVKDGDTHVLLRGDAALLDAAKGGLARVKCLSS 666
Qy 601 PDVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLHNAASYGVD 660
Db 667 PDVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLHNAASYGVD 726
Qy 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 720
Db 727 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 786
Qy 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLNLSSG 780
Db 787 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLNLSSG 846
Qy 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSTQFVRNIGLHLMDFEREQITLDLVE 840
Db 847 SFSELSVVSSSGTEGASSLEKKEVPGVDFSTQFVRNIGLHLMDFEREQITLDLVE 906
Qy 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGGTILIDLSPDDKEFQ 900
Db 907 MGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGGTILIDLSPDDKEFQ 966
Qy 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 967 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNHANE 1026
Qy 961 RMLFHGSPFNVAIHKGFDERHAYIGMGFAGIYFAENSSKSNQVYGGTGCPCVHKD 1020
Db 1027 RMLFHGSPFNVAIHKGFDERHAYIGMGFAGIYFAENSSKSNQVYGGTGCPCVHKD 1086
Qy 1021 RSCYICHRQLLCFRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1065
Db 1087 RSCYICHRQLLCFRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1131

RESULT 10
US-09-849-602-26
Sequence 26, Application US/09849602


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QY 1 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSFGEAEVNVNLLRHGADPNARDNNYT 60
Db 225 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSFGEAEVNVNLLRHGADPNARDNNYT 284
QY 61 PLHEAAIKGKIDVICIVLQHGAEPIRNTDGTALDPSAKAVLTGEYKDELLESAR 120
Db 285 PLHEAAIKGKIDVICIVLQHGAEPIRNTDGTALDPSAKAVLTGEYKDELLESAR 344
QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 180
Db 345 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 404
QY 181 PLHNACSYGHEVTELLVKGHCACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
Db 405 PLHNACSYGHEVTELLVKGHCACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 464
QY 241 NCHNKSADLAPTOLKERLAYEFKHSLLQAAEADVTRIKKHSLEMVNFKHPQTHET 300
Db 465 NCHGKSAVDMAPTPELRERLTTEYFKHSHLQAAEADLAKVKTLLALEIINFKQPSHET 524
QY 301 ALHCAAAAPYPRKQICELLRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 360
Db 525 ALHCAVASLHPKQVTELLRKGANVNEKNDFMTPLHVAERAHNDVMEVLHKGAKM 584
QY 361 NALDNLGOTSLHRAAYCGHLCRLLLSYGCDPNIISLQGFALQMGNEVQOILLQEGIS 420
Db 595 NALDTLQGTALHRAALAGHLQTCRLLLSYGDPSIISLQGFATAQMGNEAVQOILSESTP 644
QY 421 LGNSBARDQLLEAAKAGDVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 645 IRTSDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLEGRHSTPLHFAAGYNNRVSVVEYLL 704
QY 481 OHGADVHAKDGLVPLHNACSYGHEVVAELVKGHGVNVNADLWKFTPLHEAAAKGYE 540
Db 705 HHGADVHAKDGLVPLHNACSYGHEVVAELVKGHGVNVNADLWKFTPLHEAAAKGYE 764
QY 541 ICKLLQHGADPTKKNRDNTEPLDVKDGTDIQDLRGDAALLDAKKGCLARVKLSS 600
Db 765 ICKLLQHGADPTKKNRDNTEPLDVKDGTDIQDLRGDAALLDAKKGCLARVKLCT 824
QY 601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 825 PENINCRDTQGRNSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 884
QY 661 VAALLIKYNACVNTDKWFTPLHEAAQKGRTOLCALLLHAGADPTLKNQEGOTPLDLS 720
Db 885 TAALLIKYNTCVNATDKWFTPLHEAAQKGRTOLCALLLHAGADPTLKNQEGOTPLDLS 944
QY 721 ADDVSALLTAAMPSPALPCYKQPVNLGVRSFGATADALSSGSPSSLSAASSLDNLSSG 780
Db 945 ADDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTPSCLSAASSIDNLTG 997
QY 781 SPSELSSVVSSSGTGASLEKK--EVPGVDPSTITQVNRNLEHMDIFEREQITLVL 838
Db 998 PLAEALVAGSAGNAGDAAGTERKEGEVAGLDNMIISQFLKSLGLEHLRDIETEQTLDVL 1057
QY 839 VPMGHKEKEIGINAYGRHKLIKVERLISQOGLNPVLTNTSGSTLILDLSPDKE 898
Db 1058 ADMGHEELKEIGINAYGRHKLIKVERLISQOGLNPVLTNTSGSTLILDLAPEDKE 1117
QY 899 FOSVEEEMQSTVREHDDGHAGGIFNRVNIKIKQVCKNKLWERYTHRRKEVSEENHHA 958
Db 1118 YOSVEEEMQSTVREHDDGNAGGIFNRVNIQVNVNKLRECHQKEVSEENHNNH 1177
QY 959 NERMLFHGSPFNVAIIHKGDFDRHAYIGMFGAGIYFAENSKSNQYVYGGGTGCPVH 1018
Db 1178 NERMLFHGSPFNVAIIHKGDFDRHAYIGMFGAGIYFAENSKSNQYVYGGGTGCPVH 1237
QY 1019 KDRSCYIHRQILLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1065
Db 1238 KDRSCYIHRQMLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1284
```

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RESULT 12
US-09-841-835-2
; Sequence 2, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841.835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-841-835-2

Query Match 84.9%; Score 4740.5; DB 2; Length 1327;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 882; Conservative 97; Mismatches 79; Indels 9; Gaps 2;

QY 1 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSFGEAEVNVNLLRHGADPNARDNNYT 60
Db 225 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSFGEAEVNVNLLRHGADPNARDNNYT 284
QY 61 PLHEAAIKGKIDVICIVLQHGAEPIRNTDGTALDPSAKAVLTGEYKDELLESAR 120
Db 285 PLHEAAIKGKIDVICIVLQHGAEPIRNTDGTALDPSAKAVLTGEYKDELLESAR 344
QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 180
Db 345 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 404
QY 181 PLHNACSYGHEVTELLVKGHCACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
Db 405 PLHNACSYGHEVTELLVKGHCACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 464
QY 241 NCHNKSADLAPTOLKERLAYEFKHSLLQAAEADVTRIKKHSLEMVNFKHPQTHET 300
Db 465 NCHGKSAVDMAPTPELRERLTTEYFKHSHLQAAEADLAKVKTLLALEIINFKQPSHET 524
QY 301 ALHCAAAAPYPRKQICELLRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 360
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Db 525 ALHCAVASLHPKRVQVTELLRLKGANVNEKNKDFMTPLHVAARAHNDVMEVLHKGAKM 584
Qy 361 NALNLGQTSLHRAAYCHLQTCRLLSYGCDDNIIISLQGTALOMGNVNVQQLQEGIS 420
Db 585 NALDTLGTALHRAALAGHLQTCRLLSYGDPSIISLQGTAAQMGNEAVQQLSESTP 644
Qy 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYL 480
Db 645 IRTSDVYRLLEASKAGDLETVKQLCSQNVNCRDLEGRHSTPLHFAAGYNRVSVVEYL 704
Qy 481 QHGADVHAKDGGVPLHNAACSYGHEVAELLVHKGAVNVADLWKFTPLHFAAGYNRVSVVEYL 540
Db 705 HHGADVHAKDGGVPLHNAACSYGHEVAELLVHKGAVNVADLWKFTPLHFAAGYNRVSVVEYL 764
Qy 541 ICKLLHGHGADPTKKNRDGNTPLDVKDGTDIQDLRGDAALDAAKKGCLARVKLSS 600
Db 765 ICKLLHGHGADPTKKNRDGNTPLDVKEGDTDIQLLKGDAALDAAKKGCLARVQKLC 824
Qy 601 PDVNCRDTOGRHSTPLHNAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 825 PENINCRDTOGRNSTPLHNAAGYNNLEVAEYLLHGHGADVNAQDKGGLIPLHNAASYGHVD 884
Qy 661 VAALLIKYNACVNATDKWAFPLHFAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 720
Db 885 IAALLIKYNTCVNATDKWAFPLHFAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 944
Qy 721 ADDVSALLTAAMPSPALPCYKQVNLGVNVRSPGATADALSSGSPSSLSAASLDNLSG 780
Db 945 ADDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTPSCLSAASIDNLG 997
Qy 781 SFSELSVSSSGTEGASSLEKK--EVPDVFSTQFVRNLGLEHMDIFEREQITLDVL 838
Db 998 PLAELAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSJGLEHLRDIETEQITLDVL 1057
Qy 839 VEMGHKELKEIGINAYGHRHKLKGVVERLLSGQGLNPYLTLNTSGSGTILIDISPDKE 898
Db 1058 ADMGHEELKEIGINAYGHRHKLKGVVERLLSGQGTNPYLTFHCVNQGTILLDAPEDKE 1117
Qy 899 FQSVVEEMQSTVREHRDGGHAGGIFNRYNIIKIKVCNKKLWERYTHRRKEVSENNHA 958
Db 1118 YQSVVEEMQSTIREHRDGGNAGGIFNRYNIRIKVNVNKKLRERFCHRQKEVSENNHH 1177
Qy 959 NERMLFHGSPFNALIHKGDFERHAYTGGMGAGIYFAENSSKSNQYVYGTGGTGCPCVH 1018
Db 1178 NERMLFHGSPFNALIHKGDFERHAYTGGMGAGIYFAENSSKSNQYVYGTGGTGCPCVH 1237
Qy 1019 KDRSICYIHRQLLFCRVTLGKSFQFSAMQAHSPGHHSVTGRPSV 1065
Db 1238 KDRSICYIHRQMLFCRVTLGKSFQFSMTKMAHAPPGHSHSVIGRPSV 1284

RESULT 13

US-09-972-115A-8
; Sequence 8, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972.115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.1
; LENGTH: 1327
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-972-115A-8
Query Match 84.9%; Score 4740.5; DB 2; Length 1327;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 882; Conservative 97; Mismatches 79; Indels 9; Gaps 2;
Qy 1 GFGRKDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNVNLLRRHGCADPNARDNNY 60
Db 225 GFGRKDVVEYLLQNGANVHARDGGGLIPLHNACSFHAEVNVNLLRRHGCADPNARDNNY 284
Qy 61 PLHEAAIKGIDVICIVLQHGAEPTIRNTDGRALDADPSAKAVLTGEYKDELLSAR 120
Db 285 PLHEAAIKGIDVICIVLQHGADPNIRNTDGSALDADPSAKAVLTGEYKDELLSAR 344
Qy 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNRVKTIVQLLQHGADVHAKDGDV 180
Db 345 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNRVKTIVQLLQHGADVHAKDGDV 404
Qy 181 PLHNACSYGHEYTELLVHKGACVNAMDWKQFTPLHEAASKNRVEVCSLLLSYCADPTLL 240
Db 405 PLHNACSYGHEYTELLVHKGACVNAMDWKQFTPLHEAASKNRVEVCSLLLSYCADPTLV 464
Qy 241 NCHNKSADLAPTPOKRLAYBFGHSLLOAAREADVTRI KKHLSLEVMNFHQPOTHE 300
Db 465 NCHGKSADVAPTPELRELTIEFGHSLLOAAREADLAKVKKTLALEINFKQPOSHET 524
Qy 301 ALHCAAAASPYPKQKQICELLRLKGANINTEKGFPLPLHVAASEKAHNDVVEVVKHAKV 360
Db 525 ALHCAVASLHPKRVQVTELLRLKGANVNEKNKDFMTPLHVAARAHNDVMEVLHKGAKM 584
Qy 361 NALNLGQTSLHRAAYCHLQTCRLLSYGCDDNIIISLQGTALOMGNVNVQQLQEGIS 420
Db 585 NALDTLGTALHRAALAGHLQTCRLLSYGDPSIISLQGTAAQMGNEAVQQLSESTP 644
Qy 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYL 480
Db 645 IRTSDVYRLLEASKAGDLETVKQLCSQNVNCRDLEGRHSTPLHFAAGYNRVSVVEYL 704
Qy 481 QHGADVHAKDGGVPLHNAACSYGHEVAELLVHKGAVNVADLWKFTPLHFAAGYNRVSVVEYL 540
Db 705 HHGADVHAKDGGVPLHNAACSYGHEVAELLVHKGAVNVADLWKFTPLHFAAGYNRVSVVEYL 764
Qy 541 ICKLLHGHGADPTKKNRDGNTPLDVKDGTDIQDLRGDAALDAAKKGCLARVKLSS 600
Db 765 ICKLLHGHGADPTKKNRDGNTPLDVKEGDTDIQLLKGDAALDAAKKGCLARVQKLC 824
Qy 601 PDVNCRDTOGRHSTPLHNAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 825 PENINCRDTOGRNSTPLHNAAGYNNLEVAEYLLHGHGADVNAQDKGGLIPLHNAASYGHVD 884
Qy 661 VAALLIKYNACVNATDKWAFPLHFAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 720
Db 885 IAALLIKYNTCVNATDKWAFPLHFAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 944
Qy 721 ADDVSALLTAAMPSPALPCYKQVNLGVNVRSPGATADALSSGSPSSLSAASLDNLSG 780
Db 945 ADDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTPSCLSAASIDNLG 997
Qy 781 SFSELSVSSSGTEGASSLEKK--EVPDVFSTQFVRNLGLEHMDIFEREQITLDVL 838
Db 998 PLAELAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSJGLEHLRDIETEQITLDVL 1057
Qy 839 VEMGHKELKEIGINAYGHRHKLKGVVERLLSGQGLNPYLTLNTSGSGTILIDISPDKE 898
Db 1058 ADMGHEELKEIGINAYGHRHKLKGVVERLLSGQGTNPYLTFHCVNQGTILLDAPEDKE 1117
Qy 899 FQSVVEEMQSTVREHRDGGHAGGIFNRYNIIKIKVCNKKLWERYTHRRKEVSENNHA 958
Db 1118 YQSVVEEMQSTIREHRDGGNAGGIFNRYNIRIKVNVNKKLRERFCHRQKEVSENNHH 1177
Qy 959 NERMLFHGSPFNALIHKGDFERHAYTGGMGAGIYFAENSSKSNQYVYGTGGTGCPCVH 1018
Db 1178 NERMLFHGSPFNALIHKGDFERHAYTGGMGAGIYFAENSSKSNQYVYGTGGTGCPCVH 1237
Qy 1019 KDRSICYIHRQLLFCRVTLGKSFQFSAMQAHSPGHHSVTGRPSV 1065
Db 1238 KDRSICYIHRQMLFCRVTLGKSFQFSMTKMAHAPPGHSHSVIGRPSV 1284

Db 1178 NERMLFHGSPFFINAIHKGFDERHAYIGMGFGAGIYFAENSSKNQYVYGIGGTGCPH 1237
QY 1019 KDRSCVICHROLFCRVTLGKFLQFSAMKMAHSPGHHSTVGRPSV 1065
Db 1238 KDRSCVICHROLFCRVTLGKFLQFSAMKMAHSPGHHSTVGRPSV 1284

RESULT 14
US-09-972-115A-2
Sequence 2, Application US/09972115A
Patent No. 6599728
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1333
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: The 'Xaa' at location 1 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (2)..(2)
OTHER INFORMATION: The 'Xaa' at location 2 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (3)..(3)
OTHER INFORMATION: The 'Xaa' at location 3 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (4)..(4)
OTHER INFORMATION: The 'Xaa' at location 4 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (5)..(5)
OTHER INFORMATION: The 'Xaa' at location 5 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (6)..(6)
OTHER INFORMATION: The 'Xaa' at location 6 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (7)..(7)
OTHER INFORMATION: The 'Xaa' at location 7 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (8)..(8)
OTHER INFORMATION: The 'Xaa' at location 8 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (9)..(9)
OTHER INFORMATION: The 'Xaa' at location 9 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
OTHER INFORMATION: The 'Xaa' at location 10 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (10)..(10)
OTHER INFORMATION: The 'Xaa' at location 11 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (11)..(11)
OTHER INFORMATION: The 'Xaa' at location 12 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (12)..(12)
OTHER INFORMATION: The 'Xaa' at location 13 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (13)..(13)
OTHER INFORMATION: The 'Xaa' at location 14 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (14)..(14)
OTHER INFORMATION: The 'Xaa' at location 15 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (15)..(15)
OTHER INFORMATION: The 'Xaa' at location 16 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (16)..(16)
OTHER INFORMATION: The 'Xaa' at location 17 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (17)..(17)
OTHER INFORMATION: The 'Xaa' at location 18 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: The 'Xaa' at location 19 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (19)..(19)
OTHER INFORMATION: The 'Xaa' at location 20 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: The 'Xaa' at location 21 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (21)..(21)
OTHER INFORMATION: The 'Xaa' at location 22 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (22)..(22)
OTHER INFORMATION: The 'Xaa' at location 23 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (23)..(23)
OTHER INFORMATION: The 'Xaa' at location 24 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T


```

; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyzek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US 09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(11)
; OTHER INFORMATION: The 'Xaa' at location 1 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (42)-(42)
; OTHER INFORMATION: The 'Xaa' at location 42 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (98)-(98)
; OTHER INFORMATION: The 'Xaa' at location 98 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (110)-(110)
; OTHER INFORMATION: The 'Xaa' at location 110 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (114)-(114)
; OTHER INFORMATION: The 'Xaa' at location 114 stands for Asn, Ser, Thr, or Ile.
; NAME/KEY: misc feature
; LOCATION: (126)-(126)
; OTHER INFORMATION: The 'Xaa' at location 126 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (139)-(139)
; OTHER INFORMATION: The 'Xaa' at location 139 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (144)-(144)
; OTHER INFORMATION: The 'Xaa' at location 144 stands for Thr.
; NAME/KEY: misc feature
; LOCATION: (153)-(153)
; OTHER INFORMATION: The 'Xaa' at location 153 stands for Thr.
; NAME/KEY: misc feature
; LOCATION: (166)-(166)
; OTHER INFORMATION: The 'Xaa' at location 166 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (173)-(173)
; OTHER INFORMATION: The 'Xaa' at location 173 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (174)-(174)
; OTHER INFORMATION: The 'Xaa' at location 174 stands for Glu, or Lys.
; NAME/KEY: misc feature
; LOCATION: (183)-(183)
; OTHER INFORMATION: The 'Xaa' at location 183 stands for Val.
; NAME/KEY: misc feature
; LOCATION: (185)-(185)
; OTHER INFORMATION: The 'Xaa' at location 185 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (188)-(188)
; OTHER INFORMATION: The 'Xaa' at location 188 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (202)-(202)
; OTHER INFORMATION: The 'Xaa' at location 202 stands for His, or Pro.
; NAME/KEY: misc feature
; LOCATION: (204)-(204)
; OTHER INFORMATION: The 'Xaa' at location 204 stands for Glu, or Lys.
; NAME/KEY: misc feature
; LOCATION: (205)-(205)
; OTHER INFORMATION: The 'Xaa' at location 205 stands for Asn, Ser, Thr, or Ile.
; NAME/KEY: misc feature
; LOCATION: (207)-(207)
; OTHER INFORMATION: The 'Xaa' at location 207 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (211)-(211)
; OTHER INFORMATION: The 'Xaa' at location 211 stands for Gln, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (213)-(213)
; OTHER INFORMATION: The 'Xaa' at location 213 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (215)-(215)
; OTHER INFORMATION: The 'Xaa' at location 215 stands for Lys, Asn, Glu, Asp, Gln, His
; OTHER INFORMATION: , a stop codon, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (227)-(227)
; OTHER INFORMATION: The 'Xaa' at location 227 stands for His, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (228)-(228)
; OTHER INFORMATION: The 'Xaa' at location 228 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (237)-(237)
; OTHER INFORMATION: The 'Xaa' at location 237 stands for Glu, or Asp.
; NAME/KEY: misc feature
; LOCATION: (238)-(238)
; OTHER INFORMATION: The 'Xaa' at location 238 stands for Asn, Ser, Thr, Ile, Asp, Gly
; OTHER INFORMATION: , Ala, Val, His, Arg, Pro, Leu, Tyr, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (667)-(667)
; OTHER INFORMATION: The 'Xaa' at location 667 stands for Tyr, Cys, Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (725)-(725)
; OTHER INFORMATION: The 'Xaa' at location 725 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (727)-(727)
; OTHER INFORMATION: The 'Xaa' at location 727 stands for His, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (735)-(735)
; OTHER INFORMATION: The 'Xaa' at location 735 stands for Glu, or Asp.
; NAME/KEY: misc feature
; LOCATION: (741)-(741)
; OTHER INFORMATION: The 'Xaa' at location 741 stands for Met, Val, or Leu.
; NAME/KEY: misc feature
; LOCATION: (763)-(763)
; OTHER INFORMATION: The 'Xaa' at location 763 stands for Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (764)-(764)
; OTHER INFORMATION: The 'Xaa' at location 764 stands for Tyr, Cys, Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (787)-(787)
; OTHER INFORMATION: The 'Xaa' at location 787 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (788)-(788)
; OTHER INFORMATION: The 'Xaa' at location 788 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (789)-(789)
; OTHER INFORMATION: The 'Xaa' at location 789 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (790)-(790)
; OTHER INFORMATION: The 'Xaa' at location 790 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (791)-(791)
; OTHER INFORMATION: The 'Xaa' at location 791 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
```



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;; LOCATION: (792)..(792)
;; OTHER INFORMATION: The 'Xaa' at location 792 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (793)..(793)
;; OTHER INFORMATION: The 'Xaa' at location 793 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (794)..(794)
;; OTHER INFORMATION: The 'Xaa' at location 794 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (795)..(795)
;; OTHER INFORMATION: The 'Xaa' at location 795 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (796)..(796)
;; OTHER INFORMATION: The 'Xaa' at location 796 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (797)..(797)
;; OTHER INFORMATION: The 'Xaa' at location 797 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (798)..(798)
;; OTHER INFORMATION: The 'Xaa' at location 798 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (799)..(799)
;; OTHER INFORMATION: The 'Xaa' at location 799 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (800)..(800)
;; OTHER INFORMATION: The 'Xaa' at location 800 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (801)..(801)
;; OTHER INFORMATION: The 'Xaa' at location 801 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
;; LOCATION: (802)..(802)
;; OTHER INFORMATION: The 'Xaa' at location 802 stands for Lys, Asn, Arg, Ser, Thr, Ile
;; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
;; NAME/KEY: Tyr, Trp, Cys, or Phe.
Query Match 83.5%; Score 4663; DB 2; Length 1267;
Best Local Similarity 85.7%; Pred. No. 0;
Matches 914; Conservative 6; Mismatches 143; Indels 4; Gaps 2;
Qy 2 FGRKDVVEYLLONGASVQARDGGLIPLHNACSGHAEVNNLLRHGADPNARDNNWYTP 61
Db 167 FGRKDXLYLLTNGANXQXRDXGGLIPLHNACSGXAXXIXLLXHXAXPNARDNNWYTP 226
Qy 62 LHEAAIKGIDVCVLLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLESARS 121
Db 227 XKEAAIKGIXXCIVLLQHGAEPTIRNTDGTALDPSAKAVLTGEYKDELLESARS 286
Qy 122 GNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGDLVP 181
Db 287 GNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGDLVP 346
Qy 182 LHNACSGHYEVTELLVKHGACVNMADLWQFTPLHEAAKKNRVEVCSLLLSYGADPTLLN 241
Db 347 LHNACSGHYEVTELLVKHGACVNMADLWQFTPLHEAAKKNRVEVCSLLLSYGADPTLLN 406
Qy 242 CHNKSALDLATPTQLKERLAYEFKSHLSLQAREADVTRIKKHSLEVMNFKHPQTHETA 301
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Db 407 CHNKSALDLATPTQLKERLAYEFKSHLSLQAREADVTRIKKHSLEVMNFKHPQTHETA 466
Qy 302 LHCAASAPYPRKQICELLRLKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKVN 361
Db 467 LHCAASAPYPRKQICELLRLKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKVN 526
Qy 362 ALDNLGQTSLHRAAYCGHLOTCELLLSYGCDDPNIISLOGFTALOMGNENVOQLLOEGISL 421
Db 527 ALDNLGQTSLHRAAYCGHLOTCELLLSYGCDDPNIISLOGFTALOMGNENVOQLLOEGISL 586
Qy 422 GNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQ 481
Db 587 GNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQ 646
Qy 482 HGADVHAKDKGGLVPLHNACSGHYEVAELLVKHGAANNVADLWKFTPLHEAAAKGYEI 541
Db 647 HGADVHAKDKGGLVPLHNACSGHYEVAELLVKHGAANNVADLWKFTPLHEAAAKGYEI 706
Qy 542 CKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIODLLRGDAALDAKKGCLARVKLSSP 601
Db 707 CKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIODLLRGDAALDAKKGCLARVKLSSP 766
Qy 602 DNVNCRDTQGRHSTPLHLAAGYNNRVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDV 661
Db 767 DNVNCRDTQGRHSTPLHLAAGYNNRVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDV 825
Qy 662 AALLIKYNACVNATDKWAFPTPLHEAAKQKGTQLCALLAHGADPTLKNQSGQTPLDLVSA 721
Db 826 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 885
Qy 722 DNVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSPPSSPSLSAASSLDNLSGS 781
Db 886 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 945
Qy 782 FSELSSVSSSGTEGASSLEKKEVPGVDFSIOTFVRNLGLEHLMDFEREQITLDVLVEM 841
Db 946 FSELSSVSSSGTEGASSLEKKEVPGVDFSIOTFVRNLGLEHLMDFEREQITLDVLVEM 1005
Qy 842 GHKELKEIGINAYCHRHKLKIGVERLISGOQGLNPYLTNTSGSTILIDLSPDDKBFQS 901
Db 1006 GHKELKEIXINAYCHRHKLKISFERLISGOQGLNPYLTNTSGSTILIDLSPDDKBFQS 1065
Qy 902 VEEMQSTVREHRDGGHAGGIFNRYNLIKTKQYCNK---KLWERYTHRRKEVSEENHHA 958
Db 1066 VEEMQSTVREHRDGGHAGGIFNRYNLIKTKQYCNRAKIRHEERYTHRRKEVSEENHHA 1125
Qy 959 NERMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGPCVH 1018
Db 1126 NERMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGPCVH 1185
Qy 1019 KDRSCYICHRQLLFCRVTLQKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1186 KDRSCYICHRQLLFCRVTLQKSFLOFSAMKMAHSPPGHHSVTGRPSV 1232
```

Search completed: December 18, 2006, 17:37:18
Job time : 39.577 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2006, 17:27:10 ; Search time 32.8048 Seconds
(without alignments)
3123.657 Million cell updates/sec

Title: US-10-616-101-3

Perfect score: 5585

Sequence: 1 GFGKRDVVEYLLQNGASVQA.....AMKMAHSPPGHHSVTGRPSV 1065

Scoring table: , BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	877.5	15.7	1765	T42714	ankyrin 3, splice
2	877.5	15.7	1961	T42716	ankyrin 3, splice
3	875.5	15.7	4377	A55575	ankyrin 3, long sp
4	873.5	15.6	1943	T42713	ankyrin 3, splice
5	871.5	15.6	1940	T42715	ankyrin 3, splice
6	860.5	15.4	3924	S37431	ankyrin 2, neurona
7	844	15.1	1856	B35049	ankyrin 1, erythro
8	844	15.1	1880	A35049	ankyrin 1, erythro
9	839.5	15.0	1848	1 SUHUK	ankyrin 1, erythro
10	837.5	15.0	1862	S37771	ankyrin, erythrocy
11	834	14.9	1549	T13940	ankyrin - mouse
12	814.5	14.6	2039	T15347	ankyrin - fruit fl
13	814.5	14.6	2039	T15347	ankyrin-related un
14	628	11.2	791	T42691	hypothetical prote
15	545.5	9.8	1411	S30355	alpha-latroinsecto
16	514	9.2	934	H71274	probable ankyrin -
17	496.5	8.9	1062	T30255	inversin - mouse
18	491.5	8.8	1062	T14151	Inv protein - mous
19	464.5	8.3	1401	S11527	alpha-latrotoxin p
20	456.5	8.2	1188	T19552	hypothetical prote
21	451	8.1	1058	T82654	ankyrin-like prote
22	431.5	7.7	426	A82149	hypothetical prote
23	426	7.6	991	T25412	hypothetical prote
24	405.5	7.3	1184	T00253	gene Ankhzn protei
25	388	6.9	397	T46445	hypothetical prote
26	372.5	6.7	2584	T24158	hypothetical prote
27	372.5	6.7	2606	T24157	hypothetical prote
28	363.5	6.5	1031	T43458	hypothetical prote
29	350	6.3	557	T46507	hypothetical prote

30	348.5	6.2	606	2	AC2508	hypothetical prote
31	345	6.2	1423	1	T37275	death-associated p
32	336.5	6.0	1107	2	T21280	hypothetical prote
33	321	5.7	1398	2	T21884	hypothetical prote
34	310	5.6	1435	2	T32930	hypothetical prote
35	306	5.5	1322	2	A59288	myosin heavy chain
36	305	5.5	679	2	B45771	2-SA-dependent RNA
37	300.5	5.4	1016	2	T19006	ankyrin related pr
38	299.5	5.4	633	2	T27499	hypothetical prote
39	299	5.4	247	2	D84448	probable ankyrin [
40	294.5	5.3	900	2	A42024	transcription fact
41	290	5.2	1004	2	A55142	myosin-light-chain
42	287.5	5.1	656	2	A34793	sex-determining pr
43	287	5.1	1295	2	T21720	hypothetical prote
44	285	5.1	1083	2	S48460	probable membrane
45	284	5.1	237	2	T50984	related to 26s pro

ALIGNMENTS

RESULT 1

T42714

ankyrin 3, splice form 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42714

R:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.

J. Cell Biol. 130, 313-330, 1995

A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f the repeat domain.

A:Reference number: Z22237; MUID:95340633; PMID:7615634

A:Accession: T42714

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1765 <PET>

A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000029AB8; EMBL:L40632; NID:g710548; PID:

A:Experimental source: strain C57BL/6J; kidney

C:Genetics:

A:Gene: Ank3

A:Map position: 10

A:Introns: 1587/1

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

Query Match Similarity 15.7%; Score 877.5; DB 2; Length 1765;
Best Local Similarity 30.9%; Pred. NO. 4.1e-46;
Matches 277; Conservative 125; Mismatches 377; Indels 117; Gaps 22;

QY	3	GRKDVVEYLLQNGASVQARDGGLIPLHNACSFHGAEVVNLRLRHGADPNARDNNWYTP	62
DB	68	GHVEVVELLQREANVDATKKGNTALHISLAGQAEVVKVLTNGANVAQSQNGFTPL	127
QY	63	HEAAIKGKIDVICVLLQHGAEPTIRNTDGRPTALDLA-----DPSAKAVLTGYSK---KDE	114
DB	128	YMAAQENHLEVVRFLLDNGASQSLATEDGFTPLAVALQQGHQDVVLSLENDTKGKRLP	187
QY	115	LLESARSGNEEMKALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLHOGADVHAK	174
DB	188	ALHTAARKDDTKAAALLLQNDTNADVESKSGFTPLHIAAHYGNINVTALLNRAAAVDFT	247
QY	175	DKGDLVPLHNACSGHYEVTELLVKHGACVAMDLWQFTPLHGAASKNRVEVCSLLLSYG	234
DB	248	ARNDDITPLHVAASKGNANMVKLLLDORGAKIDAKTRDGLTPLHCGARSHEQVVEMLLDRS	307
QY	235	ADPTLLNCHNKSAIDLAPTQPKERLAYEFKGHSLQLQAAREADVTRIKKHLSLEMVNFKH	294
DB	308	A-PILSKTN-----GLSPHMTQGD-----HLNCVQLLQHQ	339
QY	295	-----PQTHETALHCAAAPYPRKQKQICELLKKGANINEKTEFLTPLHVAASEKAHN	347
DB	340	NVPVDVDTNLYLTALHVAAHCHGVK---VAKVLLDKKASPNAKALNGFTPLHIACKKNRI	396

Qy 348 DVEVVVHKAQNALDNLGQTSLHRAAYCGHLOTCRLLLSYSGCDPNIIISLQGFALOMG 407
 Db 397 RVWELLKHGASIQAVTESGLTPIHVAAPFMGHVNIIVSQLMHGASPNNTTNVGETALHMA 456
 Qy 408 -----NENVQQLQEGISLGNSEADRO--LLEAAKAGDVETVKKLCV--QSVNCRDIEGR 459
 Db 457 ARSQAEVVRVLYVQDGAQVEAKAKDDQTPHLSARLGKADIVQQLLQOGASPNATTS--G- 515
 Qy 460 QSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDGGVPLHNAACSYGHEVAELLVKHGAVV 519
 Db 516 -YTPLHAAAREGHEDVAFAFLDHGASLSITTKGFTPLHVAAYKGLVASLLOKSASP 574
 Qy 520 NVADLWKFPTLHAAAKGYEICKLLQHGADPTKKNRDGNTPLDL--VKGDGTDIDQLL- 577
 Db 575 DAAGKSGLTPLHVAAYHYNQKVALLLDQOGASPHAAAKNGYTPHIAAKKNQMDIATSL 634
 Qy 578 -----RGDAALLDAAKGGLARVKKLSPPD--NVNCRDTCGRHSTPLHLAAGYNN 625
 Db 635 EYGADANAVTRQGIASVHLAAQEGHVDVMSLLSRNANVLSNKG--LTPHLAAQEDR 692
 Qy 626 LEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPLHE 685
 Db 693 VNVAEVLVNOGAHVDAQTQMGYTPLVHGYCHYGNIKIVNFFLQHSKAVNAKTNGYTAHQ 752
 Qy 686 AAQKGTOLCALLAHGADPTLKNQEGOTPLDLVS-----ADVSALLTAAMPSPALP 738
 Db 753 AAQOQHTHIINVLQNNASPNELTVNGNTALAIARRLGYISVVDTLKVVTIEIMTTTIT 812
 Qy 739 SCYK---POVLNGVRSFGATADALSSGSPSSLSAASLDNLS--GSFSELSSVSSSGT 794
 Db 813 EKHQNVPTMNEVLD-----MSDDEVKASAPEKLSDGEY-----ISDGE 853
 Qy 795 EGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVLVEMGHKELKEIG 850
 Db 854 EGDKCTWFK-IPKQVEVLVK-----SEDAITGDTDKYLGPDQLKELG 894

RESULT 2
 T42716
 ankyrin 3, splice form 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42716
 R:Peterson, L.L.; John, K.M.; Lu, F.M.; Bicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, J.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ankyrin 3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A:Reference number: Z22237; MUID:95340633; PMID:7615634
 A:Accession: T42716
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1961 <PET>
 A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000027D39; EMBL:L40632; NID:g710548; PID
 A:Experimental source: strain C57BL/6J; kidney
 C:Genetics:
 A:Gene: Ank3
 A:Map position: 10
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing

Query Match 15.7%; Score 877.5; DB 2; Length 1961;
 Best Local Similarity 30.9%; Pred. No. 4,9e-46;
 Matches 277; Conservative 125; Mismatches 377; Indels 117; Gaps 22;

Qy 3 GRKDVVEYLLONGASVQARDGGLIPLHNAACSYGHEVAELLVKHGADPNARDNWNVTPL 62
 Db 68 GHVEVVEYLLQREANVDATKNGNTALHLSAQAEVVKVLTNGANVNASQNGFTPL 127

Qy 63 HEAAIKGKIDVCVILLQHGAEPTIRNTDGRALDLA-----DPSAKAVLTGEYK---KDE 114
 Db 128 YMAAQENHLEVRFLDNGASQSLATEDGFTPLAVALQGHQDVVSLLENDTKGKVRLP 187
 Qy 115 LLESARSGNEERKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLLQHGADVHAK 174

Db 188 ALHIAARDDYKAAALLQNDTNADVESKSGFTPLHIAAHYGNINVATLLNRAAAVDFT 247
 Qy 175 DKGDVPLHNAACSYGHEVTELLVHKGACVNAQMDLWQFTPLHAAAKNRVVCSELLISYG 234
 Db 248 ARNDITPLHVASKRGANVNVKLLDRGAKIDAKTRDGLTPLHCGARSQHEQVVMELDRS 307
 Qy 235 ADPTLLCNCHNSAIDLAPTPQLKERLAVFEFKGHSLLQAAAREADVTRI KKHLSLEWNVFKH 294
 Db 308 A-PILSKTKN-----GLSPLHMAQGD-----HLNCVQLLLQH 339
 Qy 295 -----PQTHETALHCAAAASPYPKRKQICELELLRKGANINEKTEFLTPHVAASEKAHN 347
 Db 340 NVPVDDVTNDYLTALHVAACHGCHK---VAKVLLDKASPNAKALNGFTPLHIAACKNRI 396
 Qy 348 DVEVVVHKAQNALDNLGQTSLHRAAYCGHLOTCRLLLSYSGCDPNIIISLQGFALOMG 407
 Db 397 RVWELLKHGASIQAVTESGLTPIHVAAPFMGHVNIIVSQLMHGASPNNTTNVGETALHMA 456
 Qy 408 -----NENVQQLQEGISLGNSEADRO--LLEAAKAGDVETVKKLCV--QSVNCRDIEGR 459
 Db 457 ARSQAEVVRVLYVQDGAQVEAKAKDDQTPHLSARLGKADIVQQLLQOGASPNATTS--G- 515
 Qy 460 QSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDGGVPLHNAACSYGHEVAELLVKHGAVV 519
 Db 516 -YTPLHAAAREGHEDVAFAFLDHGASLSITTKGFTPLHVAAYKGLVASLLOKSASP 574
 Qy 520 NVADLWKFPTLHAAAKGYEICKLLQHGADPTKKNRDGNTPLDL--VKGDGTDIDQLL- 577
 Db 575 DAAGKSGLTPLHVAAYHYNQKVALLLDQOGASPHAAAKNGYTPHIAAKKNQMDIATSL 634
 Qy 578 -----RGDAALLDAAKGGLARVKKLSPPD--NVNCRDTCGRHSTPLHLAAGYNN 625
 Db 635 EYGADANAVTRQGIASVHLAAQEGHVDVMSLLSRNANVLSNKG--LTPHLAAQEDR 692
 Qy 626 LEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPLHE 685
 Db 693 VNVAEVLVNOGAHVDAQTQMGYTPLVHGYCHYGNIKIVNFFLQHSKAVNAKTNGYTAHQ 752
 Qy 686 AAQKGTOLCALLAHGADPTLKNQEGOTPLDLVS-----ADVSALLTAAMPSPALP 738
 Db 753 AAQOQHTHIINVLQNNASPNELTVNGNTALAIARRLGYISVVDTLKVVTIEIMTTTIT 812
 Qy 739 SCYK---POVLNGVRSFGATADALSSGSPSSLSAASLDNLS--GSFSELSSVSSSGT 794
 Db 813 EKHQNVPTMNEVLD-----MSDDEVKASAPEKLSDGEY-----ISDGE 853
 Qy 795 EGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVLVEMGHKELKEIG 850
 Db 854 EGDKCTWFK-IPKQVEVLVK-----SEDAITGDTDKYLGPDQLKELG 894

RESULT 3
 A55575
 ankyrin 3, long splice form - human
 N:Alternate names: ankyrin G
 C:Species: Homo sapiens (man)
 C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 31-Dec-2004
 C:Accession: A55575
 R:Kordeli, E.; Lambert, S.; Bennett, V.
 J. Biol. Chem. 270, 2352-2359, 1995
 A:Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax
 A:Reference number: A55575; MUID:95138209; PMID:7836469
 A:Accession: A55575
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-4377 <KOR>
 A:Cross-references: UNIPROT:Q12955; UNIPARC:UPI000013C497; GB:U13616; NID:g608024; PID:n
 C:Genetics:
 A:Gene: GDB:ANK3
 A:Cross-references: GDB:424503; OMIM:600465
 A:Map position: 10q21-10q21
 C:Superfamily: EGF homology

C;Keywords: alternative splicing; peripheral membrane protein

F:73-105/Domain: ankyrin repeat homology <AN01>
F:106-138/Domain: ankyrin repeat homology <AN02>
F:139-171/Domain: ankyrin repeat homology <AN03>
F:172-200/Domain: ankyrin repeat homology <AN04>
F:201-233/Domain: ankyrin repeat homology <AN05>
F:234-266/Domain: ankyrin repeat homology <AN06>
F:267-299/Domain: ankyrin repeat homology <AN07>
F:300-332/Domain: ankyrin repeat homology <AN08>
F:333-365/Domain: ankyrin repeat homology <AN09>
F:366-398/Domain: ankyrin repeat homology <AN10>
F:399-431/Domain: ankyrin repeat homology <AN11>
F:432-464/Domain: ankyrin repeat homology <AN12>
F:465-497/Domain: ankyrin repeat homology <AN13>
F:498-530/Domain: ankyrin repeat homology <AN14>
F:531-563/Domain: ankyrin repeat homology <AN15>
F:564-596/Domain: ankyrin repeat homology <AN16>
F:597-629/Domain: ankyrin repeat homology <AN17>
F:630-662/Domain: ankyrin repeat homology <AN18>
F:663-695/Domain: ankyrin repeat homology <AN19>
F:696-728/Domain: ankyrin repeat homology <AN20>
F:729-761/Domain: ankyrin repeat homology <AN21>
F:762-794/Domain: ankyrin repeat homology <AN22>
F:795-827/Domain: ankyrin repeat homology <AN23>

Query Match 15.7%; Score 875.5; DB 2; Length 4377;
Best Local Similarity 30.5%; Pred. No. 2.3e-45;
Matches 273; Conservative 126; Mismatches 362; Indels 135; Gaps 21;

Qy 3 GRKDVVEYLLQNGASVQARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNNWYTPL 62
Db 85 GHVEVSELLQREANVDAATKKGNTALHSLAGQAEVVKVLTNGANVNAQSQNGFTPL 144

Qy 63 HEAAIKGKIDVICVILQHGAEPTIRNTDGTALDLA-----DPSAKAVLTGEYK---KDE 114
Db 145 YMAAQENHLEVVEVFLDNGASQSLATEDGFTPLAVALQOQHDQVVSLLLENDTKGKRLP 204

Qy 115 LLESARGSGNEKEMKALLTPLNVNCHASDGRKSTPLHLAAGNVRVKIVOLLQHGADVHAK 174
Db 205 ALHTAARKDDTKAALLQNDNADVESKSGFTPLHIAAHYGNINVTALLNRAAADFT 264

Qy 175 DKGLVPLHNACSGHYEVTELLVKHGACVNMADLQFTPLHEAASKNRVVCVCSLLLSYG 234
Db 265 ARNDITPLHVASKRGANVMVLLDRGAKIDAKTRDGLTPLHCGARSHEQVEMVLLDRA 324

Qy 235 ADPTLLCHNKSAIDLAFTPOLKERLAYEFKGHSLQAAAREADVTRIKKHLSLEWVNFKH 294
Db 325 A-PILSKTKN-----GLSPLHMAATQGD-----HLNCVQLLIQH 356

Qy 295 -----PQTHETALHCAASPYPKRKQICELLIRKGANINEKTEPLTPLHVASEKAHN 347
Db 357 NVPVDDVTNDYLTALHVAHCHGYK---VAKVLDKKAANPAKALNGFTPLHIAACKNRI 413

Qy 348 DVVEVVKHEAKVNALDNLGOTSUHLRAAYCGHLOTQCRLLSYGCDPNIIISLQGFALQMG 407
Db 414 KVMELLKHGASIQAVTESGLTPIHVAFMGHVNIQVLSLMEHGHASPTNTNVRGETALHMA 473

Qy 408 -----NENVQQLQEGISLGNSEADRO---LLEAAKAGDVETVKKLCVV-QSNCRDIEGR 459
Db 474 ARSQGAQVVRVYLQDGAQVEAKAKDDQTPHISARLGRADIVQQLQOQASFNAAATTSG- 532

Qy 460 QSTPLHFAAGNVRVSVVEYLLQHGADVHAKDKGGLVPLHNACSGHYEVAELLVKHGAVV 519
Db 533 -YTPHLHSAAREGHEVAAFLDHGASUSITTKKFTPLHVAAKYKGKUEVANILLQKASGP 591

Qy 520 NVADLWKEFTPLHEAAAKGYEICKLLQHGADPTKKNRDGNTPLDL-VKQGDTDIQILL- 577
Db 592 DAAGKSGLTPLHVAHYDNQKVALLLDQGHASPHAAKNGYTPHLHIAKKNQMDIATILL 651

Qy 578 -----RGDAALLDAKKGCLARVKKLSPPD-NVNCRDQTQGRHSTPLHLAAGVNN 625
Db 652 EYGADANAVTRQGIASVHLAAQEGHVDVMSLLGRNANVNLNKSQ--LTPLHLAAQEDR 709

Qy 626 LEVAEYLLQHGADVNAQDKGGLIPLHNAAASYGHVDVVAALLIKYACVNAKTWAFPTPLHE 685
Db 710 VVNAEVLVNGAHVDAQTKMGYTPFLHVGCHYGNIKIVNFLQHSKAKNAKTNGYTPHLQ 769

Qy 686 AAQKGRQLCALLAHGADPTLKNQSGQTPDL-----VSADDVSALLT-AAMPSPALP 738
Db 770 AAQOQGHTHIINVLLQNNASPNELTVNGNTALGIARRLGYSVVDPTLKIIVTETMTTITVT 829

Qy 739 SCYK---POVLNGVRSFGATADALSSGSPSSLSAASSLDNLGSGFSELSSVSSSGTE 795
Db 830 EKHKNVPETNEVLD-----MSDEVRKANAPENLSDG----- 863

Qy 796 GASSLEKKEVGVDFSITQFVRNLGLEHLMDFEREQ-ITLDVLVEMGHKELKEIG 850
Db 864 -----EVIDSVERGEDAMTGTDKYLGPDQLKEIG 893

RESULT 4
T42713
ankyrin 3, splice form 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42713
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f
the repeat domain.
A:Reference number: Z22237; MUID:95340633; PMID:7615634
A:Accession: T42713
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1943 <PE>
A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000028367; EMBL:L40632; NID:G710548; PID:
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 855/1
C:Function:
A:Description: supposed to play an important role in the polarized distribution of many i
A:Note: major kidney ankyrin
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 15.6%; Score 873.5; DB 2; Length 1943;
Best Local Similarity 30.6%; Pred. No. 8.6e-46;
Matches 274; Conservative 122; Mismatches 365; Indels 135; Gaps 21;

Qy 3 GRKDVVEYLLQNGASVQARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNNWYTPL 62
Db 68 GHVEVSELLQREANVDAATKKGNTALHSLAGQAEVVKVLTNGANVNAQSQNGFTPL 127

Qy 63 HEAAIKGKIDVICVILQHGAEPTIRNTDGTALDLA-----DPSAKAVLTGEYK---KDE 114
Db 128 YMAAQENHLEVVEVFLDNGASQSLATEDGFTPLAVALQOQHDQVVSLLLENDTKGKRLP 187

Qy 115 LLESARGSGNEKEMKALLTPLNVNCHASDGRKSTPLHLAAGNVRVKIVOLLQHGADVHAK 174
Db 188 ALHTAARKDDTKAALLQNDNADVESKSGFTPLHIAAHYGNINVTALLNRAAADFT 247

Qy 175 DKGLVPLHNACSGHYEVTELLVKHGACVNMADLQFTPLHEAASKNRVVCVCSLLLSYG 234
Db 248 ARNDITPLHVASKRGANVMVLLDRGAKIDAKTRDGLTPLHCGARSHEQVEMVLLDRA 307

Qy 235 ADPTLLCHNKSAIDLAFTPOLKERLAYEFKGHSLQAAAREADVTRIKKHLSLEWVNFKH 294
Db 308 A-PILSKTKN-----GLSPLHMAATQGD-----HLNCVQLLIQH 339

Qy 295 -----PQTHETALHCAASPYPKRKQICELLIRKGANINEKTEPLTPLHVASEKAHN 347
Db 340 NVPVDDVTNDYLTALHVAHCHGYK---VAKVLDKKAANPAKALNGFTPLHIAACKNRI 396

Qy 348 DVVEVVKHEAKVNALDNLGOTSUHLRAAYCGHLOTQCRLLSYGCDPNIIISLQGFALQMG 407

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Db 397 RVMLLLKHGASIQAVTESGLTPIHVAAPFMGHVNIIVSQLMHHGASPNITNVGETALHMA 456
Qy 408 -----NEWVQQLQGGISLGNSEADQ--LLEAAKAGDVETVKKLCIV-QSVNCRDIEGR 459
Db 457 ARSGQAEVVRVIVDQGAQVEAKKDDQTPHLSARLGKADIIVQQLLQCGASPNAAATTS- 515
Qy 460 QSTPLHFAAGYNRVSVVEYLLQHGADVHAKDGGGLVPLHNACSYGHEVAELLVKHGAVV 519
Db 516 -YTPLHLAAREGHEDVAAPLLOHGASLSITTTKGGFTPLHVAAGYKLEVASLLOKQAS 574
Qy 520 NVADLWKFTPLHAAAKGKEICKLLQHGADPTKKNRDNTPDL-VKDGDTDIQDILL- 577
Db 575 DAAGKSGLTPLHVAHYDNQKVALLLQDGASPHAAAKNGYTPHLIAAKNQMDIATSL 634
Qy 578 -----RGDAALDAKKGCLARKYKLSPPD-VNCRDITQGRHSTPLHLAAGYNN 625
Db 635 EYGADANAVTRQGIASVHLAAQEGHVDVMSLLSRNANVNLNKG--LTPHLAAQEDR 692
Qy 626 LEVAEYLLQHGADVNAQDKGGLIPLHNAASCHVDVAALLIKYNACVNATDKWAFPLHE 685
Db 693 VNVAEVLVNOGAHVDAQTKMGYTPLVHVGCHYGNIKIVNPLQHSKAKVNAKTNGYTAHQ 752
Qy 686 AAQKGTQCALLAHAGADPTLKNQEGOTPLDVS-----ADDVSALLTAAMPSPALP 738
Db 753 AAQGGHTHIINVLQNNASPNELTVNGTALAIARLGLYISVVDTLKVTEEIMTTIT 812
Qy 739 SCYK---POVLNGVRSPGATADALSGSPSSLSAASLDNLS-GSFSSELSSVSSGT 794
Db 813 EKHKMNPETMNEVLDD-----MSDDEVKASAPEKLSDEY-----ISDGE 853
Qy 795 EGASSELKEKVEPGVDFSTIQFVRNLGLEHMDIFEREQITLDVIVEMGHKELKEIG 850
Db 854 EG-----EDAITGDTDKYLGPDQLKELG 876

RESULT 5
T42715
Ankyrin 3, splice form 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42715
J:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.
J:Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; PMID:95340633; PMID:7615634
A:Accession: T42715
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1940 <PET>
A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000029ABD; EMBL:L40632; NID:g710548; PID
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 834/1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 15.6%; Score 871.5; DB 2; Length 1940;
Best Local Similarity 28.3%; Pred. No. 1.1e-45;
Matches 320; Conservative 159; Mismatches 464; Indels 189; Gaps 35;

Qy 3 GRKDVVEYLLQNGASVQARDGGLIPLHNACSFHGAEVNLLLRHGDAPNARDNNYITPL 62
Db 68 GHVEVVELLQREANVDATKGNATLHIASLAGQAEVVKLVTVNGANVNAQSQNGFTPL 127

Qy 63 HBAATKGKIDVCIVLLQHGAEPTINTDGRALDLA-----DPSKAVLTGYK---KDE 114
Db 128 YMAAQENHLEVVRFLLDNGASQSLATEDGFTPLAVALQGHQDVVSLLENDTKGKVRLP 187
Qy 115 LLESARSNGEEKWALLPLNVLNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAK 174
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Db 188 ALHIAARKDDTKAAALLQNDTNADVESKSGFTPLHIAAHYGNINVATLLNRAAAVDFT 247
Qy 175 DKGDVPLHNACSYGHEVTELLVKGACVNAAMDLMQFTPLHFAAASKNRVEVESCILLSYG 234
Db 248 ARNDITPLHVAKRGNNANVVKLLDRGAKIDAKTRDGLTPLHCGARSGBEQVVEMLLDRS 307
Qy 235 ADPTLLNCHNKSAIDLAPTPQLKERLAYBFKGHSLLOAAREADVTRIKKHLSELMVNFKH 294
Db 308 A-PILSKTKN-----GLSPHMAATQGD-----HLNCVQLLQH 339
Qy 295 -----POTHETALHCAAAAPYKPKQICEILLRKGANINEKTEKFLTPLHVAASEKAHN 347
Db 340 NVPVDVTDNYLTALHVAACHGHYK---VAKVLLDKKASPNKALANGFTPLHIACKNRI 396
Qy 348 DVVEVVVHKAENALDNIGQTSLHRAAYCGHLOTCRLLLSYGCDDPNISLQGFALOMG 407
Db 397 RVWELLKHGASIQAVTESGLTPIHVAAPFMGHVNIIVSQLMHHGASPNITNVGETALHMA 456
Qy 408 -----NEWVQQLQGGISLGNSEADQ--LLEAAKAGDVETVKKLCIV-QSVNCRDIEGR 459
Db 457 ARSGQAEVVRVIVDQGAQVEAKKDDQTPHLSARLGKADIIVQQLLQCGASPNAAATTS- 515
Qy 460 QSTPLHFAAGYNRVSVVEYLLQHGADVHAKDGGGLVPLHNACSYGHEVAELLVKHGAVV 519
Db 516 -YTPLHLAAREGHEDVAAPLLOHGASLSITTTKGGFTPLHVAAGYKLEVASLLOKQAS 574
Qy 520 NVADLWKFTPLHAAAKGKEICKLLQHGADPTKKNRDNTPDL-VKDGDTDIQDILL- 577
Db 575 DAAGKSGLTPLHVAHYDNQKVALLLQDGASPHAAAKNGYTPHLIAAKNQMDIATSL 634
Qy 578 -----RGDAALDAKKGCLARKYKLSPPD-VNCRDITQGRHSTPLHLAAGYNN 625
Db 635 EYGADANAVTRQGIASVHLAAQEGHVDVMSLLSRNANVNLNKG--LTPHLAAQEDR 692
Qy 626 LEVAEYLLQHGADVNAQDKGGLIPLHNAASCHVDVAALLIKYNACVNATDKWAFPLHE 685
Db 693 VNVAEVLVNOGAHVDAQTKMGYTPLVHVGCHYGNIKIVNPLQHSKAKVNAKTNGYTAHQ 752
Qy 686 AAQKGTQCALLAHAGADPTLKNQEGOTPLDVS-----ADDVSALLTAAMPSPALP 738
Db 753 AAQGGHTHIINVLQNNASPNELTVNGTALAIARLGLYISVVDTLKVTEEIMTTIT 812
Qy 739 SCYK---POVLNGVRSPG-----ATADALSS-----GP----- 763
Db 813 EKHKMNPETMNEVLDDMSDEGDKCTWFKIPKQVEVLVKSSEDITGDTDKYLGPDQLKEL 872
Qy 764 ---SSPSSLSAASLDNLSGFSSELSSVVS-----SSGTEGASSELKEKVEPGVDFSTIQF 815
Db 873 GDDSLPAEGYVGFSLGARSASLRSFSSDRSYTLNRSYARDSMMIEELLVPSKEQHLT-F 931
Qy 816 VNLGLEHMDIFEREQITLDV-----VEMGHKELKEIGINAYG-----HRHKL 861
Db 932 TREFDSDSLRH-YSWAADTLDNVNLVSSPVHSGF--LVSPFMDARGSGMRSGRHGMR 988
Qy 862 -----KGVERLISQOGLNPYLTNTSSGRTILDSPDDKEFQS-VEEEMQSTV 910
Db 989 IPPRCKTAPTRITCRVLKHKHLANPPMVMEGEGSLARLVEWGPAGQFLGPVIEIP--- 1045
Qy 911 REHRDGGHAGGIFNRYNLIKIQVCNKKLWE--RYTHRRKEVSE-----ENHNHANERML 963
Db 1046 -----HFGSMRGKREILVLRSENGETWKEHQFDSKNEDLAELLNGMBELDLSPEEL- 1097
Qy 964 FHGSPFNVAIIHKGFDERHAYIGGMFGAGIYFAENS---SKSNQYVYVIGGG 1012
Db 1098 --GTRICRIITKDFPQ-----YFAVWSRIKQESNQ--IGPEGG 1132
```

RESULT 6

S37431

Ankyrin 2, neuronal long splice form - human

N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid

N;Contains: ankyrin 2, short form

C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
 C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
 R:Chan, W.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37431
 A:Accession: S37431
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-3924 <CHA>
 A:Cross-references: UNIPROT:Q01484; UNIPARC:UPI0000125B19; EMBL:226634; NID:G406287; PID:J. Cell Biol. 114, 241-253, 1991
 R:Oto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
 A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
 A:Reference number: A39643; MUID:91302466; PMID:1830053
 A:Accession: A39643
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2077 <OT1>
 A:Cross-references: UNIPARC:UPI0000177547; GB:X56957
 A:Accession: B39643
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1443, 3585-3924 <OTT>
 A:Cross-references: UNIPARC:UPI0000177548; EMBL:X56958
 R:Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward, Genomics 10, 858-866, 1991
 A:Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
 A:Reference number: A40334; MUID:92009921; PMID:1833308
 A:Accession: A40334
 A:Molecule type: DNA
 A:Residues: 463-474, 'PE', 477-495 <TSE>
 A:Cross-references: UNIPARC:UPI000016A55B; GB:M37123; NID:G178647; PIDN:AAA62828.1; PID:R:Chan, W.; Kordeli, E.; Bennett, V.
 J. Cell Biol. 123, 1463-1473, 1993
 A:Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and se
 A:Reference number: A49462; MUID:94075409; PMID:8253844
 A:Accession: A49462
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-3924 <RES>
 A:Cross-references: UNIPARC:UPI0000125B19; EMBL:226634; NID:G406287; PIDN:CAA81387.1; PI
 C:Genetics:
 A:Gene: GDB:ANK2
 A:Cross-references: GDB:127607; OMIM:106410
 A:Map position: 4q25-4q27
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:2-3924/Product: ankyrin 2, long form #status predicted <MAT>
 F:2-1443, 3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
 F:63-95/Domain: ankyrin repeat homology <AN01>
 F:96-128/Domain: ankyrin repeat homology <AN02>
 F:129-161/Domain: ankyrin repeat homology <AN03>
 F:162-190/Domain: ankyrin repeat homology <AN04>
 F:191-223/Domain: ankyrin repeat homology <AN05>
 F:232-264/Domain: ankyrin repeat homology <AN06>
 F:265-297/Domain: ankyrin repeat homology <AN07>
 F:298-330/Domain: ankyrin repeat homology <AN08>
 F:331-363/Domain: ankyrin repeat homology <AN09>
 F:364-396/Domain: ankyrin repeat homology <AN10>
 F:397-429/Domain: ankyrin repeat homology <AN11>
 F:430-462/Domain: ankyrin repeat homology <AN12>
 F:463-495/Domain: ankyrin repeat homology <AN13>
 F:496-528/Domain: ankyrin repeat homology <AN14>
 F:529-561/Domain: ankyrin repeat homology <AN15>
 F:562-594/Domain: ankyrin repeat homology <AN16>
 F:595-627/Domain: ankyrin repeat homology <AN17>
 F:628-660/Domain: ankyrin repeat homology <AN18>
 F:661-693/Domain: ankyrin repeat homology <AN19>
 F:694-726/Domain: ankyrin repeat homology <AN20>
 F:727-759/Domain: ankyrin repeat homology <AN21>
 F:760-792/Domain: ankyrin repeat homology <AN22>
 F:793-825/Domain: ankyrin repeat homology <AN23>

	Query Match	15.4%	Score 860.5;	DB 2;	Length 3924;
	Best Local Similarity	29.8%	Pred. No. 1.7e-44;		
	Matches 283;	Conservative 127;	Mismatches 386;	Indels 153;	Gaps 21;
QY	3	GRKDVVEYLLQNGASVQARDGGGLIPLHNACSGHAEVWVNLRLRHGADPNARDNNWYTP	62		
DB	75	GHVGLVQELLGRGSDVSATKKGNTALHIAISLAGQAEVVKVKEGANINAQSQNGFTPL	134		
QY	63	HEAAIKGKIDVICVLQHGABPTIRNTDGR-----ALDLADPSAKAVLTGEYKDEL---	115		
DB	135	YMAAQENHIDVVKYLLNGANQSTATEDGFTPLAVALQOQHNOVAIILENDTKGKRLP	194		
QY	116	-LESARSGNEEKMMALLTPLNVNCHASDGRKS-----TPHLHAAGYNNRVKIVQL	163		
DB	195	ALHTAARKDDTKSAALLQ---NDHNADVQSKMMVNRRTTESGFTPLHTAAHYGNVNVATL	251		
QY	164	LLQHGADVHAKDGDVPLHNACSGHYEYVTELLVKGACVNMMDLWQFTPLHEAASNR	223		
DB	252	LLNRGAADVFTARNGITPLHVASKRGNTNMVKLLDRGGQIDAKTRDGLTPLHCAARSGH	311		
QY	224	VEVCSLLLSYGADPTLLNCHNKSALDAPTQLKERLAYEFKSHSLLOQAAREADVTRIKK	283		
DB	312	DQVVELLLERGA-PILARTKN-----GSLPHMAAQGDHVECVK	349		
QY	284	HLSELMVNFKHP-----QTHETALHCAAAAPYKPKKQICELLRLKRGANINEKTEFLTPL	338		
DB	350	HL-----LQHKAPVDVDTLDYLTALHVA--HCGHYRVTKLLDKRANPNARALNGFTPL	402		
QY	339	HVASEKAHNDVVEVVVXHEAKVNDLNGOTSLHRAAYCGHLOTCRLLLSYGCDNIIISL	398		
DB	403	HIACKNRKIKVMELLVKYGASIQAITESGLTPIHVAAPFMGHLNIVLLLLONGASPDVTNI	462		
QY	399	QGFTALOMGN-----ENVQQLLOEGI-----SIGNSEADROLLE----	432		
DB	463	RGETALHMAARAGQVYVVRCLLRNGALVDARAREEQTPHLHTASRLGKTEIVOLLQHMWH	522		
QY	433	-----AAKAGDVETVKLCTQVSNCRDIEGRQSTPLHFAAGYNNRVSVVEY	478		
DB	523	PDAATTNGYTPHLHSAREGQVDVASVLEAGAHSLATK-KGFTPLHVAAYKGSIDVAKL	581		
QY	479	LLQHGADVHAKDGGVPLHNACSGHYEYVTELLVKGACVNMMDLWQFTPLHEAASNR	538		
DB	582	LLQRRRAADSAGKNGLTPLHVAHYDNQKVALLEKASPHATAKNGYTPHLHTAAKKNQ	641		
QY	539	YEICKLLLOHGADPTKNGRDNTPDLV-KDGTDDIQDLRGDAALLDAKKGCLARVKK	597		
DB	642	MQIASTLLNGAETNIVTKQGVTPHLASQBGHTDMVTLLDKGANIHMSTKSGL----	696		
QY	598	LSSPDVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYG	657		
DB	697	-----TSLHAAQEDKXNVADILTKHGADQDAHTKLGTYPLIVACHYG	739		
QY	658	HVDVAALLIKYNCVATDKWAFPTPLHEAAQKGTQLCALLLAHAGADPTLKNQEQOTPLD	717		
DB	740	NVKMVFLLKQGANVNAKTNGYTPHLHQAQOQHTHIINVLLQHGAKPNATTANGNTALA	799		
QY	718	L-----VSADDVSALLTAAMPSPALPSCYKQVINGVRSPCATADALSSGSPSSLSA	771		
DB	800	IAKELGYISVVDTLKVVTEVTTTTTITEK-----HKLNVPTMTTEVL-----DVSD	847		
QY	772	ASSLDNLGSGFSEL-----SSVSSSGTEGASSLEKKEVPGVDFRISITOPV--RN	818		
DB	848	EGDDTMTGQGEYLRPEDUKELGDDSLPSSQFDDGMNLYLSLEGGRSDSLRFSFSDRS	907		
QY	819	LGLEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERL	867		
DB	908	HTLSHAS--YLKDSAVMDDSVVIPSQVSTLAKAERNYSYLSWGTENL	954		

RESULT 7
 B35049
 ankyrin 1, erythrocyte splice form 3 - human

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N:Contains: ankyrin 2.2, erythrocyte

C:Species: Homo sapiens (man)

C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998

C:Accession: B35049

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A:Title: cDNA sequence for human erythrocyte ankyrin.

A:Reference number: A35049; MUID:90175370; PMID:1689849

A:Accession: B35049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1856 <LAM>

A:Cross-references: UNIPARC:UPI0000177546

C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900

A:Map position: 8p11.2-8p11.2

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>

F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

F:44-76/Domain: ankyrin repeat homology <AN01>

F:77-109/Domain: ankyrin repeat homology <AN02>

F:110-142/Domain: ankyrin repeat homology <AN03>

F:143-171/Domain: ankyrin repeat homology <AN04>

F:172-204/Domain: ankyrin repeat homology <AN05>

F:205-237/Domain: ankyrin repeat homology <AN06>

F:238-270/Domain: ankyrin repeat homology <AN07>

F:271-303/Domain: ankyrin repeat homology <AN08>

F:304-336/Domain: ankyrin repeat homology <AN09>

F:337-369/Domain: ankyrin repeat homology <AN10>

F:370-402/Domain: ankyrin repeat homology <AN11>

F:403-435/Domain: ankyrin repeat homology <AN12>

F:436-468/Domain: ankyrin repeat homology <AN13>

F:469-501/Domain: ankyrin repeat homology <AN14>

F:502-534/Domain: ankyrin repeat homology <AN15>

F:533-567/Domain: ankyrin repeat homology <AN16>

F:568-600/Domain: ankyrin repeat homology <AN17>

F:601-633/Domain: ankyrin repeat homology <AN18>

F:634-666/Domain: ankyrin repeat homology <AN19>

F:667-699/Domain: ankyrin repeat homology <AN20>

F:700-732/Domain: ankyrin repeat homology <AN21>

F:733-765/Domain: ankyrin repeat homology <AN22>

F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 15.1%; Score 844; DB 2; Length 1856;

Beat Local Similarity 25.7%; Pred. No. 5.5e-44;

Matches 281; Conservative 151; Mismatches 355; Indels 306; Gaps 28;

QY 3 GRKDVVEYLLONGASVQARDGGLIPLHNACSFGHAENVNLLRHGADPNARDNNWYTP 62

DB 89 GQDEVVELVNGVNVNAQSQGFTPLYMAAQENHLEVVKFLLENGANQNVATEDGFTPL 148

QY 63 HEAAIKGKIDVICVILLOHGAETI-----RNTDGTALDLADPSAKAVLTGEYK 113

DB 149 AVALQOQHENVVAHLINYGKVRPLPALHIAARNDTFTA-----AVLLQNDPNP 199

QY 114 ELLESARGNEEKWALLTPLNVNCHASD-----GRKS-----TPLHLAAGY 155

DB 200 DVL--SKTG-----FTPLHIAHYENLVNAQQLLNKSSVNFPPQNGITPLHIAARR 249

QY 156 NRKTVQLLQHGADVHAKDGLVPLHNACSFGHYEVTELVKYGACVNAVDLMQFTPL 215

DB 250 GNVIMVRLLDGAGIETKTDELTPHCAARNGHVRISILLDHGAPQAKTKNGLSPI 309

QY 216 HEAAKRNVEVCSLLSYCADPTFLNCHNKSIDAIDAPTQLKERLAYEFKSHLLQARE 275

DB 310 HMAAGDHLDCVRLLLQDYDAE-----ID----- 332

QY 276 ADVTRIKKHLSEVMVNFKHPQTHETALHCAASPYKPKQICELLIRKGANINEKTKPL 335

DB 333 -DIT-----LDHLTPHVA--HGHHRVAKVLLDKGAKPNSRALNGF 372

QY 336 TPLHVASEKAHNDVVEVVKHEAKVNALDNLGOTSLHRAAYCGHLQTCRLLLSVGCDPNI 395

DB 373 TPLHACKQNHVRVMEELLTKTGASIDAVTESGLTPLVASFMLGHLFIVKLLQORGASPNV 432

QY 396 ISLQGFALQMG-----NENVQQLQEQ-----GISLGNSEADRLQLE- 432

DB 433 SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDOTPLHCAARIGHTNNVKKLLEN 492

QY 433 -----AAKAGDVETVKKLCTVQ--SVNCRDIEGROSTPLHFAAGYNRVS 474

DB 493 NANPNLATTAGHTPLHIAAREGHVETVLALLEKEASQACWTKKG--FTPLHVAAYGKVR 550

QY 475 VVEYLLQHGADVHAKDGGVPLHNACSFGHYEVAELLVKGAVNVNADLWK--FTPLHEA 533

DB 551 VAEILLERDAHPNAAGKGLTPLHVAVHNHNDIVKLLIPRGGSPH--SPAANGTTPHIA 609

QY 534 AAKGYEICKLLLOHGADPTKKNRDGNTPLDL--VKDGDITDIQLLRGDAALLDAAKKGCL 592

DB 610 AKQNVAVARSLLQYGGSANAESVQGVTPHLAAQEGHAEVALL----- 654

QY 593 ARVKLSSPDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHN 652

DB 655 -----LSKQANGNLGNKSG--LTPLHLVAQEGHVPVADVLIKHGVMVDATTRMGYTPHV 707

QY 653 AASYGHVDVAALLIKYNACVNATDKWAFPLHAAQKGRGTQLCALLAHGADPTLKNQEG 712

DB 708 ASHYGNIKLVKRFLLQHQADVNAKTKLGYSPLHQAQOQGHDTIVTLLKNGASPNVSSDG 767

QY 713 QTPDL-----VSADVDVSALLTAMPPSALPSC----- 740

DB 768 TTPLAIAKRLGIVSDTVLKVTDTSFVLVSDKHEMSFETVDEILDVSEGEELISF 827

QY 741 -----YKQVNLNGVRSPGATADALSSGSPSSSLSS-----AASSLDN 777

DB 828 KAERRDSRDVBEKELDFVPKLDQVVESPA-----PRIPCAMPETVWIRSEREQ 879

QY 778 LSGSFELSSVSSSGTEGASSLEKEVEQVDFSIQFVRLNLEHLMDFEREQITLDV 837

DB 880 ASKEYDEDSLIPSSPATETSDNISPVASPVHTGFLVSEF----- 918

QY 838 LVEMGHKELKEIGINAYGHRHKLKGVE-----RLISGQGLNPVLTNTSG 884

DB 919 -----VDARGSNRSGRHNGLRVVIPTCAAPTRICLVKPKQLSTPPPLAEEG 970

QY 885 STILIDLSP-----DDKEFQSEEEEMQSTVREHRRDGHGAGGIF 923

DB 971 LASRIIALGFTGAQFLSPVIVEIPHPFASHGRGDRDLVLRSENGSVWKEHR----- 1021

QY 924 NRYNLIKIQKVCN 936

DB 1022 SRYGESYLDQILN 1034

RESULT 8

A35049

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N:Contains: ankyrin 2.2, erythrocyte

C:Species: Homo sapiens (man)

C:Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004

C:Accession: A35049

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A:Title: cDNA sequence for human erythrocyte ankyrin.

A:Reference number: A35049; MUID:90175370; PMID:1689849

A:Accession: A35049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1880 <LAM>

A:Cross-references: UNIPROT:P16157; UNIPARC:UPI0000177545; GB:M28880

C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing; cytoskeleton
F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
F:2-1513.1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 15.1%; Score 844; DB 2; Length 1880;
Best Local Similarity 25.7%; Pred. No. 5.6e-44;
Matches 281; Conservative 151; Mismatches 355; Indels 306; Gaps 28;

QY 3 GRKQVVEYLQNGASVQARDGGLPLHNCASFGEHAEVWVLLRHGADPNARDNNYTP 62
DB 89 GQDEVVRELWYGANVNAQSGKFTPLYNAAQENHLEVVKFLLNGANGQVATEDGFTPL 148

QY 63 HEAAIKGKIDVCI VILQHGABPTI-----RNTDGRITLADLADPSAKAVLTGEYKD 113
DB 149 AVALQGHENVAHLINVTGKVRPLPALHIAARNDDTRTA-----AVLLQNDNP 199

QY 114 ELLESARGSENEKMMALLTPLNVNCHASD-----GRKS-----TPLHLAAGY 155
DB 200 DVL--SKTG-----FTPLHIAHYENLVNAQLLNRGSSVNFPPQNGITPLHIAARR 249

QY 156 NRKVIQLLOLHGADVHAKDGLVPLHNCASYGHEVTELLVKGACVNMMDLMOFTPL 215
DB 250 GNVMVRLLDGQAQITETKTDELTPHCAARNGHVRISSEILLDHGAPITQAKTKNGLSPI 309

QY 216 HEAAKQNRVECSLLSYGADPTLNCNKSADLAPTLPOLKRLAYEFKSHLSLQAARE 275
DB 310 HMAAQDHLDCVRLLLQYDAB-----ID----- 332

QY 276 ADVTRIKKLSLEWNVFKHPQHTALHCAASAPYKPKQICELLRLKGANINEKTEPL 335
DB 333 -DIT-----LDHLPLHVA--HCHHRVAKVLLDKGAKNSALNGF 372

QY 336 TPLHVAEKANDVVEVVKHBAKVNALDNLQOTSLHRAAYCCHLQTCRLLSYCCDPNI 395
DB 373 TPLHIACKGNHVRMELLKTKGASIDAVTESGLTPLHVASPMGLPIVKNLLQRCASPNV 432

QY 396 ISLQFTALOMG-----NENVOQLLOE-----CISLGNSEADQLILR- 432
DB 433 SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDQTPHLHCAARTGHTNMVKKLEN 492

QY 433 -----AAKAGDVETVKKLCVQ--SVNCRDIEGRQSTPLHFAAGNVRVS 474
DB 493 NANPNLATTAGTTPHLHIAAREGHVETVLALLEKEASQACWTKG--FTPLHVAAYKGV 550

QY 475 VVEYLLQHGADVHAKDGLVPLHNCASYGHEVTELLVKGACVNVNADLMK-FTPLHEA 533
DB 551 VAEILLERDAHPNAAKNGLTPLHVAHVHNNLDIVKLLPRGSGSPH-SPAWNNGYTPHLIA 609

QY 534 AAKGYEICKLLQHGADPTKKNRDGNTPLDL-VKGDGTDIQDLLRGDAALLDAAKKGCL 592
DB 610 AKQNVQVARSLLQVGGSAANAESVQGVTPPLHLAAQEGHAEMVALL----- 654

QY 593 ARVKKLSFDDNNCRDGTGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLH 652
DB 655 -----LSKQANGNLGKSG--LTPLHLVAQEGHVFADVLLKHGVMVDATTRMGYTPLHV 707

QY 653 AASYGHVDVAALLIKYNACVNAATDKWFTPLHEAAQKGRTOCALLLAHGADPTLKNOEG 712
DB 708 ASHYGNIKLVFLLQHQADVNAKTKLGYSPLHQAQQGHTDITVYLLKNGASPNVSSDG 767

QY 713 QTPLDL-----VSADVSALLTAAMPSPALPSC----- 740
DB 768 TTPLAIKRLGLVISVTDVLKVVTDETSFVLVSDKHRMSFPETVDEILDVSEDEGEELISF 827

QY 741 -----YKQVNLGVRSPPATADALSSGSPSSPSLS-----AASLDN 777
DB 828 KAERRDRDVEKEKELDFVPKLDQVVEPAI-----PRIPCAMPETVIRSEEQEQ 879

QY 778 LSGSFSELSVVSSSGTEGASLEKKEKVPVDFSTQFVRLNGLHLMIDIFEREQITLDV 837
DB 880 ASKEYDESLIPSSPATETSDNISVSPVHTGFLVSEFM----- 918

QY 838 LVEMGHKELKEIGINAYGHRHKLKGV-----RLISGQOGLNPYLTNTSG 884
DB 919 -----VDARGGMRGSRHNLRLVPPPTCAAPTITCLVKKPKQLSTPPPLAESEG 970

QY 885 SGTILDLSP-----DDKEFQSVBEEMOSTVREHRRDGGHAGGIF 923
DB 971 LASRIIALGPTGAOFLSPVIVEIPHFAHSGRGDRELVLVLRSENGSVWKEHR----- 1021

QY 924 RRYNLIKQKVCN 936
DB 1022 SRYGESYLDQILN 1034

RESULT 9
SJHUK
ankyrin 1, erythrocyte splice form 1 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N:Contains: ankyrin 2.2
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S08275; A33219; PC2220; A35443
R:Lux, S.E.; John, K.M.; Bennett, V.
Nature 344, 36-42, 1990
A:Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure w
A:Reference number: S08275; MUID:90158830; PMID:2137557
A:Accession: S08275
A:Molecule type: mRNA
A:Residues: 1-1881 <LUI>
A:Cross-references: UNIPROT:P16157; UNIPARC:UPI0000167B64; EMBL:X16609; NID:g28701; PIDN:
A:Accession: A33219
A:Molecule type: protein
A:Residues: 2-7,'X',9-17,'X',19-20,'T',22-30,733-749,'A',751-753,828-833,'X',835-855,'X',
X,1367,1383-1427,1601-1630,1686-1698,'D',1700,1763-1772 <LUX>
A:Cross-references: UNIPARC:UPI0000173DC3; UNIPARC:UPI0000173DC4; UNIPARC:UPI0000173DC5;
DCA; UNIPARC:UPI0000173DCB; UNIPARC:UPI0000173DCC; UNIPARC:UPI0000173DCD; UNIPARC:UPI0000173DCE;
A>Note: 845-Arg and 1392-Thr were also found
R:Hermann, J.; Barel, M.; Prade, R.
Biochem. Biophys. Res. Commun. 204, 453-460, 1994
A:Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A:Reference number: PC2220; MUID:95071348; PMID:7526850
A:Accession: PC2220
A:Molecule type: protein
A:Residues: 910-929 <HER>
A:Cross-references: UNIPARC:UPI0000173DDO
R:Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A:Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A:Reference number: A35443; MUID:90285190; PMID:2141335

A:Accession: A35443
A:Molecule type: protein
A:Residues: 'X', 'S', 'Y', '7-12', '403-417', 'X', '419-422', 'H', '424', 'LQ', '797-800', 'L', '802-814', '862-863',
A:Cross-references: UNIPARC:UPI0000173DD1; UNIPARC:UPI0000173DD2; UNIPARC:UPI0000173DD3;
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing; phosphoprotein
F:2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F:2-1512, 1675-1881/Product: ankyrin 2, erythrocyte #status predicted <MAT2>
F:2-827/Domain: 89k #status predicted <DOM1>
F:2-827/Region: anion exchange protein binding
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
F:828-1382/Domain: 62k #status predicted <DOM2>
F:828-1382/Region: spectrin binding
F:1383-1381/Domain: 55k #status predicted <DOM3>

Query Match 15.1%; Score 842; DB 1; Length 1881;
Best Local Similarity 25.5%; Pred. No. 7.5e-44;
Matches 279; Conservative 152; Mismatches 356; Indels 306; Gaps 27;
QY 3 GRKDYVEYLLONGASVQARDGGLIPLHNACSFGEAEVYNLLRHGADPNARDNNYTP 62
DB 89 GQDEVVRELNVYGVANVNAQSGFTPLYMAAQENHLEVVKFLENGANGNVATEDGFTPL 148
QY 63 HEATKGIKIDVICVLLQHGAEPTI-----RYTDGRTALDLADPSAKAVLTGEYK 113
DB 149 AVALQOQGHENVAHLINTGTGKVKRLPALHIAARNDTRTA-----AVLLQNDPNP 199
QY 114 ELLSARGSENEKQWALLTPLNVNCHASDGRKS-----TPLHLAAGY 155
DB 200 DVL--SKTG-----FTPLHIAHYENLVNAQVLLNRGASVNTTPQNGITPLHIAER 249
QY 156 NRKIVVQLLQHGADVHAKRGLDPLHNACSYGHEVTELVKRGACVNAVDLWQFTPL 215
DB 250 GNVMVRLLDGAGIETKTDELTPHCAARNGHVRISILLDHGAPIQAKTKNGLSPI 309
QY 216 HEASKNRVEVCSLLSAGADPTLNCNCHKSALDIAPTQPKERLAYEPKGHSLQAARE 275
DB 310 HMAAQGDHLDCVRLLLQYDAE-----ID----- 332
QY 276 ADVTRI KGHLSLEMYNFKHPQTHETALCAAASPYKPKQICELLRLKGANINEKKEPL 335
DB 333 -DIT-----LDHLLTPLHVA-----HCGHHRVAKVLLDQKAKPNSRALNGF 372
QY 336 TPLHVASEKAHNDVVEVVVGHBAKYNLDNLGQTSLSHRAAYCGHLQTCRLLLSYGCDFNI 395
DB 373 TPLHTACKNHRVVMELLKTGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNV 432

QY 396 ISLQGFALQMG-----NENVQOLLQ-----GISLGNSEADROLLE- 432
DB 433 SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDQTPHCAARIGHNVMKLLLEN 492
QY 433 -----AAKAGDVETVKKLCTVQ-SVNCRDIEGROSTPLHFAAGYNRVS 474
DB 493 NANPNLATTAGHTPLHIAAREGHVEITLALLEKEASQACWTKKG--FTPLHVAAYKVKR 550
QY 475 VVEYLLQHGADVHAKRGLDPLHNACSYGHEVTELVKRGACVNAVDLWQ-FTPLHVA 533
DB 551 VAELLERDAHPNAAGKNGLTPLHVAHNNLDIVKLLPRGGSPH-SPAWNGYTPHLHIA 609
QY 534 AAKGYEICKLLOHGADPTKKNRDGNTPLDL-VKDGDTDIQDLRGDAALLDAKKGCL 592
DB 610 AKONQVEVARSLLQYGGSSANAESVQGVTPHLHAAQEGHAEWVALL----- 654
QY 593 ARVKLSSPDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHN 652
DB 655 -----LSKQANGNLGNKSG--LTPLHVAQEGHVPVADVLIKHGVMDATTRMGYTPHV 707
QY 653 AASYGHVDVAALLIKYNACVNAQDKWAFPLHBAOKGRTQOLCALLAHGADPTLKNQEG 712
DB 708 ASHYGNIKLVKFLQHQADVNAKTKLGYSPLHQAQOQGHDTIVTLLKNGASPNVSSDG 767
QY 713 QTPLDL-----VSADDVSALLTAAMPSPALPSC----- 740
DB 768 TTPLAIAKRLGIVSDTVLVKVTDETSFVLVSDKHRMSFPETVDEILDVSEDEGEELISP 827
QY 741 -----YKQVNLNGVSPGATADALSSQSPSPSSLS-----AASLDN 777
DB 828 KAERDRSDVDEKELLDVFKLDQVVEPAI-----PRIPCAMPETVWIRSEBEQ 879
QY 778 LSGSFSELSVSSVSSGTEGASLEKKEVPGVDPSITQFVNLGLEHLMDFEREQITLDV 837
DB 880 ASKEYDEDSLIPSPATETSDNISPVASPVHTGLVSEFM----- 918
QY 838 LVEMGHKELKETGINAYGHRHKLKQVE-----RLISGQGLNPYLTLNTSG 884
DB 919 -----VDARGGSMRSGRHNGLRVVIPTCAAPTRITCRILVKPKOKJSTPPPLASEEG 970
QY 885 SGTILIDLSP-----DDKEFQSVBEEMQSTVREHRDGGHAGGIF 923
DB 971 LASRIIALGPTGAQFLSPVIVEIPHFASHGRGDRELVLVLRSENGSVWKEHR----- 1021
QY 924 NRYNLIKIOKVCN 936
DB 1022 SRYGESYLDQILN 1034

RESULT 10

S37771
ankyrin, erythrocyte - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37771
R:Birkmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J. Biol. Chem. 268, 9533-9540, 1993
A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found am
A:Reference number: S37771; MUID:93252825; PMID:8486643
A:Accession: S37771
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1848

A:Cross-references: UNIPROT:Q61302; UNIPARC:UPI0000028360; EMBL:X69063; NID:G311816; PIDN
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:48-80/Domain: ankyrin repeat homology <AN01>
F:81-113/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN03>
F:147-175/Domain: ankyrin repeat homology <AN04>
F:176-208/Domain: ankyrin repeat homology <AN05>
F:209-241/Domain: ankyrin repeat homology <AN06>
F:242-274/Domain: ankyrin repeat homology <AN07>

F:275-307/Domain: ankyrin repeat homology <AN08>
 F:308-340/Domain: ankyrin repeat homology <AN09>
 F:341-373/Domain: ankyrin repeat homology <AN10>
 F:374-406/Domain: ankyrin repeat homology <AN11>
 F:407-439/Domain: ankyrin repeat homology <AN12>
 F:440-472/Domain: ankyrin repeat homology <AN13>
 F:473-505/Domain: ankyrin repeat homology <AN14>
 F:506-538/Domain: ankyrin repeat homology <AN15>
 F:539-571/Domain: ankyrin repeat homology <AN16>
 F:572-604/Domain: ankyrin repeat homology <AN17>
 F:605-637/Domain: ankyrin repeat homology <AN18>
 F:638-670/Domain: ankyrin repeat homology <AN19>
 F:671-703/Domain: ankyrin repeat homology <AN20>
 F:704-736/Domain: ankyrin repeat homology <AN21>
 F:737-769/Domain: ankyrin repeat homology <AN22>
 F:770-802/Domain: ankyrin repeat homology <AN23>

Query Match 15.0%; Score 839.5; DB 2; Length 1848;
 Best Local Similarity 29.5%; Pred. No. 1e-43;
 Matches 237; Conservative 127; Mismatches 262; Indels 177; Gaps 20;

QY 3 GRKDVVEYLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNWYTP 62
 DB 93 GODEVRELVNNGANNAQSGKFTPLYNAAQENHLEVVVKFLLNGANQNVADEGFTPL 152
 QY 63 HEAAIKGKIDVICVLLQHGAEPTI-----RNTDGRALDLADPSAKAVLTGEYK 113
 DB 153 AVAQOQHENVVAHLINVTGKVRPLPALHIAARNDDTRTA-----AVLLQNDPNP 203
 QY 114 ELLESARGNEEKMMALLTPLNVNCHASGRKS-----TPHLAAGY 155
 DB 204 DVL--SKTG-----FTPLHIAAHYENLVNVAQLLNRGASVNFPPQNGITPLHIA 253
 QY 156 NRVKIVQLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPL 215
 DB 254 GNVMVRLLDLDRGAQIETRTKDELTPHCAARNGHVRISAILLDHGAPIOAKTKNGLSPI 313
 QY 216 HEAAKSRVEVCSLLSYGADPTLLNCHNKSAIDLAPTQPKERLAYEFKGHSLLOAARE 275
 DB 314 HMAAQGDHLDVRLLLQYNAB-----ID----- 336
 QY 276 ADVTRIKKLSLEMVNFKHPQTHETALHCAASPYPRKQICELLRKGANINEKTEFL 335
 DB 337 -DIT-----LDHLTPHVA--HCGHVRVAKVLLDKGAPNSRALNGF 376
 QY 336 TPLHVAEKAHNDVVEVVKHAKVNALDNLGQTSIHAAYCGHQLTCRLLLSYCCDNI 395
 DB 377 TPLHTACKNHIRVNMELLTKTGASIDAVTESGLTPLHVASFMGHLPIVKNILLQRGASPNV 436
 QY 396 ISLOGFTALOM-----GNENVQOLLQEGISLGNSEAD-----ROLLE- 432
 DB 437 SNVKVETPLHMAARAGHTEVAKYLLQNKAKANAKAKDDOTPLHCAARIGHGTGWKVLLEN 496
 QY 433 -----AAKAGDVEVTKLCTVQ--SVNCRDIEGRQSTPLHPAAGYNRVS 474
 DB 497 GASPNLATTAGHTPLHTAAREGHVDTALALLEKEASQACWTKKG--FTPLHVAAYGKVR 554
 QY 475 VVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNVNADLWK--FTPLHEA 533
 DB 555 LAELLEHDHAPNAAGKNGLTPLHVAVHNNLIDIVKLLLPGRGSPH-SPAWNGYTPHLIA 613
 QY 534 AAKGYEIKLLOHGADPTKKNRDGNTPLDI--VKGDTDIDQLLGRDAALLDAKKGCL 592
 DB 614 AKQNGIEVARSLLQYGGGNAESVGVFTPLHAAQEGHTEMVALL----- 658
 QY 593 ARVKKLSPPDNVNCRDTOQRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHN 652
 DB 659 -----LSQANGNLGNKSG--LTPLHLVSOEGHVPVADVLKGVTVDAFTMGVTPHLV 711
 QY 653 AASYGHVDVAALLIKYNAQVATDKWATFTPLHAAQKGTQICALLAHGADPTLKNQEG 712
 DB 712 ASHYGNIKLVKFLQHQADVNAKTKLGYSPHQAQOQGHDTIVTLLKNGASPNVSSNG 771

QY 713 OTPLDL-----VSADDVSALLT 729
 DB 772 TTPLAIARLGLYISVTDVLKVT 794

RESULT 11

I49502
 ankyrin - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I49502
 R:White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
 Mamm. Genome 3, 281-285, 1992
 A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory doma
 A:Reference number: I49502; MUID:92345717; PMID:1386265
 A:Accession: I49502
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1862 <RES>
 A:Cross-references: UNIPROT:Q02357; UNIPARC:UPI000002921E; GB:M84756; NID:gi91939; PIDN:
 C:Genetics:
 A:Gene: Ank-1
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:40-72/Domain: ankyrin repeat homology <AN01>
 F:73-105/Domain: ankyrin repeat homology <AN02>
 F:106-138/Domain: ankyrin repeat homology <AN03>
 F:139-167/Domain: ankyrin repeat homology <AN04>
 F:168-200/Domain: ankyrin repeat homology <AN05>
 F:201-233/Domain: ankyrin repeat homology <AN06>
 F:234-266/Domain: ankyrin repeat homology <AN07>
 F:267-299/Domain: ankyrin repeat homology <AN08>
 F:300-332/Domain: ankyrin repeat homology <AN09>
 F:333-365/Domain: ankyrin repeat homology <AN10>
 F:366-398/Domain: ankyrin repeat homology <AN11>
 F:399-431/Domain: ankyrin repeat homology <AN12>
 F:432-464/Domain: ankyrin repeat homology <AN13>
 F:465-497/Domain: ankyrin repeat homology <AN14>
 F:498-530/Domain: ankyrin repeat homology <AN15>
 F:531-563/Domain: ankyrin repeat homology <AN16>
 F:564-596/Domain: ankyrin repeat homology <AN17>
 F:597-629/Domain: ankyrin repeat homology <AN18>
 F:630-662/Domain: ankyrin repeat homology <AN19>
 F:663-695/Domain: ankyrin repeat homology <AN20>
 F:696-728/Domain: ankyrin repeat homology <AN21>
 F:729-761/Domain: ankyrin repeat homology <AN22>
 F:762-794/Domain: ankyrin repeat homology <AN23>

Query Match 15.0%; Score 837.5; DB 2; Length 1862;
 Best Local Similarity 29.5%; Pred. No. 1.4e-43;
 Matches 237; Conservative 127; Mismatches 262; Indels 177; Gaps 20;

QY 3 GRKDVVEYLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNWYTP 62
 DB 85 GODEVRELVNNGANNAQSGKFTPLYNAAQENHLEVVVKFLLNGANQNVADEGFTPL 144
 QY 63 HEAAIKGKIDVICVLLQHGAEPTI-----RNTDGRALDLADPSAKAVLTGEYK 113
 DB 145 AVAQOQHENVVAHLINVTGKVRPLPALHIAARNDDTRTA-----AVLLQNDPNP 195
 QY 114 ELLESARGNEEKMMALLTPLNVNCHASGRKS-----TPHLAAGY 155
 DB 196 DVL--SKTG-----FTPLHIAAHYENLVNVAQLLNRGASVNFPPQNGITPLHIA 245
 QY 156 NRVKIVQLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPL 215
 DB 246 GNVMVRLLDLDRGAQIETRTKDELTPHCAARNGHVRISAILLDHGAPIOAKTKNGLSPI 305
 QY 216 HEAAKSRVEVCSLLSYGADPTLLNCHNKSAIDLAPTQPKERLAYEFKGHSLLOAARE 275
 DB 306 HMAAQGDHLDVRLLLQYNAB-----ID----- 328
 QY 276 ADVTRIKKLSLEMVNFKHPQTHETALHCAASPYPRKQICELLRKGANINEKTEFL 335

Db 329 -DIT-----LDHLPVAA-----HGHHRVAKVLLDKGAPNSALNGF 368
Qy 336 TPLHVASEKANDVVEVVKHAKVNALDNLGQTSLHRAAYCGHILQTCRLLLSYGCDPNI 395
Db 369 TPLHTACKNHRVWELLKTKGASIDAVTESGLTPLHVASFHGLPIVKNLLQORGASPNV 428
Qy 396 ISLQGFALOM-----GNENVQQLLEGISLGNSEAD-----RQLLE- 432
Db 429 SNVKVETPLHMAARAGHTEVAKYLLQNKAKANAKAKDDQTPHCAARIGHTGMVKLLLEN 488
Qy 433 -----AAKAGDVETVKLCVQ--SVNCRDIEGRQSTPLHFAAGVNRVS 474
Db 489 GASPNLATTAGHTPLHTAAREGHVDITALALLEKEASQACWTYKG--FTPLHVAAYKVR 546
Qy 475 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVNVADLWK-FTPLHHEA 533
Db 547 LAELLEHDHAPNAAGKNGLTPLHVAVHHNLDIVKLLPRGSPH-SPAWNRYTPLHTA 605
Qy 534 AAKGYEICKLLQHGADPTKQNRDQNTPLDL-VKQDGTDIQDILLRGDAALLDAAKKGCL 592
Db 606 AKQNGIEVARSLLOYGGSANASVQGVTPPLHAAQEGHTEMVALL----- 650
Qy 593 ARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGLIPLHN 652
Db 651 -----LSQANGNLGNKSG--ITPLHLSVQEGHVLVADVLIKGVTVDTATRGYTPLVH 703
Qy 653 AASYGHVDVVAALLIKYNACVNATDKWAFPTPLHHEAAQKGTQICALLAHAGADPTLKNQEG 712
Db 704 ASHYGNILKVLKELLQHQADVNAKTKLGYSPHQAQOQGTDIVTLLKNGASPNESVSG 763
Qy 713 QTPDL-----VSADDVSGALLT 729
Db 764 TPLTAIAKELGYISVTDVLKVV 786

RESULT 12
T13940
Ankyrin - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13940
R:Dubreuil, R.R.; Yu, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
A:Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Drosophila
A:Reference number: Z17820; PMID:95024098; PMID:7937942
A:Accession: T13940
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1549 <DUB>
A:Cross-references: UNIPROT:Q24241; UNIPARC:UPT000007E386; EMBL:L35601; NID:g557083; PIR:13940
C:Genetics:
A:Cross-references: FlyBase:FBgn0011747

Query Match 14.9%; Score 834; DB 2; Length 1549;
Best Local Similarity 27.4%; Pred. No. 1.7e-43;
Matches 298; Conservative 165; Mismatches 470; Indels 154; Gaps 32;

Qy 3 GRKDVVEYLLONGASVOARDGGLIPLHNACSPGAEVNNLLRHGADPNARDNNMYTPL 62
Db 84 GYVDICELLRRGIKIDNATKGNATLHSLAGQHDVINGQLLYNANVQSLNGFTPL 143
Qy 63 HPAALIKGIDVICVLQHGAEPIRNTDGRALDLA-----DPSAKAVLTGEYK----KDE 114
Db 144 YMAAQENHDNCCRTLLANGANPSLSTEDGTPLAVAMQOQHDKIYAVLLENDVRGKVRLP 203
Qy 115 LLESARSGNEEKQMAILLPLNVNCHASDGRKSTPLHAGYNRVKIVQLLQHGADVHAK 174
Db 204 ALHIAAKQNDVNAKLLQHDHPNADIVSGSGFTPLHIAHYGNVDIATLLNNKADNVY 263
Qy 175 DKGDVPLHNACSYGHYEVELLVKHGACVNAMDLWQFTPLHFAASKNRVVEVCSLLISY 234
Db 264 AGNITPLHVACKWGLSLCTLLCRGAKIDATRDGLTPLHCAASRGHVEVIKHLQQN 323

Qy 235 ADPTLLNCHN-KSAIDLAPTOLKERLAYEFKXHSILQARBADVTRI KKHLSLE----- 288
Db 324 A-PILTKYKXGSLAHMAAQE-----HDEAHLHLLDNKAPVDEVTVLYLTALHVAACH 376
Qy 289 -----MVNFK-HPQTHE-----TALHCAAAAPYPRKQICELLURKGANINEKTEFL 335
Db 377 GHVKVAKLLDYKANPNARALNGFTPLHIAACK--NRIMVVELLIKHGANIGATTESGL 433
Qy 336 TPLHVASEKANDVVEVVKHAKVNALDNLGQTSLHRAAYCGHILQTCRLLLSYGCDPNI 395
Db 434 TPLHVASFPGCINIVYLLQHEASADLPTIRGETPLHAAARANOADIIRLLR-SAKVDA 492
Qy 396 ISLQGFAL-----OMGNEN-VQQLLEGISLGNSEAD--QLLEAAKAGDVETVKLCV 448
Db 493 IVREGQTPHVASRLGNINIMLLQHGAEINAQSNKYSAHLIAKEGENIVQVLLLEN 552
Qy 449 QSVNCRDIEGRQSTPLHFAAGYNRVSVEYLLQHGADVHAKDKGGLVPLHNACSYGHYE 508
Db 553 GAEN-NAVTKGFTPLHIAKYGKQNVQILLQNGASIDFQGNQDVTPLHVATHYNNPSI 611
Qy 509 AELLVKGAVNVADLWKFTPLHHEAAKGYEICKLLQHGADPTKQNRDQNTPLDL-VK 567
Db 612 VELLKNGSSPNLCARNGQCAIHIACKNYLETAMQLQHGADVNIISKSGFPLHAAQ 671
Qy 568 DGDGTIDQILLRGDAALLDAAKKGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLE 627
Db 672 GGNVDMVQQLLEGYVISAANKGL-----TPLHVAQAEGHVL 708
Qy 628 VAEYLLQHGADVNAODKGLIPLHNAAASYGHVDVVAALLIKYNACVNATDKWAFPTLH 687
Db 709 VSQILLLEGANISERTNGYTPPLHMAAHYGHLDLVKFFIENDADIEWSSNIGYTPHQA 768
Qy 688 QKQRTQCALLAHAGADPTLKNQEGTPLDVSADDSALLTAAMPSPALPSCYKQVPLN 747
Db 769 QQGHIMIINLLLRKANPNALTQDGNATLHASN-----LGYYTVMESLUKITVSTSVIN 822
Qy 748 G-----VRSPGATADALSSGSPSSLSAAS-----SLDNLSGSFSELSSVVS 790
Db 823 SNIGAIIEKLVKWTPELMQETLLSDDESDCDLLDHNHYKYWATDDLKANYQDQKNFD 882
Qy 791 SSGTE-----GASLEKKEVPGVDFSTQFVRNIGLEHLM--IFEREQITDLVLVEMGHK 844
Db 883 TTNTDHLDTDVSVLNKEILPEMESCIELTE---IGHKPDNVVIARSQVHLGLVSPF--- 936
Qy 845 ELKEIGINAYHRRKLIKGYE-----RLISGOOGLNPYLTNTSGSGTILID 891
Db 937 LVDARGGSMRGYRHNQVRIIVPPKACAEPTITCRYVKPQVRVNPPLMEGEALVSRILE 996
Qy 892 LSPDDKEFOS---VEEEMOSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRK 948
Db 997 MSPVDQMFSLPITLEVPHYGTLRK-----NEREII-ILRSDNGESWREH-NLYK 1043
Qy 949 EVSEENHNHANERMLPHGSPFVNAIHKGDFERHAYIGMGAGIYFAENSSKSNQVYVG 1008
Db 1044 DIIGEDINQTEE---FHSDRIVR-IVTQNVPHFAVV-----SRVRQEVHV 1085
Qy 1009 IG--GGT 1013
Db 1086 IGPDGGT 1092

RESULT 13
T15347
Ankyrin-related unc-44 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15347; T15346; T15345; A57282; B57282; C57282
R:Gottung, S.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid B0350.
A:Reference number: Z18332
A:Accession: T15347

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2039 <GAT>
A:Cross-references: UNIPROT:Q17489; UNIPARC:UPI0000077B65; EMBL:U50071; NID:g1208871; PID:g1208871
A:Accession: T15346
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1000, 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVA
32, 'S', 2034-2035, 'GSPTSRVPEHRHSQHDHGGST' <CA2>
A:Cross-references: UNIPARC:UPI0000077BDB; EMBL:U50071; NID:g1208871; PID:g1208875; PIDN
A:Accession: T15344
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTIVAESTSEQVPE', 1934-1935, 'E
<GA3>
A:Cross-references: UNIPARC:UPI000007878C; EMBL:U50071; NID:g1208871; PID:g1208874; PIDN
A:Accession: T15345
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE
PTRSRVPEHRHSQHDHGGST' <CA4>
A:Cross-references: UNIPARC:UPI000007D1A6; EMBL:U50071; NID:g1208871; PID:g1208876; PIDN
A:Otsuka, A.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpo
J. Cell Biol. 129, 1081-1092, 1995
A>Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Cae
A:Reference number: A57282; MUID:95263663; PMID:7744957
A:Accession: A57282
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-852, 'GGG', 856-1000, 'SKLQHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWE
'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
A:Cross-references: UNIPARC:UPI0000080E35; GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:
A:Accession: B57282
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E
V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'STRSRVPEHRHS', 1984-1985, 'EDHEGS', 1
A:Cross-references: UNIPARC:UPI000017754A; GB:U21731
A:Accession: C57282
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, '
4, 'TIV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESES', 1944, 'REDDGTIVTT', 194
A:Cross-references: UNIPARC:UPI0000076E32; GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:
C:Genetics:
A:Gene: CESP:unc-44
A:Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979
A:Superfamily: ankyrin; ankyrin repeat homology
F:164-192/Domain: ankyrin repeat homology <AN04>
F:358-390/Domain: ankyrin repeat homology <AN1>
F:391-423/Domain: ankyrin repeat homology <AN11>
Query Match 14.6%; Score 814.5; DB 2; Length 2039;
Best Local Similarity 26.1%; Pred. No. 4.4e-42;
Matches 301; Conservative 156; Mismatches 418; Indels 279; Gaps 36;
QY 3 GRKDVVEYLLONGASVQARDGGLIPLHNACSGHAEVNNLLRHGADPNARDNNWTPL 62
DB 77 GHSEVVELIKRQAVDAATRKGNALHTIASLQSLVITLVENGANNVNVQSVNGFTPL 136
QY 63 HEAAIKGKIDVCLVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGCEYKDELLESARG 122
DB 137 YMAQENHEEVKYLKHGNALSTEDGFTPLAVA-----LQOG 176
QY 123 NEEKMMALLTPLNVNCHASDGRKSTP-LHLAAGYNRVKIVQLLQHGADVHAKDGLVP 181
DB 177 HDRVVAVLE-----NDSKGKVRLLPALHIAAKDDTTAATLLQNEHPDVTSGGFTP 230
QY 182 LHNACSYGHEVTELLVKGACVNDMLWQFTPLHEAASKNRVESCLLSLYGADPTLIN 241
DB 231 LHIAAHYGHENVQQLLEKGANVNYQARHNISPLVATKWGRTNMANLLSRGA-----IID 287
QY 242 CHNKSAIDLAPTQLKERLAYEPFKHSLLOQAAREADVTRIKKHLISLEWNVFKHPQTHETA 301

288 SRTKDLL-----TP 296
302 LHCAASAPVKRKOICELLRRKGANINEKTEFLTPLHVASEKAHNDVVVVVKEAKYN 361
297 LHCAARSGH---DQVVDLLVQGAIPISAKTKNGLAPLHWAAGDHVDAARTLLYHRAPVD 353
362 --ALDNLQOTSLHRAAYCGHJQTCRLLSYGCOPNIIISLQGFALOMGNEN-----410
354 DVTVDYL--TPLHVAACHGVKRVAKLLDORSAPNSRALNGFTPLHIAACKNRIKIVVELL 411
411 -----VQOLLQEGIS-----IGNSEADROLLEAAKAGDVETVKLCTVOSVNCRDIE 457
412 LKYRAAIEATTESGLTPLHVAAFMGAINIIVYLQOGANPDVETV-----456
458 GROSPTLHFAAGYNRVSVVYLLQHGADVHAKDGLVPLHNACSYGHEVAELLVKHGA 517
457 -RGFTPLHLAARANOTDVRVLIRNGAKVDAQARELOTPPLHIASRLGNTDVIILLQAGA 515
518 VVNADLWKFTPLHEAAAAGKYEICLLLQHGADPTKKNRDGNTPLDLV-KDGDTDIQL 576
516 NSNATTRDNYSELHIAAKEGQEVAGILLDHADKTLTKGFTPLHLASKYGNLEVVRL 575
577 L--RGDAALLDAKKGCLARVKLSSPDNVNCRDQGRHS--TPLHLAAGYNNLEVAEYLL 633
576 LLERGTVP-----DIEGKNQVTPHVAAHYNNDKVAMLLL 610
634 QHGADVNAODKGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFPLHEAAOKGRTO 693
611 ENGASAKAAKNGYTPHLHIAKKNQMEIATLLQKADPNAKSRAGFTPLHLASAQEGHKE 670
694 LCALLLHAGADPTLNQBGQTPDLVVSADD-----VSALLTAAMPSPALPS 739
671 ISGLLIENGSDVGAKANNGLTAMHLCAQEDHVPVAQILYNNCAEINSKTNAGYTPPLHV-A 729
740 CYKQVQLNGVR---SPGATADALSSGSPSSLSAASSLDNLSGSFSELSVSVSSSGTEG 796
730 CHFGQ-LNNVKPLVENGADVGCEKTRASYTPPLHQAACQGHNCVRYLLE-----NG 778
797 ASSLEKKEVPGVDFSIOTFVRNLG---LEHLMDFPEREQITDLVLVEMGHKELKEIGIN 852
779 ASPNQATATGQTPLSIAQ---RLGVSVVETURTVTITVTITTTTVDERYKQNPPEANW 835
853 -----AYGHRKLI-----KGVERLISSGQGLNPYLTINTSG 884
836 EWFSEDEGAAEHAHAEKDFSDNLTQGLQDSTGVHMTGEOQLQORSQELENG 895
885 -----SGTILIDSPDKFOSVEEMQS-----TVREHRDG--GHAGIFNRYNLIKTO 932
896 AIPKINSQ---GMSF-EKEFAKIPVATSPSIATNSQSFGIAPRAGSISGQFOQPLH 950
933 KYCNKKLWERYTHRRKE--VSEENHNHANERMLFHGS-----PFVNAIHKGF-----DE 980
951 GAGPEDNLEELVRRANQHPINAGNYDNGVAMLENGHADNVPIGHVTPOTPSLISFLVDA 1010
981 RHAYTIGSMFGAGIYPAENSNSKSNQVYVYGIGGTGCPVHKDRSCYICHRQLLCFVRLGKS 1040
1011 RCGAMRGCHSVRIIVPRASQ-----PIR-----VTCRY-LRKD 1046
1041 FLQFSAMKVAHSP 1054
1047 -----KLAHPPP 1053

RESULT 14

T42691
hypothetical protein DKFp434D2328.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
R:Accession: T42691
R:Biocheck, H.; Boscher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A:Reference number: Z22230

A:Accession: T42691
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-791 <AAA>
A:Cross-references: UNIPROT:Q9UFA4; UNIPARC:UPI000006DC92; EMBL:AL133087
A:Experimental source: adult testis; clone DKFZp434D2328
C:Genetics:
A:Note: DKFZp434D2328.1

Query Match		11.2%;	Score 628;	DB 2;	Length 791;
Best Local Similarity		27.7%;	Pred. No. 4.3e-31;		
Matches 232;		Conservative 119;	Mismatches 313;	Indels 174;	Gaps 28;
QY	3	GRKDVVEYLQNGASVQARDGGLIPLHNACSFHAEVNVLLRHGADPNARDNNYTP	62		
DB	14	GOINVGKLLNLGVDEINVGNTALHIACVNGQDAVVELIDYGANVPQNNNGFTPL	73		
QY	63	HEAAIKGKIDVCI-VLLOHGABPTIRNTDGRALDLADPSAKAVLTGEYKDELL----	116		
DB	74	HFAAATHGALCLELVNNGADVNTQSKDGKSPHM-----TAVHGRTRSQTLIQNGG	127		
QY	117	-----SSARGNEKEMWALT-----PIN-----VNCHA-----	140		
DB	128	EIDCVDKDGNTEPLHVAARYGHELLINTLITSGADTAKCGIHSMFPLHAAALNAHSDCCRK	187		
QY	141	--SDGRK-----STP-----LHLAAGYNRVKIVOLLQHGADVH	172		
DB	198	LLSSGQKYSIVSLFNEHVSLSAFBIDTPDKFGRITCLHAAAAGGVNVECIKLQSSGADPH	247		
QY	173	AKDGDVPLHNACSYGHVEVELLVKHGACVNMALMQFTPLHAAASKNRVEVCSSLIS	232		
DB	248	KDKCGRTPLHYAANCHFHCIETIVTGANVNETDDMGRTALHYAASD-----	297		
QY	233	YGADPTLL-NCHNKSAIDLAPTPOLKER---LAYEFKGHSLLLQAAREADVTRIKKLSLE	288		
DB	298	MDRNKNTILGNAHDNSE-ELERARELKEKATCLCF-----LLQ-----	335		
QY	289	MVNFKHQPTHE-----TALHCAAASYPYKQKQICELLKRGANINKEKFTLT--PLHVAS	342		
DB	336	--NDANPSIRDKEGYNSIHYAAAYGH---RQCLELLELRTNSGFESDGAATKSPHLHAA	390		
QY	343	EKAHNDVVEVVKHEAKVNALDNLGQTSIHRAAAYCGHLQTCRLLSYCDPNIISIQGT	402		
DB	391	YNGHQALEVLLQSLVDIDIRDEKGRDALDLAFAFGHTECEVALIN-----QGAS	440		
QY	403	ALQMGNNVQQLQBGISLNSSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRST	462		
DB	441	IFVKDNTKRTPLHASVINGHTLCRLLEIAD-----NPEADVVKDAQGQ--T	487		
QY	463	PLHFAAGYNRVSVVEYLLQHGADVHAKKGLVPLHNACSYGHEVAELLVKHGAVNVA	522		
DB	488	FLMLAVAYGHDIAVSLLEKEANVDVTDILGCTALHRTGIMTGHCEVCQMLLEQEVSI	547		
QY	523	DLWKFTPLHAAAAGKYBEICKLLQLHG--ADPTKKNRDNTPLO--LVKDGDTDIQDL	577		
DB	548	DSRGRTPLHYAARGHATWSELLOWALSEEDCCFDNQGYTPLHWACVNGNENCIEVLL	607		
QY	578	R-----GD-----AALLDAAKKGCLARVKKLSPPDNVNCRDTOGRHSTPLHLAAG	622		
DB	608	EOKCFRKFIGNPFTPLHCAIINDHG--NCASLLILGAIIDSSIIVSCRDDKGR--TPLHAAAF	663		
QY	623	YNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLI-KYNAVCNATDKWAPT	681		
DB	664	ADHVECLQLLRHSAPVNAVDSNGKTALMMAAENGQAGADVILVNSAQADLTIVKDKLNT	723		
QY	682	PLHBAAGKRTQLCALLAHGADPTL--KNQEGOTPLDLVSADDSALLTAAMPSSA	736		
DB	724	PLHLACSGHEKCALLIDKIQDBESLINEKNALQTPLHYAARNGLKVVVEELLAKGA	781		

RESULT 15
S30355
alpha-latroinsectotoxin precursor - black widow spider (fragment)

C:Species: Latrodectus mactans tredecimguttatus (black widow spider)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: S30355; S29864
R:Kiyatkin, N.; Dulubova, I.; Grishin, E.
Eur. J. Biochem. 213, 121-127, 1993
A:Title: Cloning and structural analysis of alpha-latroinsectotoxin cDNA. Abundance of ar
A:Reference number: S30355; MUID:93238678; PMID:8477689
A:Accession: S30355
A:Molecule type: mRNA
A:Residues: 1-1411 <KIY>
A:Cross-references: UNIPROT:Q02989; UNIPARC:UPI000007A3C2; EMBL:Z14086; NID:G9536; PIDN:(
A:Note: it is uncertain whether Met-26 is the initiator or whether translation is initial
C:Keywords: presynaptic neurotoxin
F:533-565/Domain: ankyrin repeat homology <AN1>
F:1001-1032/Domain: ankyrin repeat homology <AN2>
F:1146-1178/Domain: ankyrin repeat homology <AN3>

Query Match		9.8%;	Score 545.5;	DB 2;	Length 1411;
Best Local Similarity		23.7%;	Pred. No. 1.5e-25;		
Matches 239;		Conservative 136;	Mismatches 378;	Indels 257;	Gaps 33;
QY	11	LLQNGASVQARDGGLIPLHNACSFHAEVNVLLR-----HGADPNARDNNYTPLHE	64		
DB	486	LQNGANVSETELGRAIHAASAGNYDVGELLNKDINLEKADKN-----GYTELHI	540		
QY	65	AAIKGKIDVICIVLLQHGABPTIRNTDGRALDLADPSAKAVLTGEYKDELLSARSNE	124		
DB	541	AADSNKDNFVFLIGNADV-----RTKSDLFTP-----LHLAARDLT	581		
QY	125	EKMWALLTEPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGLVPLHN	184		
DB	582	DVTQTLIDITEIDLNAQDKSGFTPLHLSISSTSETAAILIRNTNAVNIKSKVGLTPEHL	641		
QY	185	ACSYGHEYTELLVKHGACVNMALMQFTPLHAAASKNRVEVCSSLISYGADPTLLCHN	244		
DB	642	ATLQNNLSVSKLAGGAYLNDGDANGMTPLHYAAMTGNLEWVDFLL-----N	689		
QY	245	KSALDIAPTPQKBE-----RLAYEFKGHSLQ-----	271		
DB	690	QQYININATKEKWTPLHLAILFKNDVAERLLSDENLIRLETNGGINPLHLASATGN	749		
QY	272	-----AAREADVTRI-KKHLSELMVNFKPHQTHETALHCAAASPYPKKQICELLRK	323		
DB	750	KQLVTELLAKNADVTRLTSGFS-----ALHLGIIG---KNEEIPFFFLVEK	792		
QY	324	GANINKEKTEFTPLHVASEKARNDDVVEVVVHAEKVNALDNLGQTSLHRAAYCGHLQTC	383		
DB	793	GAVNDKINSVTPPLHFAAGLCKANIFRLLSRGADIKAEDINSQMPIHEAVSNGHLEIV	852		
QY	384	RLLSYCGDPNIISIQGFTALQNGNENVOQLQOE-GISLNSSEADRLLEAAKAGDVETV	442		
DB	853	RILIEK--DPSLM-----NVKNIRNEYPFYLAVERKYKIDIFYFVSKD----	893		
QY	443	KKLCTVQSVNCRDIEGRSTPLHFAAGYNRVSVVEYLLQHGADVHAKD-----	490		
DB	894	-----ANNVEVDHNGNTLLHLSSTGELEVVFQMONGANFRLLKNRERKTFDILAIE	945		
QY	491	-----KGLVPLHNACSYGHEVAELLVKHGAVNVDLWKFT	528		
DB	946	NGRLNIVAFVEKKNVNLQAAHRGKTILYHAICDSAKYDKIEIVKYFIEKLNESEC--N	1002		
QY	529	PLHAAAAGKYBEICKLLQ-HGADPTKKNRDGN--TPLDLVKOG-----DTIQDLRG	579		
DB	1003	PLHAAAHAHLDLVKYFVQERGINFAEFNEENQASPFCTIHGAPCGYSIDCDTPDRLEV	1062		
QY	580	DAALDAAKKGCLARVKKLSSP-DNVNCRDTOGRHSTPLHLAGYNVLEVAEYLLQHGAD	638		
DB	1063	VEYLS-----KIPDINGKC-DVQ--ENTPITVAIFANKVSLNVLVIGAD	1106		
QY	639	VNAQDKGGLIPLHNAASYGHVDVAALLIK-YNACVNATDKWAPTPLHAAKGRTOCAL	697		
DB	1107	PNQVQDGD--PPLVIAARQGRFEIVRCLIEVHKVDINTRNKERTALHAAARNDFMDVVKY	1165		

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:21:50 ; Search time 213 Seconds
(without alignments)
4625.078 Million cell updates/sec

Title: US-10-616-101-3
Perfect score: 5585
Sequence: 1 GGRKDVVEYLQNGASVQA.....AMKMAHSPGHHSVTGRPSV 1065

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt.7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5582	99.9	1166	1 TNKS2_HUMAN	Q9h2k2 homo sapien
2	5350	95.8	1167	2 Q800E0 CHICK	Q800e0 gallus gall
3	4742.5	84.9	1320	2 Q8PFX2 MOUSE	Q6pfx9 mus musculu
4	4740.5	84.9	1327	1 TNKS1_HUMAN	Q95271 homo sapien
5	4732.5	84.7	1327	2 Q4G0F2 HUMAN	Q4g0f2 homo sapien
6	4730.5	84.7	1266	2 Q800D9 CHICK	Q800d9 gallus gall
7	4674.5	83.7	1303	2 Q5XGK5 XENLA	Q5xgk5 xenopus lae
8	4631.5	82.9	1212	2 Q4RG97 TETNG	Q4rg97 tetradon n
9	4532.5	81.2	1055	2 Q59FX0_HUMAN	Q59fx0 homo sapien
10	4136.5	74.1	976	2 Q8BX62 MOUSE	Q8bx62 mus musculu
11	3849	68.9	1168	2 Q7PYH8 ANOGA	Q7pyh8 anopheles g
12	3706.5	66.4	1181	2 Q9VBP3 DROME	Q9vbp3 drosophila
13	3706.5	66.4	1181	2 Q9XZ37 DROME	Q9xz37 drosophila
14	3179	56.9	1047	2 Q4S372 TETNG	Q4s372 tetradon n
15	2833	50.7	589	2 Q3UES3 MOUSE	Q3ues3 m adult mal
16	2731	48.9	601	2 Q8BXH7 MOUSE	Q8bxh7 mus musculu
17	1883	33.7	408	2 Q6P537 MOUSE	Q6p537 mus musculu
18	1795.5	32.1	471	2 Q4FZM0 XENLA	Q4fzm0 xenopus lae
19	886	15.9	1806	2 Q574D8 RAT	Q574d8 rattus norv
20	886	15.9	1984	2 Q574D7 RAT	Q574d7 rattus norv
21	877.5	15.7	1765	2 Q4U258 MOUSE	Q4u258 mus musculu
22	877.5	15.7	1961	2 Q4U256 MOUSE	Q4u256 mus musculu
23	876.5	15.7	1861	2 Q7Z3G4 HUMAN	Q7z3g4 homo sapien
24	875.5	15.7	1726	2 Q8VC68 MOUSE	Q8vc68 mus musculu
25	875.5	15.7	4377	1 ANK3_HUMAN	Q12955 homo sapien
26	873.5	15.6	1861	2 Q5CZH9 HUMAN	Q5czh9 homo sapien
27	873.5	15.6	1943	2 Q4U259 MOUSE	Q4u259 mus musculu
28	871.5	15.6	1940	2 Q4U257 MOUSE	Q4u257 mus musculu
29	867.5	15.5	1136	2 Q9N180 BOVIN	Q9n180 bos taurus
30	865	15.5	4372	2 Q5VXD5 HUMAN	Q5vxd5 homo sapien
31	864.5	15.5	2622	2 Q70511_RAT	Q70511 rattus norv

RESULT 1

ID	TNKS2_HUMAN	STANDARD;	PRT;	1166 AA.
AC	Q9H2K2; Q9H8P2; Q9HAS4;			
DT	27-MAR-2002, integrated into UniProtKB/Swiss-Prot.			
DT	01-MAR-2001, sequence version 1.			
DT	07-MAR-2006, entry version 41.			
DE	Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1-interacting ankyrin-related ADP-ribose polymerase 2) (Tankyrase-like protein) (Tankyrase-related protein2).			
DE	protein) (Tankyrase-related protein2).			
GN	Name=TNKS2; Synonyms=PARP5B, TANK2, TNKL;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Fetal brain;			
RX	MEDLINE=21072550; PubMed=11205898;			
RA	Monz D., Munia A., Contesse N., Fischer U., Steudel W.-I., Feiden W.,			
RA	Glass B., Meese E.U.;			
RT	"Novel tankyrase-related gene detected with meningioma-specific sera.";			
RL	Clin. Cancer Res. 7:113-119(2001).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Mammary carcinoma;			
RX	MEDLINE=21190090; PubMed=11294570; DOI=10.1038/sj.gene.6363722;			
RA	Kuimov A.N., Kuprash D.V., Petrov V.N., Vdovichenko K.K.,			
RA	Scanlan M.J., Jongeneel C.V., Lagarkova M.A., Nedospasov S.A.;			
RT	"Cloning and characterization of TNKL, a member of tankyrase gene family.";			
RT	Genes Immun. 2:52-55(2001).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.			
RC	TISSUE=Liver;			
RX	MEDLINE=21264473; PubMed=11278563; DOI=10.1074/jbc.M009756200;			
RA	Lyons R.J., Deane R., Lynch D.K., Ye Z.-S.J., Sanderson G.M.,			
RA	Eyre H.J., Sutherland G.R., Daly R.J.;			
RT	"Identification of a novel human tankyrase through its interaction with the adaptor protein Grb14.";			
RL	J. Biol. Chem. 276:17172-17180(2001).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.			
RC	TISSUE=Placenta;			
RX	MEDLINE=21443728; PubMed=11454873; DOI=10.1074/jbc.M105968200;			
RA	Kaminker P.G., Kim S.-H., Taylor R.D., Zebardjian Y., Funk W.D.,			
RA	Morin G.B., Yaswen P., Campisi J.;			
RT	"TANK2, a new TRF1-associated poly(ADP-ribose) polymerase, causes rapid induction of cell death upon overexpression.";			
RL	J. Biol. Chem. 276:35891-35899(2001).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE, FUNCTION, AND INTERACTIONS WITH TRF1 AND			

RP LNPEP/OTASE.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=1216613461; PubMed=11802774; DOI=10.1042/0264-6021:3610451;
 RA SbioD J.I., Lodish H.F., Chi N.-W.;
 RT "Tankyrase-2 oligomerizes with tankyrase-1 and binds to both TRF1
 RT (telomere-repeat-binding factor 1) and IRAP (insulin-responsive
 RT aminopeptidase).";
 RL Biochem. J. 361:451-459 (2002).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA Yin Y., Gelmann E.P.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15164054; DOI=10.1038/nature02462;
 RA Deloukas P., Earthrowl M.E., Grafham D.V., Rubinfeld M., French L.,
 RA Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
 RA Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
 RA Taylor A., Battles J., Bird C.P., Ainscough R., Almeida J.P.,
 RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Baggeley C.L., Bailey J.,
 RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
 RA Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,
 RA Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
 RA Corby N., Coulson A., Dhani P., Dutta I., Dunn M., Faulkner L.,
 RA Frankish A., Frankland J.A., Garner P., Garnett J., Gribble S.,
 RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.B.,
 RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
 RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
 RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,
 RA Lee H.M., Leongamert D.A., Laird G., Lloyd C., Lloyd D.M.,
 RA Loveland J., Lovell J., McLaren S., McIay K.E., McMurray A.,
 RA Mashregi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
 RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,
 RA Pellan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
 RA Sarafidou T., Sehra H.K., Shownkeen R., Skuce C.D., Smith M.,
 RA Stranding L., Sycamore N., Tester J., Thorpe A., Torcaso W.,
 RA Tracey A., Tromans A., Toolas J., Wall M., Walsh J., Wang H.,
 RA Weinstein K., West A.P., Willey D.L., Whitehead S.J., Wilming L.,
 RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
 RA Siebert R., Fichtel K., Bentley D., Durbin R., Hubbard T.,
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 10.";
 RL Nature 429:375-381 (2004).
 RN [8]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 838-1151.
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Inose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RL cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 RN [9]
 RP FUNCTION, AND ADP-RIBOSYLATION.
 RX MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002;
 RA Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
 RT "Role for the related poly(ADP-ribose) polymerases tankyrase 1 and 2
 RT at human telomeres.";
 RL Mol. Cell. Biol. 22:332-342 (2002).
 CC 1- FUNCTION: May regulate vesicle trafficking and modulate the
 CC subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP
 CC activity and can modify TRF1, and thereby contribute to the
 CC regulation of telomere length.
 CC 2- CATALYTIC ACTIVITY: NAD(+) + (ADP-D-riboseyl)(n)-acceptor =
 CC nicotinamide + (ADP-D-riboseyl)(n+1)-acceptor.
 CC 3- SUBUNIT: Oligomerizes and associates with TNKS. Interacts with the
 CC cytoplasmic domain of LNPEP/Otase in SLC2A4/GLUT4-vesicles. Binds
 CC to the N-terminus of Grb14 and TRF1 with its ankyrin repeat
 CC region.
 CC 4- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and
 CC with juxtanuclear SLC2A4/GLUT4-vesicles. Also found around the
 CC pericentriolar matrix of mitotic centrosomes. During interphase, a
 CC small fraction of TNKS2 is found in the nucleus, associated with
 CC TRF1.
 CC 5- TISSUE SPECIFICITY: Highly expressed in placenta, skeletal muscle,
 CC liver, brain, kidney, heart, thymus, spinal cord, lung, peripheral
 CC blood leukocytes, pancreas, lymph nodes, spleen, prostate, testis,
 CC ovary, small intestine, colon, mammary gland, breast and breast
 CC carcinoma, and in common-type meningioma. Highly expressed in
 CC fetal liver, heart and brain.
 CC 6- PTM: ADP-ribosylated (-auto).
 CC 7- SIMILARITY: Contains 15 ANK repeats.
 CC 8- SIMILARITY: Contains 1 PARP catalytic domain.
 CC 9- SIMILARITY: Contains 1 SAM (sterile alpha motif) domain.
 CC 10- SIMILARITY: Contains 1 SAM (sterile alpha motif) domain.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC -----
 CC EMBL: AF305081; AAG25674.1; ALT_INIT; mRNA.
 CC EMBL: AF264912; AAG44694.1; -; mRNA.
 CC EMBL: AF229636; AAK13463.1; -; mRNA.
 CC EMBL: AF342982; AAK25811.1; -; mRNA.
 CC EMBL: AF309033; AAK82330.1; -; mRNA.
 CC EMBL: AF438201; AAL40795.1; -; mRNA.
 CC EMBL: AL359707; CAC78760.1; -; Genomic DNA.
 CC HSSP: P16157; IN11.
 CC EMBL: AK023746; BAB14665.1; ALT_INIT; mRNA.
 CC HSSP: P16157; IN11.
 CC Ensembl: ENSG00000107854; Homo sapiens.
 CC HGNC: HGNC:15677; TNKS2.
 CC MIM: 607128; gene.
 CC InterPro: IPR001290; PARP.
 CC InterPro: IPR012317; PARP_catalytic.
 CC InterPro: IPR011660; SAM.
 CC InterPro: IPR011510; SAM_2.
 CC Pfam: PF00023; Ank; 17.
 CC Pfam: PF00644; PARP; 1.
 CC Pfam: PF07647; SAM_2; 1.
 CC SMART: SM00248; ANK; 15.
 CC SMART: SM00454; SAM; 1.
 CC PROSITE: PS0297; ANK_REPEAT; 1.
 CC PROSITE: PS0088; ANK_REPEAT; 15.
 CC PROSITE: PS1059; PARP_CATALYTIC; 1.
 CC PROSITE: PS10105; SAM_DOMAIN; 1.
 CC ADP-ribosylation; ANK repeat; Chromosomal protein;
 CC Glycosyltransferase; Golgi stack; NAD; Nuclear protein; Repeat;
 CC Telomere; transferase.
 CC CHAIN 1 1166 Tankyrase 2.
 CC REPEAT 57 89 /FTid=PRO_0000211334.
 CC REPEAT 90 122 ANK 1.
 CC REPEAT ANK 1.

248 PLHNACSYGHVEYTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCISLLSYGADPTLL 307
241 NCHNKSADLAPTOLKERLAYEFKGHSLLOAREADVTTRIKKHISLEWNPVKHPQTHET 300
308 NCHNKSADLAPTOLKERLAYEFKGHSLLOAREADVTTRIKKHISLEWNPVKHPQTHET 367
301 ALHCAAAAPYKPKKQICELLIRKGANINEKTEFLTPLVHASEKAHNDVVEVVVKEAKV 360
368 ALHCAAAAPYKPKKQICELLIRKGANINEKTEFLTPLVHASEKAHNDVVEVVVKEAKV 427
361 NALDNLGOTSLEHRAAYCCHLOTICRLLSYGCDPNIIISLQGFALOMGNENVOQLQEGIS 420
428 NALDNLGOTSLEHRAAYCCHLOTICRLLSYGCDPNIIISLQGFALOMGNENVOQLQEGIP 487
421 LGNSEADQLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
488 LGNSDADRQLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 547
481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGVNVDLWKFTPLHEAAAKGKYE 540
548 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGVNVDLWKFTPLHEAAAKGKYE 607
541 ICKLLQHGADPTKKNRDGNTPLDVLKDGDDTDIQLLRGDAALLDAAKKGCLARVKLLSS 600
608 ICKLLQHGADPTKKNRDGNTPLDVLKDGDDTDIQLLRGDAALLDAAKKGCLARVKLLSS 667
601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
668 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 727
661 VNAALLKYNACVNAQDKGLIPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 720
728 VNAALLKYNACVNAQDKGLIPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 787
721 ADDVSALLTAAMPSPALPSCYPQVNLVGRSPGATADALSSGPPSPSLSAASSLDNLSSG 780
788 ADDVSALLTAAMPSPALPSCYPQVNLVGRSPGATADALSSGPPSPSLSAASSLDNLSSG 847
781 SFSELSVSSVSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHMLDIFEREQITLDVLVE 840
848 SFSELSVSSVSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHMLDIFEREQITLDVLVE 907
841 MGHKELKEIGINAYGHRHKLKGVVERLSGQOGLNPYLTLNTSSGTTLLDLSDDKEQF 900
908 MGHKELKEIGINAYGHRHKLKGVVERLSGQOGLNPYLTLNTSSGTTLLDLSDDKEQF 967
901 SVEEEMQSTVREHROGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNANE 960
968 SVEEEMQSTVREHROGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNANE 1027
961 RMLFHGSPFVNAIHHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGTCGCPVHKD 1020
1028 RMLFHGSPFVNAIHHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGTCGCPVHKD 1087
1021 RSCYICHRQLLECRVTGLKSFLOFSAMKVAHSPGHSHSVTGRPSV 1065
1088 RSCYICHRQLLECRVTGLKSFLOFSAMKVAHSPGHSHSVTGRPSV 1132

RESULT 3
Q6PFX9 MOUSE PRELIMINARY; PRT; 1320 AA.
AC Q6PFX9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE Tks protein.
GN Name=Tks;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

Query Match 84.9%; Score 4742.5; DB 2; Length 1320;
Best Local Similarity 82.7%; Pred. No. 1e-271;
Matches 882; Conservative 98; Mismatches 78; Indels 9; Gaps 2;
QY 1 GFGRKDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNVLLLRHGDAPNARDNNYIT 60
DB 218 GFGRKDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNVLLLRHGDAPNARDNNYIT 277
QY 61 PLHEAAIKGKIDVCIVLLOHGAEPITRTDGRALDADPSAKAVLTGEYKDDLELSAR 120
DB 278 PLHEAAIKGKIDVCIVLLOHGAEPITRTDGRALDADPSAKAVLTGEYKDDLELSAR 337
QY 121 SGNEEKVALLTFLPNVNVCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 180
DB 338 SGNEEKVALLTFLPNVNVCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 397

[1] NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2] NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

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EMBL; BC057370; AAH57370.1; -; mRNA.
HSSP; Q00420; 1ANC.
Ensembl; ENSMUSG00000031529; Mus musculus.
MGI; MGI:1341087; Tks.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003950; P:NAD+ ADP-ribosyltransferase activity; IEA.
GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
InterPro; IPR002110; ANK.
InterPro; IPR001290; PARP.
InterPro; IPR012317; PARP_catalytic.
InterPro; IPR001660; SAM.
InterPro; IPR011510; SAM_2.
Pfam; PF00023; Ank; 19.
Pfam; PF07647; SAM 2; 1.
PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 15.
SMART; SM00454; SAM; 1.
PROSITE; PS00297; ANK_REPEAT; 1.
PROSITE; PS00088; ANK_REPEAT; 15.
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PROSITE; PS01059; PARP_CATALYTIC; 1.
ANK repeat; Repeat.
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DR HSSP; P16157; IN11.
DR Ensemble; ENSG00000173273; Homo sapiens.
DR HGNC; HGNC:11941; TNKS.
DR MIM; 603303; Gene.
DR GO; GO:0000783; C:chromosome, telomeric region; IDA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IDA.
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DR GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM_2.
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DR Pfam; PF00023; ANK; 19.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM 2; 1.
DR SMART; SM00248; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS02997; ANK_REPEAT; 1.
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DR PROSITE; PS1059; PARP_CATALYTIC; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ADP-ribosylation; Alternative splicing; ANK repeat;
KW Chromosomal protein; Glycosyltransferase; Golgi stack; NAD;
KW Nuclear protein; Phosphorylation; Repeat; Telomere; Transferase.
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FT REPEAT 215 247
FT REPEAT 248 280
FT REPEAT 281 313
FT REPEAT 368 400
FT REPEAT 401 433
FT REPEAT 434 466
FT REPEAT 521 556
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FT REPEAT 683 715
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FT DOMAIN 1030 1089
FT DOMAIN 1112 1317
FT COMPBIAS 9 14
FT COMPBIAS 27 34
FT COMPBIAS 128 134
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FT MUTAGEN 1184 1184
FT MUTAGEN 1291 1291
SQ SEQUENCE 1327 AA; 142011 MW; E14DE985C710B957 CRC64;
Query Match 84.9%; Score 4740.5; DB 1; Length 1327;
Best Local Similarity 82.7%; Pred. No. 1.3e-271;
Matches 882; Conservative 97; Mismatches 79; Indels 9; Gaps 2;
QY 1 GFGKDDVVEYLLQNGASVQARDGGIPLHNACSFHAEVYNLLLRHGDAPNARDNNYNT 60
DB 225 GFGKDDVVEYLLQNGANVHARDGGIPLHNACSFHAEVSVLLCCGADPNARDNNYNT 284
QY 61 PLHEAAIKGKIDVICVLLQHGABPTTRNTDGTALDADPSAKAVLTGEYKDELLESAR 120
DB 285 PLHEAAIKGKIDVICVLLQHGADPNTRTDGKSALDADPSAKAVLTGEYKDELLEAAR 344
QY 121 SGNEEKWALLTPLNPNVCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDKGDLV 180

DB 345 SGNEEKWALLTPLNPNVCHASDGRKSTPLHLAAGYNRVIRIVOLLQHGADVHAKDKGGLV 404
QY 181 PLHNACSYGHEVTELLVHGACVNMADLWQFTPLHEAASKNRVEVCSSLSSVGADFTLL 240
DB 405 PLHNACSYGHEVTELLVHGACVNMADLWQFTPLHEAASKNRVEVCSSLSSVGADFTLV 464
QY 241 NCHNKSALDAPTPOLKERLAYEFKCHSLQQAAREADVTRI KKHLSLEMYNFKHPQTHET 300
DB 465 NCHGKSAVDMAPTPELRELTTFYFKHSLQQAAREADLAKVKTLALUEIINFQPOSHET 524
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DB 525 ALHCAVASLHPKEKQVTELLLRKANVNEKDFMTPLHVAERAHNDVVELHKGAKM 584
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DB 585 NALDNLGQTSALHRAALAGHLQTCRLLLSYGSDPSIISLOGFTAAOMGNEAVQOILSESTP 644
QY 421 LGNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHPAAGYNRVSVVEYLL 480
DB 645 IRTSDVDYRLLEASKAGDLLETVKQLCSSQNVNCRDLEGRHSTPLHPAAGYNRVSVVEYLL 704
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QY 601 PDNVNCRDITQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
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DB 885 IAALLIKYNTCVNATDKWFTPLHEAAAKGRTQCALLLAHAGADPTMKNOEGQTFPLDLAT 944
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DB 945 ADDIRALLIDAMPPEALPTCFKPOAT-----VVSASLISPASITFSCLSAASIDNLTG 997
QY 781 SFSELSSVSSSGTEGASSLEKK--EVPVGDFRITQFVRNLGLEHMDIFEREQITLDVL 838
DB 998 PLAEAVGASNAGDGAAGTERKEGEVAGLDWMISQPLKSLGLEHLRDI FETEQITLDVL 1057
QY 839 VENGHKEKEIGINAYGHRHKLKIGVERLISGQGLNPYLTNTSGSTILIDLSPDDKE 898
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QY 899 FQSVESQMSTVREHRDGGHAGGIFNRYNLLKTKQVCNKKLWERYTHRRYKVESENHHA 958
DB 1118 YQSVESQMSTIREHRDGGNAGGIFNRYNRIQKVNNKKLREFFCHROKVESENNHHH 1177
QY 959 NERMLFHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSCKSNQVYVGGTGGCPVH 1018
DB 1178 NERMLFHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSCKSNQVYVGGTGGCPH 1237
QY 1019 KORSICYCHROLQLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1065
DB 1238 KORSICYCHROLFCRVTLGKSFLOFSAMKMAHAPGHHSVIGRPSV 1284
RESULT 5
Q4G0F2 HUMAN
ID Q4G0F2.HUMAN PRELIMINARY; PRT; 1327 AA.
AC Q4G0F2_
DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 30-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase.
GN Name=TNKS;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
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 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin J.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.

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CC -----
 CC EMBL; BC098394; AAH98394.1; -; mRNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR012317; PARP_catalytic.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00023; Ank; 18.
 DR Pfam; PF00644; PARP; 1.
 DR Pfam; PF07647; SAM 2; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 15.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 15.
 DR PROSITE; PS51059; PARP_CATALYTIC; 1.
 DR PROSITE; PS51059; SAM_DOMAIN; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 1327 AA; 141980 MW; 21A9309DF979CA21 CRC64;

Query Match 84.7%; Score 4732.5; DB 2; Length 1327;
 Best Local Similarity 82.6%; Pred. No. 46-271;
 Matches 881; Conservative 97; Mismatches 80; Indels 9; Gaps 2;

QY 1 GFRKDVVEYLLQNGASVQARDGGGLPLHNACSGHAEVNVLLRHGADPNARDNNYTT 60
 DB 225 GFRKDVVEYLLQNGASVQARDGGGLPLHNACSGHAEVNVLLRHGADPNARDNNYTT 284
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 DB 285 PLHEAAIKGKIDVCIVLLQHGADPNIRNTDGSALDLADPSAKAVLTGEYKKDELLEAR 344
 QY 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDGLV 180
 DB 345 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDGLV 404

QY 181 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
 DB 405 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLSYGADPTLV 464
 QY 241 NCHNKAIDLAAPTOLKERLAYEPKSHSLQAAREADVTRIKCHLSLEWVNFKPHQTHET 300
 DB 465 NCHGKSAVDMAPTPELRERLTPEFKSHSLQAAREADLAKVKTKLTALBTIINFKQPSHET 524
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 DB 525 ALHCAVASLHPRKQIVTELLIRKGANVNEKNKQFTPLHVAARAHNDVMEVLHKGAKM 584
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 DB 595 NALDTLGTALHRAALAGHLTCRLLLSYSGDSPISIIISQGFATQAQMGNEAVQQLISESTP 644
 QY 421 LGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVVEYLL 480
 DB 645 IRTSDVDYRLLEASKAGDLETVKLCSSQNVNCRDLEGRHSTPLHFAAGYNNRVSVVEYLL 704
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 DB 765 ICKLLQHGADPTKKNRDGNTPLDLVKEGDDTDIODLLRGDAALLDAAKKGCLARVKLCT 824
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 DB 825 PENINCRDPTQGRNSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGGGLPLHNAASYGHVD 884
 QY 661 VAALLIKYCNVATDKWAFPLHEAAKQGTQICALLLAHGADPTLKNQSGQTPDLVLS 720
 DB 885 IAALLIKYCNVATDKWAFPLHEAAKQGTQICALLLAHGADPTLKNQSGQTPDLAT 944
 QY 721 ADDVSALLTAAMPSPALPCYKPOVLNGLVRSFGATADALSSGSPSSLSAASSLDNLSSG 780
 DB 945 ADDTRALLIDAMPPEALTCTCKPOAT-----VVSASLISPASTPSCLSAASSIDNLTG 997
 QY 781 SFSBELSVVSSSGTEGASSLEKK--EVPGVDFSITQFVRNLGLEHLMDFEREQITLDVL 838
 DB 998 PLAGLAVGSGASNAGDGAAGTERKEGEVAGLDWNIISQPLKSLGLEHLRDFIETEQTLDVL 1057
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 DB 1238 KDRSCYICHRQLLFCRVTLGKSFLOPSAMKVAHSPGHHSVTGRPSV 1284
 RESULT 6
 Q800D9 CHICK PRELIMINARY; PRT; 1266 AA.
 AC Q800D9;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 14.
 DE Tankyrase 1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.

OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BJ20021450;
RA De Rycker M., Venkatesan R.N., Wei C., Price C.M.;
RT "Vertebrate tankyrase domain structure and sterile alpha motif (SAM)-
RL mediated multimerization";
RL Biochem. J. 372:87-96(2003).
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CC -----
DR EMBL; AY142108; AAN41651.1; -; mRNA.
DR HSSP; P16157; IN11.
DR Ensembl; ENSGALG00000011438; Gallus gallus.
DR DR; GO:0005634; C:nucleus; IEA.
DR DR; GO:0003950; P:NAD+ ADP-ribosyltransferase activity; IEA.
DR DR; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR DR; InterPro; IPR002110; ANK.
DR DR; InterPro; IPR001290; PARP.
DR DR; InterPro; IPR012317; PARP_catalytic.
DR DR; InterPro; IPR001660; SAM.
DR DR; InterPro; IPR011510; SAM_2.
DR DR; Pfam; PF00023; ANK; 19.
DR DR; Pfam; PF0644; PARP; 1.
DR DR; Pfam; PF07647; SAM_2; 1.
DR DR; PRINTS; PR01415; ANKYRIN.
DR DR; SMART; SM00248; ANK; 15.
DR DR; SMART; SM00454; SAM; 1.
DR DR; PROSITE; PS0297; ANK_REPEAT; 1.
DR DR; PROSITE; PS0088; ANK_REPEAT; 15.
DR DR; PROSITE; PS1059; PARP_CATALYTIC; 1.
DR DR; PROSITE; PS0105; SAM_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1266 AA; 136212 MW; 14B8617BF930E6E0 CRC64;

Query Match 84.7%; Score 4730.5; DB 2; Length 1266;
Best Local Similarity 82.6%; Pred. No. 4.8e-271;
Matches 881; Conservative 97; Mismatches 80; Indels 9; Gaps 2;

QY 1 GFGKRDVVEYLLQNGASVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARDNNWYT 60
DB 164 GFGKRDVVEYLLQNGASVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARDNNWYT 223
QY 61 PLHEAAIKGIDVCIVLQHGAEPIRNTDGTALDADPSAKAVLTGEEKDLEESAR 120
DB 224 PLHEAAIKGIDVCIVLQHGADPNIRNTDGSALDADPSAEAVLTGEEKDLEESAR 283
QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDKGLV 180
DB 284 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDKGLV 343
QY 181 PLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHEAASKRVEVCSLLLSYGADPTLL 240
DB 344 PLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHEAASKRVEVCSLLLSYGADPTLV 403
QY 241 NCHNKSALDAPTPOLKRLAYEFKHSLLQAREADVTRIKKHLSLEMVNFKPQTHET 300
DB 404 NCHGKSAVMDAPTPELRRLTYEFKHSLLQAREADLAKVKTALALEINFKPQSHET 463
QY 301 ALHCAASPYKPKKOICELLRLKGANINEKTEFLTPLHVAEKANDVVEVVKHEAVK 360
DB 464 ALHCAVAAVHPKPKQVTELLRLKGANVNEKNDFMTPLHVAEKAHNDVVEVHLKHGAKM 523
QY 361 NALDNLGOTSLHRAAYCGHLOTCRLLLSYGCDPNTIISLQGTALQNGENVNOLLQEGIS 420
DB 524 NALDNLGOTSLHRAALAGHLQTCRLLNVGSDPSIISLQGTAAQIGNEAVQILSESTP 583
QY 421 LGNSEADPQLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHPAAGYNNRVSVVEYLL 480
DB 584 VRTSDVDYRLLEAKAGDLETVKQLCSPQNVNCRDLEGRHSTPLHPAAGYNNRVSVVEYLL 643
QY 481 QHGADVHAKDKGLVPLHNACSYGHVEVAELLVKHGAVNVNADLWKFTPLHEAAAKGKYE 540

DB 644 HHGADVHAKDKGLVPLHNACSYGHVEVAELLVRHGASVNVADLWKFTPLHEAAAKGKYE 703
QY 541 ICKLLLOHGADPTKKNRDNCTPLDLVKDGDITDIODLLRGDAALLDAKKGCLARVKKLSS 600
DB 704 ICKLLLOHGADPTKKNRDNCTPLDLVKEGDITDIODLLRGDAALLDAKKGCLARVKKLCT 763
QY 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
DB 764 PENINCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 823
QY 661 VAALIKKNACVNAATDKWAFTPLHEAAQKGTQLCALLAHAGADPTLKNOEGOTPLDLVS 720
DB 824 IAALLIKKNTCVNATDKWAFTPLHEAAQKGTQLCALLAHAGADPTLKNOEGOTPLDLAT 883
QY 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVSPCATADALSSGSPSSLSAASLNLG 780
DB 884 ADDIRALLIDAMPPEALPTCFKQAT-----VWSAISLSPASTPSCLSAASIDNLGT 936
QY 781 SPSELSSVVSSSGTEGASLEKK--EVPGVDFRSITQFVRNLGLEHLMDFPEREQTILDLV 838
DB 937 PLAEALVAGGASNTGDGAETERKEGEVSGLDNITQFLKSLGLEHLRDLFETEQITLDVL 996
QY 839 VEMGHKELKEIGINAYGHRHKLKIGVERLISQOGLNPNYLTNTSGSTLIDLSDDKE 898
DB 997 ADMGHEELKEIGINAYGHRHKLKIGVERLLGGQGTNPVLTFCVSGQGTLLDLAPDKE 1056
QY 899 FQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKIQKCNKLMERYTHRRKEVSEENHHA 958
DB 1057 YQSVSEEMQSTIREHRDGGNAGGIFNRYNVIQKVNNKLRERFCHROKEVSEENHHH 1116
QY 959 NERMLFHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGTCPCPVH 1018
DB 1117 NERMLFHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGTCGPTH 1176
QY 1019 KDRSCYICHRQLLCRVTLGKSLFQSFAMKMAHSPGHHSVTGRPSV 1065
DB 1177 KDRSCYICHRQLLCRVTLGKSLFQSFAMKMAHSPGHHSVIGRPSV 1223

RESULT 7
Q5XGK5 XENLA
ID Q5XGK5 XENLA PRELIMINARY; PRT; 1303 AA.
AC Q5XGK5
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE LOC495279 protein.
GN Name=LOC495279;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE-Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC084432; AAH84432.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 18.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS0297; ANK_REPEAT; 1.
DR PROSITE; PS00088; ANK_REPEAT; 15.
DR PROSITE; PS01059; PARP_CATALYTIC; 1.
DR PROSITE; PS01005; SAM_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1303 AA; 140271 MW; 5F4C3FE9329D5F8B CRC64;

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Db 201 GFGKDVVEYLLQNGASVQARDGGGLPLHNACSFGEAEVNVNLLRHGADPNARDNNYNT 260
Qy 61 PLHEAAIKGKIDVCIIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKKDELLESAR 120
Db 261 PLHEASIKGKIDVCIIVLLQHGADPSIRNTDGSALDLADPSAKAVLTGEYKKDELLEAAR 320
Qy 121 SGNEEKMALITPLNVNCHASDGRKSTPLHLAAGNVRVKIVOLLQHGADVHAKDKGLV 180
Db 321 SGNEEKMALITPLNVNCHASDGRKSTPLHLAAGNVRVKIVOLLQHGADVHAKDKGLV 380
Qy 181 PLHNACSYGHVEVTELLVKGHCACVNMADLWQPTPLHEAASKNRVEVCSSLLSYGADPTLL 240
Db 381 PLHNACSYGHVEVTELLVKGHCACVNMADLWQPTPLHEAASKNRVEVCSSLLSHGADPTLV 440
Qy 241 NCHNKAISDALPTPOLKRLAYEFKSHLSLQAAAREADVTIRKCHLSLEWNVFKHPQTHET 300
Db 441 NCHGSAVDMAPTPELKERLSYEFKSHLSLQAAAREADLAKVKKTLALRIINFKPQSHET 500
Qy 301 ALHCAAAASYPKPKQICELLRLKGANINEKTEFTPLHLVASEKANNDDVVEVVKGEAKV 360
Db 501 ALHCAVASLHPKPKQITELLRLKGSVNEKNKDFMTPLHLVASERAHNDVVEVLHGKGAKM 560

Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYSGDPNIIISLQGFALQMGNNVQQLLOEGIS 420
Db 561 NTLDTLIGOTALHRAALGGHLQTCRLLLSYSGDSASISVLSQGFATAAQMGNEAVQQLNESTP 620
Qy 421 LGNSEARQLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 621 VRTSDVYRLLEASKAGDLDIVKQLCSSQNNVNCRDLEGRHSTPLHFAAGYNRVSVVEYLL 680
Qy 481 OHGADVHAKDKGLVPLHNACSYGHYEVAELLVKGHCACVNVADLWKFPTPLHEAAKAGKYE 540
Db 681 HHGADVHAKDKGLVPLHNACSYGHYEVAELLVKGHCACVNVADLWKFPTPLHEAAKAGKYE 740
Qy 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAKKGKGLARVKLSS 600
Db 741 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAKKGKGLARVKLCT 800
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 801 QENINCRDTCGRNSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 860
Qy 661 VAALLIKYNACVNATDKWAFPTPLHEAAKQKGTQLCALLLAHGAADPTLKNQSGQTPDLVLS 720
Db 861 IAALLIKYNACVNATDKWAFPTPLHEAAKQKGTQLCALLLAHGAADPTLKNQSGQTPDLVLS 920
Qy 721 ADDVSALLTAAMPSPALPCVKPQVLNGVRSPGATADALSGSPSSPSLSAASSLSDNL-SG 780
Db 921 ADDIRALLIDAMPPEALPSCFKPOAT-----VVSASIIISPASTPSCLSAASSIDNL-TG 973
Qy 781 SFSELSVSVSSSGTEGASSLEKK--EVPGVDFTITQVRNINQSLGLEHMDIPFREQITLDVL 838
Db 974 PLAEAVGVGSNAGDGAAGTERKEGEVTCIDMNTNQSLGLEHMDIPFREQITLDVL 1033
Qy 839 VEMGHKEIKETGINAYGHRHKLKGVVERLISGQQLNPLYTLNTSGSTILIDLSPDDKE 898
Db 1034 ADMGHEELKEIGINAYGHRHKLKGVVERLISGQQLNPLYTLNTSGSTILIDLSPDDKE 1093
Qy 899 FQSVVEEMQSTVREHRDGHAGGIENRYNLIKQVCNKKLWERYTHRRKEVSEENHHA 958
Db 1094 HQSVVEEMQSTVREHRDGHAGGIENRYNLIKQVCNKKLWERYTHRRKEVSEENHHA 1153
Qy 959 NERMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSCKSNQYVYGGGTGCPVH 1018
Db 1154 NERMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSCKSNQYVYGGGTGCPVH 1213
Qy 1019 KDRSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGPHSHSVTGPRSV 1065
Db 1214 KDRSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGPHSHSVTGPRSV 1260
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Q4RG97_TETNG PRELIMINARY; PRT; 1212 AA.
AC Q4RG97;
DT 19-JUL-2005, integrated into UniProtKB/TREMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Chromosome 12 SCAF15104, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00034904001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=9988;
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RN NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biewont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Craud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Landier E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; CAAB01015104; CAG12585.1; -; Genomic DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00023; Ank; 15.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM 2; 1.
DR PRINTS; PRO1415; ANKRYIN.
DR SMART; SM00248; ANK; 13.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS0297; ANK REP REGION; 1.
DR PROSITE; PS0088; ANK REPEAT; 13.
DR PROSITE; PS1059; PARP CATALYTIC; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ANK repeat.
FT NON TER 1 1
FT NON TER 1212 1212
SQ SEQUENCE 1212 AA; 131719 MW; 9733077F92C219 CRC64;

Query Match 82.9%; Score 4631.5; DB 2; Length 1212;
Best Local Similarity 77.2%; Pred. No. 3.3e-265;
Matches 872; Conservative 103; Mismatches 78; Indels 77; Gaps 7;

QY 3 GRKDVVEYLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYTP 62
DB 50 GEKTWNTFLOTGANVHARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYTP 109

QY 63 HEAAIKGKIDVICIVLLQHGAEPTINTDGTALDADPSAKAVLTGEYKDBELLESARG 122
DB 110 HEAAIKGKIDVICIVLLQHGADPNIRNTDGSALDADPSAKAVLTGEYKDBELLESARG 169

QY 123 NEEKMALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDGLVPL 182
DB 170 NEEKMALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDGLVPL 229

QY 183 HNACSYGHEVTELVKHGACVNMALWQFTPLHEAASKNRVEVCSLLISYGADPTLLNC 242
DB 230 HNACSYGHEVTELVKHGACVNMALWQFTPLHEAASKNRVEVCSLLISYGADPTLLNC 289

QY 243 HNKSADLAPTQKRLAYEFGKSHLSLQAAREADVTRIKGHLSEMVNFKIPQTHETAL 302
DB 290 HSKSAVDMAPTPELKDRLTYEFKGSHLSLQAAREADVTRIKGHLSEMVNFKIPQTHETAL 349

QY 303 -----HCAAASPYPKRKQICELLRLKGNINEKTEFLTPHVASEKAHNDVVEV 353
DB 350 MLKVAAVFQHCVAVPHPKQVTELLRLKGNINDKNDPMTPLHVAERAHNDLLEVL 409

QY 354 VKHEAKVNALDNLGOTSLHRAAYCGHLOTCRLLLSYGCDFPNIISLQGTALQWGNVQ 413
DB 410 QKHGAKVNAADTLGQTLHRAALAGHIQTKULLLSYGADPAIVSLQGTAAQWGNVQ 469

RESULT 9

Q59FX0 HUMAN PRELIMINARY; PRT; 1055 AA.
ID Q59FX0 HUMAN PRELIMINARY; PRT; 1055 AA.
AC Q59FX0;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
DE variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain.
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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414 LLEQGISLGNSEADRLLEAAKAGDVETV-----KKLCTVQ 449
DB 470 ILNENVPTNNSVDYRFLFAAAGDLDTVQVSWSLALRLVSEGMRLQKVLVSQQQLCSPQ 529
QY 450 SYNCRDIDEGRQSTPLHFAAGYNNRVSVVEYLQHGADVHAKDKGLVPLHNACSYGHEVA 509
DB 530 NVNCRDLGEGHSTPLHFAAGYNNRVAVVEYLLHHGADVHAKDKGLVPLHNACSYGHEVA 589
QY 510 ELLVKGAVNVVADLWKFTPLHEAAAKGYEYCKLLQHGADPTKKRDGNTPLDLVKDG 569
DB 590 ELLVRHGASVNVADLWKFTPLHEAAAKGYEYCKLLQHGADPTKKRDGNIPLDMVKDG 649
QY 570 PDDIOLLDGDAALDAKGLARVKKLSPPNVNCRDTQGRHSTPLHLAAGYNNLEVA 629
DB 650 PDDIOLLDGDAALDAKGLARVKKLSPPNVNCRDTQGRHSTPLHLAAGYNNLEVA 709
QY 630 EYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFTPLHEAAQK 689
DB 710 EYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFTPLHEAAQK 769
QY 690 GRTQICALLLAHGAADPTLKNQSGQTPLD-----LVSADDV 724
DB 770 GRTQICALLLAHGAADPTLKNQSGQTALDLATVNLPLFIYSTLYSRRAGHVFWLLQADDI 829
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DB 880 LTELAAAVSTGSSGVADGATGSEKEGEMTLDWNISQFLKSLGLDLRDLIFEREQITL 939
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DB 1000 DKEYOSVEEEMQSTVREHSDGGHAGGIFNRYNLTIKQVCKNKKLWERYTHRRKEVSEENH 1059
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DB 1060 NHNEMMLFHGSPFFVNAIHKGFDERHAYIGMFGAGIYGAENSSKSNQVYVGGGTGC 1119
QY 1016 PVHKORSCHVCHRQLLPCRVTLGKSFLOPSAKMAHSPGHHSVTGRPSV 1065
DB 1120 PTHKORSCHVCHRQLLPCRVTLGKSFLOPSAKMAHSPGHHSVTGRPSV 1169

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CC EMBL; AB209339; BAD92576.1; -; mRNA.
 CC GO; GO:0003634; C:nucleus; IEA.
 DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR001290; PARP.
 DR InterPro; IPR012317; PARP_catalytic.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR011510; SAM_2.
 DR Pfam; PF00023; ANK; 17.
 DR Pfam; PF00644; PARP; 1.
 DR Pfam; PF07647; SAM 2; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 13.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00297; ANK REP REGION; 1.
 DR PROSITE; PS00088; ANK REPEAT; 13.
 DR PROSITE; PS1059; PARP CATALYTIC; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW ANK repeat.
 FT NON TER 1 1
 SQ SEQUENCE 1055 AA; 115234 MW; 9210519D299EB805 CRC64;
 Query Match 81.2%; Score 4532.5; DB 2; Length 1055;
 Best Local Similarity 82.6%; Pred. No. 28-259;
 Matches 842; Conservative 93; Mismatches 75; Indels 9; Gaps 2;
 QY 49 ADPNARDNNYTPLEHAAIKGKIDVICVILLOHGAEPTRINTDGTALDIDADPSAKAVLTG 108
 DB 1 ADPNARDNNYTPLEHAAIKGKIDVICVILLOHGAEPTRINTDGTALDIDADPSAKAVLTG 60
 QY 109 EYKDELLESARSNGNEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHG 168
 DB 61 EYKDELLEARSNGNEKLMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHG 120
 QY 169 ADVHAKDGDVPLHNACSYGHEVTELLVKGACVNMADLNOQTPLEHAASKNVEVCS 228
 DB 121 ADVHAKDGDVPLHNACSYGHEVTELLVKGACVNMADLNOQTPLEHAASKNVEVCS 180
 QY 229 LLLSYGADPTLNLCHNKSADIDLAPTPOLKRLAYEPKSHLSLQAAAREADVTRIKKLSLE 288
 DB 181 LLLSHGADPTLVNCHGKSAVDNAPTELPRLERTYEPKSHLSLQAAAREADVTRIKKLSLE 240
 QY 289 MYNFKHPQTHETALHCAASVPYKQKQICELLRLKGANINEKTKPLPLHLVASEKANND 348
 DB 241 IINFQKQPSHETALHCAVASLHPKQKQVTELLRLKGANVNEKNKDFMTPLHVAASRAHND 300
 QY 349 VVEVVVHKEKYNALDNLGOTSILHRAAYCGHLOTCELLLSYCGDPNIIISLOGFTALQNGN 408
 DB 301 VMEVLHKGAKGNALDNLGOTSILHRAALAGHLOTCELLLSYSGDSPSIISLOGFTAAQNGN 360
 QY 409 ENVQQLLOQGISLGNSEADROLLEAKAGDVETVKLCTVQSVNCRDIEGRSTPLHFAA 468
 DB 361 EAVQQLSESTPIRSDVDYRLLEKASKAGDLFTVQKCSSQNVNCRDIEGRSTPLHFAA 420
 QY 469 GYNRVSVVEYLLQHGADVHAKDGGVPLVPLHNAACSYGHEVABELLVKGAVNVNADLWKP 528
 DB 421 GYNRVSVVEYLLHHGADVHAKDGGVPLVPLHNAACSYGHEVABELLVKGAVNVNADLWKP 480
 QY 529 PLHEAAAKGYEICKLLQHGADPTKKNRDGNTPDLVKGDTDQDLRGDAALLDAK 588
 DB 481 PLHEAAAKGYEICKLLKHGADPTKKNRDGNTPDLVKGDTDQDLRGDAALLDAK 540
 QY 589 KCLARVKLSLSDNVNCRDITGRSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLI 648
 DB 541 KCLARVKLSLSDNVNCRDITGRSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLI 600
 QY 649 PLHNAASYGHVDVAALLIKYNACVNATDKWATPPLHEAAQKGRTOQLCALLAHGADPTLK 708
 DB 601 PLHNAASYGHVDVAALLIKYNTCVNATDKWATPPLHEAAQKGRTOQLCALLAHGADPTMK 660

QY 709 NOEGOTPLDLYSADDVSALLTAAPPSPALPSYCKPQVLNGVRSPGATADALSSGSSPSS 768
 DB 661 NOEGOTPLDLYSADDVSALLTAAPPSPALPSYCKPQVLNGVRSPGATADALSSGSSPSS 713
 QY 769 LSAASSLNLGSLFSFSLSSVSSSGTEGASLEKK--EVPGVDFITQFVRLGLEHMD 826
 DB 714 LSAASSIDNLGTPLAELAVGASNAGDGAAGTERKEGEVAGLDNMISQPLKSLGLEHMD 773
 QY 827 IFERQITLDVLVNGHKLKEIGINAYGHRHKLKGVERLISGOGLNPLYLTNTSGS 886
 DB 774 IFETEQITLDVLADMGHEELKEIGINAYGHRHKLKGVERLISGOGLNPLYLTNTSGS 833
 QY 887 TILIDLSPODKFOSVEEMOSTVREHRDGGHAGIFNRYNLIKIQKVNKKLWERYTHR 946
 DB 834 TILDLAPEDKEYQSVSEEMOSTVREHRDGGHAGIFNRYNLIKIQKVNKKLWERYTHR 893
 QY 947 RKEVSEENHNHNERMLFHGSPFVNAILHKGFDERHAYIGMGFGAGIYFAENSSKSNQV 1006
 DB 894 RKEVSEENHNHNERMLFHGSPFVNAILHKGFDERHAYIGMGFGAGIYFAENSSKSNQV 953
 QY 1007 YGIGGGTCGPVHKDSCYICHROLLFCRVTLGKSLQFSAMKMAHSPCHHSVTRGPSV 1065
 DB 954 YGIGGGTCGPVHKDSCYICHROLLFCRVTLGKSLQFSAMKMAHSPCHHSVTRGPSV 1012
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 Q8BX62_MOUSE PRELIMINARY; PRT; 976 AA.
 AC Q8BX62;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 20.
 DE 0 day neonate cerebellum cDNA, RIKEN full-length enriched library,
 DE clone: C230076123 product: tankyrase, TRF1-interacting ankyrin-related
 DE ADP-ribose polymerase, full insert sequence.
 GN Name=Trks;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Cerebellum; STRAIN=C57BL/6J;
 RX MEDLINE=92729253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-2;
 RA Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning."
 RL Methods Enzymol. 303:19-44(1999).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
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 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,

Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Sano S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Spierling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale J.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
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 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RX RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
 RG "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566 (2005).
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 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Ciothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierka R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mikl H., Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
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 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RX Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuura Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690 (2001).
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 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsuoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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 EMBL: AK048860; BAC33475.1; -; mRNA.
 HSSP: Pf6157; 1N11.
 Ensembl: ENSMUSG00000031529; Mus musculus.
 MGI: MGI:1341087; Tnks.
 GO: GO:0005634; C:nucleus; IEA.
 GO: GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 GO: GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 InterPro: IPR002110; ANK.
 InterPro: IPR001290; PARP.
 InterPro: IPR012317; PARP catalytic.
 InterPro: IPR001660; SAM.
 InterPro: IPR011510; SAM_2.
 Pfam: PF00023; Ank; 15.
 Pfam: PF00644; PARP; 1.
 Pfam: PF07647; SAM_2; 1.
 PRINTS: PR01415; ANKYRIN.
 SMART: SM00248; ANK; 12.
 SMART: SM00454; SAM; 1.
 PROSITE: PS02297; ANK_REPEAT; 1.
 PROSITE: PS00088; ANK_REPEAT; 12.

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Db 531 LLEHGAEVHASKDGGVPLHNACSYGHVEVTELLVKGAVNVNADLWKFTPLHEAAAKG 590
Qy 539 YEICKLLOHGADTKKRDGNTPLDLVKDGTDIQDILLRGDAALLDAKKGCLARVKL 598
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Db 651 VSDAUNICRDQGRNSTPLHLAAGVNNLEVAEYLLEHADVNAQDKGLIPLHNAASYGH 710
Qy 659 VDVAALLIKYNACVNAATDKAFTPLHEAAQKRTQLCALLAHGADPTLKQBGQTPDL 718
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Qy 719 VSADVVALLTAAPPSALPSCYKPVQVLNGVRSPGATADALSSGSPSSLSAASSLDNL 778
Db 771 ATABDVKCLLDAM-----VASQGTVAGGTAAAGAGAGTSGGGILSANGTL--L 816
Qy 779 SGSPSELSSVVS-----SSGTEGASSL-----EKKEVPG 807
Db 817 ATSCSPTEVTLTGASMTLSVPVQPLPVRSCLSPAQGAENVVDGIVDHDDKMPSPS 876
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Db 877 IESSVSVFLTSQLLEHLIDLFEREQITWDILAEMGHEDLKQGVSAVYFRHKILKGIATL 936
Qy 868 -ISGQOGLNPYLTNTSGSHTLIDSPDDKEFQSVSEEMQSTVREHDDGGHAGIFNRY 926
Db 937 RATTGLGLTP-----NPGTLLVDLLPDDKEFLAVEEEMQATIREHDDNGHSGYFNRY 989
Qy 927 NILKIQVCKNKKLWERYTHRKEVSEENHNANERMLFHGSPFFVNAITHKGFDERHAYIG 986
Db 990 NIVRIQVQNKKLWERYVHRKQEISEENHQASERMLFHGSPFFVNAIVQKGFDERHAYIG 1049
Qy 987 GMFAGIYFAENSKSNQYVYIGGGTQCPVHKDKRSCYICHRQLLFCRVTLGKSPLOFSA 1046
Db 1050 GMFAGIYFAENSKSNQYVYIGGGIGGICPTHKDKSCYQCHRQLLCLRALGKSPLOFSA 1109
Qy 1047 MKMAHSPGHHSVTCRPS 1064
Db 1110 MKMAHAPGHHHSVTCRPS 1127

RESULT 12

Q9VBP3 DROME

ID Q9VBP3 DROME PRELIMINARY; PRT; 1181 AA.
AC Q9VBP3;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 32.
DE CG4719-PA.

GN Name=tankyrase; ORFNames=Dmel CG4719;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN NUCLEOTIDE SEQUENCE.

RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballev R.M., Baeu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Berkeley Drosophila Genome Project;

RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,

RA Hoskins R., Scapleton M., Pacleb J., Park S., Svirskas R., Smith E.,

RA Yu C., Rubin G.

RA "Drosophila melanogaster release 4 sequence."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mammel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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RA Wang Z.-Y., Wessarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnik S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnik S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
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RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Scapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.

DR GO:0006471; P:protein amino acid ADP-ribosylation; IEA.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR012317; PAMP_catalytic.

DR Pfam; PF00023; Ank; 13.

DR Pfam; PF00644; PAMP; 1.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SMO0248; ANK; 9.

DR PROSITE; PS50297; ANK REP REGION; 1.

DR PROSITE; PS50088; ANK_REPEAT; 10.

DR PROSITE; PS51059; PAMP_CATALYTIC; 1.

KW ANK repeat. 1047 1047

FT NON TER

SQ SEQUENCE 1047 AA; 114477 MW; 09E9D3AE198C75E7 CRC64;

Query Match 56.9%; Score 3179; DB 2; Length 1047;

Best Local Similarity 59.1%; Pred No. 3e-179;

Matches 652; Conservative 68; Mismatches 134; Indels 250; Gaps 17;

Qy 108 GEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRKIVOLLQH 167

Db 18 GEYKDELLEARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRKIVOLLQH 77

Qy 168 GADVHAKDKGDLVPLHNAACSGHYEVTLLVK----- 199

Db 78 GADVHAKDKGGLVPLHNAACSGHYEVTLLVTHHTRAQTHTCGYEWTLARPLTLEA 137

Qy 200 -----HGACVNMDLWOFTPLHEAASKNRVEVCSLLSYGADPTLNCNKSALDAPT 253

Db 138 ETVSPQHGACVNMDLWOFTPLHEAASKNRVEVCSLLSHGADPTLNCNKSVDMAPT 197

Qy 254 POLKERLAYEPKSHLSQAAREADVTRIKGHLSEVMNFKHPQTHETALHCAAAAPYK 313

Db 198 PELKERLTYEPKSHLSQAAREADVAKAKSVLEIIFKHPHTHETAL----- 246

Qy 314 KOICELLURKGANINEKTYEFLPLHVAASEK-----AHNDVVEVVVVKHAKVNALDNLGOT 369

Db 247 -----LHDSASRGGCGGAHNDIMEVLQKHGAKVNALDTLGTOT 282

Qy 370 SLHRAAYCGHLTCRLLLSYGCNPNIISLQGTALQMGNNVQQLQSGISLGNSEADRO 429

Db 283 ALHRAAMAGHLHTCKLLIGYGADSLVSLQGTAAQMGNEAVQQLSENVPVRSNDVDR 342

Qy 430 LLEAAKAGDVETVKLCVTQSVNCRDIEGROSTPLHFAAGYNNRVSVYLLQHGADVHAK 489

Db 343 LLEAAKAGDLTQVSLCTPQNVNCRDLGSRHSTPLHFAAGYNNRVSVYLLHGHADVHAK 402

Qy 490 DKGLVPLHNAACSGHYEVAELLVKHGVANNVADLWKFTPLHEAASKYIECKILLQHG 549

Db 403 DKGLVPLHNAACSGHYEVAELLVRHGASVNVADLWKFTPLHEAASKYIECKILLKHG 462

Qy 550 ADPTKKNRDGNTPLDLVKDGTDTODLARGDAALLDAAKKGLARVKKLSGPDVNCBRT 609

Db 463 ADPTKKNRDGNTPLDLVKDGTDTODLARGDAALLDAAKKGLARVKKLSGPDVNCBRT 522

Qy 610 QGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDAALLIKYN 669

Db 523 QGRNSTPLHLAAGYNNLEVAEYLLHGHADVNAQDKGGLIPLHNAASYGHVDIALLIKHN 582

Qy 670 ACVNATDKWFTPLHEAASKGTQICALLAHGADPTLKNEGOTPLDLVS----- 720

Db 593 TCVNATDKWFTPLHEAASKGTQICALLAHGADPTMRNEGOTPLDLATAPVVFDROR 642

Qy 721 -----ADVSALLTAAMPSSALPSCKYKQVNLGVRSPGATADALSGSPSSPS 767

Db 643 MYDSVSVPPPSQADDIRALLIDAMPDPALPSCLKPQ-----ATVWVSGG----- 688

Qy 768 SILSAASSLDNLGSGFSELSSVSSVSGTGTGASLEKKEVP-----GVDFSIQT----- 814

Db 689 --ECQRCRRRCHLAVPVAVLIPVCGQQHQRPDHPAPRPHGCRGHRISGRDVRVQEGGR 746

Qy 815 -FVRNLGLEHLMIDIFEREQITLDVLVEMGHKEL-KEIGI----- 851

Db 747 RYRRAFAAGH-----DHQPLPEESGAGTPPHLPERADFPSPGRGH 788

Qy 852 ---NAYGHRHKLINGVERLISGOOGLN-----PYLTNTSGSTILIDLSPDKKF 899

Db 789 GARAEGRHQRRLRPPAQAQDQGHREAAAGRTARWKPVDLPPLRPGN----- 834

Qy 900 QSVEEEMQSTVREHRDQGHAGGIFNRNIIKIQVCNKKLWE-----RYTHRRKEYSEE 953

Db 835 -----RPDRPGSRQGV-----PVCGGAAEHHPRAPRWRRRRSLOPL 873

Qy 954 NHNANERMLF-----HGSPFVNALIHKGFDERHAYIGGMFGAGI 993

Db 874 QHOGVACGFRAADRDDEPALTVCVFLADSEGSFPFNAIHKGFDERHAYIGGMFGAGI 933

Qy 994 YFAENSSKSNQYVYIGGGTGCVPVHDKRSCYIC-----ROLFCRVTLGKSF 1041

Db 934 YFAENSSKSNQYVYIGGGTGCVPVHDKRSCYICVCHRSADVNGGCLCARQMLFCRVTLGKSF 993

Qy 1042 LOFSAMKVAHSPGHSHVTCRPSV 1065

Db 994 LOFSAMKVAHSPGHSHVTCRPSV 1017

RESULT 15

Q3UES3_MOUSE

ID Q3UES3_MOUSE PRELIMINARY; PRT; 589 AA.

AC Q3UES3;

DT 11-OCT-2005, integrated into UniProtKB/TREMBL.

DT 11-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 6.

DE Adult male liver tumor cDNA, RIKEN full-length enriched library,

DE clone: C730001F05 product: Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase

DE II) (TNKS-2) (TNF1-interacting ankyrin-related ADP-ribose polymerase

DE 2) (Tankyrase-like protein) (Tankyrase-related protein) homolog

DE (Fragment).

GN Name=Tnk2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.;"

RL Methods Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RC PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K.,

RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,

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RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX PubMed=1614073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
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RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
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RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
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RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
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RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
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RA Muramatsu M., Hayashizaki Y.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AK149368; BAF28838.1; -; mRNA.
CC MGI: MGI:1921743; Tnks2.
CC GO: GO:0005634; C:nucleus; IEA.
CC GO: GO:0003950; P:NAD+ ADP-ribosyltransferase activity; IEA.
CC GO: GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR012317; P:PARP_catalytic.
CC InterPro: IPR001660; SAM_2.
CC Pfam: PF00023; Ank; 5.
CC Pfam: PF00644; P:PARP; 1.
CC Pfam: PF07647; SAM_2; 1.
CC PRINTS: PR01415; ANKYRIN.
CC SMART: SM00248; ANK; 4.
CC SMART: SM00454; SAM; 1.
CC PROSITE: PS00297; ANK_REPEAT; 1.
CC PROSITE: PS00088; ANK_REPEAT; 4.
CC PROSITE: PS1059; P:PARP_CATALYTIC; 1.
CC PROSITE: PS0105; SAM_DOMAIN; 1.
KW ANK repeat.
FT NON_TER 1
SQ SS_SEQUENCE 589 AA; 64051 MW; AF630275E3C75124 CRC64;
Query Match 50.7%; Score 2833; DB 2; Length 589;
Best Local Similarity 96.8%; Pred. No. 4e-159;
Matches 536; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Db	54	GHVGLVQELLGRGSSVDSATKKGNLTALHIASLAGQAEVVKVLVKEGAINAQSQNGFTPL	113
QY	63	HEAAITKGIDVICVILLQHGAEPTTINTDGR-----ALDLADPSAKAVLTGEYKKDEL---	115
Db	114	YMAQENHIDVVKYLLLENGANQSTATEDGFTPLAVALQOQHNOQAVAILLENDTKGVRLP	173
QY	116	-----LESARSNGEEKMALLTPLNVNCHASDGRKS-----TPLHLAAGYNRKVIQOL	163
Db	174	ALHIAARKDDTKSAALLQ-----NDHNADVDSKMMVNNTTSGFTPLHIAAHYGNVNATL	230
QY	164	LIQHGADVHAKDGDVPLHNACSYGHVEYVELLVKHGACVNAMLWQFTPLHAAASKNR	223
Db	231	LLNRGAADVFTARNGITPLHVASKRGYTNVVKULLDRGGQIDAKTRDGLTPLHCAARSGH	290
QY	224	VEVCSLLSYGADPTLLNCHNKSADLAPTQPKERLAYEFKGHSLLQAAREADVTRIKK	283
Db	291	DQVVELLERGA-PLIARTKN-----GLSPLHMAAQGDHVECVK	328
QY	284	HUSLEWNVNFKHP-----QTHETALHCAASAPYPKRKQICELLRLKGNANTNEKTKFTPL	338
Db	329	HU-----LOHKA FVDDVDLYLTLALHVA-----HCHGYRVTKLLDKKANPNARALNGFTPL	381

QY **DG**

339 HVASEKAHNDVVEVVVVKHEAKYNALDNLNGOTSLHRAAYCGHLQTCLLLSYCDPNISL 398
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dg 382 HTACKKVRIKWELLKVYGASIQAITESGLTPIHVAAPMGHLNVLILLONGASPDTVTNI 441
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Qy 399 QGFALTOMGN-----ENVQOILQEGI-----SIGNSADRQLLE---- 432
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 442 RGETALHMAARAGOVVEVRCCLRNGALVDARAREEQTLPHIASRLGKTBIIVOLLQHMAH 501
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 433 -----RAKAGDVETVKLCCTVQSNCNRDIEGROSTPLHPFAAGNVRYSVVEY 478
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 502 PDAATNNRVTPLIHSABEGOVDVASULLBAGAASHLATK-KGTPTLVHAUKTGSLDVDKL 560
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 479 LLQGADVHADKKGGIPLPHTACSGHYEVAEALLVKHGAVVNVDLKRFPTLPHEAAKGK 538
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 561 LLORRARAADSAGKVGLTPLHVAAHYDNQKVALILLEKGAIPHATAKNGYTPLLHIAAQQNQ 620
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 539 YEICKLLLHQGDAPTCKNRDGNTPLDLV-KDDTDIDLLRGDAALLDKAQGCCLARVKX 597
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Dd 621 MQIASTLLNYGAETNVTIKOGVTPPLHASOECHTMVTTLLLDKGANIHMSTKSGL- 675
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 598 LSPPDNVCNCRDTGRHSTPLHLAGYNNLEVARYLLQHDGVNAQDKGGLIPLNHAASYG 657
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 676 -----TSUHLAAQSDKNVNAVAILTKHGADAQNHTKLGTYTPLIVACHYG 718
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 658 HYDVAALLKYACVNATOKMFTPLHEAAAQKRTOLCALLLAHGADPTLKNOGEQTPLD 717
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 719 NVKWVFLLKQGANVNAKTNKGYTPLHQAAQGHITHINVLQHGAKPNATTANGNTALA 778
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Qy 718 L-----VSADDVSALLTAAMPSPSALPCSKPVOLNUGVRSFGATADALSGBPSSPSLSA 771
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 779 IAKRLGISVWDITKVVTEVTTTTTIITEK-----HKLNVPETMTFVL-----DVSD 826
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 772 ASSIDLNLGSFSSEL-----SSVYSSTCSEGASSLEKEKPEVGPDSFITQFV--RN 818
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 827 BEGDDTMDGGBYLPRDELKELGDDLSPSQFLDGMNLYLRYSLEGSRDSLASFSSDRS 886
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 819 LGLEHLMDFIFEREQITLDVLVENGHKELKEIGINAYCHRHKLIKGVREL 867
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 887 HTLSHAS--YLRUSANVMDSVVIPISHOVSTLAKEAERNRYRLSWGENTENL 933
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 2

US-11-050-875-628
; Sequence 628, Application US/11050875
; Publication No. US20060263786A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 1847.1001
; CURRENT APPLICATION NUMBER: US/11/050,875
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1583
; SEQ ID NO 628
; LENGTH: 1880
; TYPE: PR1
; ORGANISM: Homo sapiens
US-11-050-875-628

Query Match 15.1%; Score 842; DB 7; Length 1880;
Best Local Similarity 25.5%; Pred. No. 3.3e-45;
Matches 279; Conservative 152; Mismatches 356; Indels 306; Gaps 27;

Qy 3 GRKDVBYYLLQNGASVOARDGGGLIPHNACSFGHAEVNNLLRHGADDPWARDNWYTPL 62
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 88 GODEVRELVNYSVANQAQSKGFTPLYMAAQENHLEHVFKFLLENGANQNATEDGTFPL 147
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 63 HEAAIKGKIDVICVILLOHGAEPFI-----RNTDERTALDLADPSAKAVLTGEVKXD 113
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 148 AVALOQGHENVAHLINYGTKYRKRLPALHTAARNDDRITA-----AVLLQNDPNP 198
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 114 ELLESARSNEEKMWALLITPLNVNCHASDGRKS-----TPULHLAGY 155
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

199	DVL--SKTG-----FTPLHIAAHYENLVNAQALLNARGASVNFTPQNGITPLHIASRR	248
156	NRVKIVQLLOHGADVHAKDGLVPLHNACSYGHYEVTELLVKHGACVNMADLQFTPL	215
249	GNVIMVRLLDORGAQIETKTDELTPLHCAARNGHVRISIELLDGAPITQAKTNGLSPI	308
216	HEAASNRVEVCSILLISYGADPTLLNCHNKSAIDLAPTQPKERLAYEPKGHSLQAARE	275
309	HMAAQGDHLDCVRLLLQYDAE-----ID-----	331
276	ADVTRIKXHLSEMWNFKHQPTHETALHCAASPYPKPKQICELLRLKGANINKEKPL	335
332	-DIT-----LDHLTPLHVA--HCGHHRVAKVLLDKGAKPNSRALNGF	371
336	TEPLHVASEKAHNDVVVVVKHBAKNALDNLGOTSLHRAAYCGHLOTCELLISYGCDPNI	395
372	TEPLHIACKGNHVRVMEILLKTGASIDAVTESGLTPLHVASFHGLPIVKNLLQRGASPNV	431
396	ISLQGFALOMG-----NENVQOLQOE-----GISLGNSEADROLLE-	432
432	SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDQTPLHCAARIQHTNMVKLLLEN	491
433	-----AAKAGDVETVKKLCTVQ--SVNCRDIEGRQSTPELHFAAGYNRVVS	474
492	NANPNLATTAGHTPLHIAAREGHVETVLALLEKEASQACMTKKG--FTPLHVAAKYGVKVR	549
475	VVEYLLQHGADVHAKDGGVLPLHNACSYGHYEVAELLVKHGAVNVNADLWK--FTPLHEA	533
550	VAELLERDAHENAAGKNGLTPLHVAVHNHNDIVKLLPRGGSPI--SPAWNRYTEPLHIA	608
534	AAKGXEICKLLOHGADPTKKNRGNTPLDI--VKDGDTDIODLRGDAALLDAKKGCL	592
609	AQONQVEVARSLLQYGGSSANASSVQGVTPPLHAAQEGHAEMVALL-----	653
593	ARVKCLSSPDNVNCRDIOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHN	652
654	-----LSKQANGNLGNKSG--LTPLHLVAQEGHVPVADVLINXGVNMDATTRMGYTPLHV	706
653	AASYGHVDVAAILLIKYNACVNATDKWAFTEPLHEAAQKGTQLCALLAHGADPTLKNQEG	712
707	ASHYGNIKLVKFLLOHQADVNAKTKLGYSPLHQAOQOQHTDITVLLLLKNGASPNESVSDG	766
713	QTPLDL-----VSADDDVALLTAMPSPALPSC-----	740
767	TTPLATAKRLGYSVTEVVLKVTDTEISFVLSVDKXHRMSPEETVDEILDVSEDEGBELISF	826
741	-----YKPOVLNGVRSPGATADALSGPSPSPSLUS-----AASLDN	777
827	KAERRDSRDVEBEKLLDFVKLDQVVESPA-----PRIPCAMPETVWIRSEBEQ	878
778	LSGSFBELSVSVSSGTGASLEKEVEPCVDFSIITQFVRNLGLEHLMDFEREQITLDV	837
879	ASKEYDEDSLIPSPATETSDNISPVASPVHTGFLVSFM-----	917
838	LVEMGHKELKEIGINAYGHRHKLIKGVE-----RLISQOGLNPXYLLNTSG	884
918	-----VDARGSGRSGRNGRLRVVIPPRTCAAPTRICRLVKPQKLTSTPPPLAESEG	969
885	SGTILIDLSP-----DDKEFQSVSEENQOSTVREHRDGGHAGGIF	923
970	LASRIIALGPTGAQFLSPVIVEIPHFAHGGRDRELVLVLRSENGSVWKEHR-----	1020
924	NRYNILKIQKVCN	936
1021	SRYESYLDQILN	1033

RESULT 3
US-11-050-875-629
; Sequence 629, Application US/11050875
; Publication No. US20060263786A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER

```

; FILE REFERENCE: 1847.1001
; CURRENT APPLICATION NUMBER: US/11/050.875
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1583
; SEQ ID NO 629
; LENGTH: 1881
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-875-629

```

Query Match	15.1%	Score	842;	DB	7;	Length	1981;
Best Local Similarity	25.5%	Pred.	No. 3.3e-45;				
Mismatches	152;	Mismatches	356;				
Conservative	279;	Indels	306;	Gaps	27;		

Qy	3	GRKDVVYLLQNGASVQARDGGGLPLHNASCFGHAEEVVNLLLRHGDAPNARDWNWYTPL	62
Db	89	GQDEVRELNYGANNVAQSQKGFPTPLMAAQENHLEVVFKFLLENGANQNVATEDGFPTPL	148
Qy	63	HEAAIKGIDVCIVLLOHGAEPTI-----RNTDGTALDLADPSAKAVLTGEYKDD	113
Db	149	AVALOQGHENVVAHLINYGTKVKRPLPALHIAARNDTRTA-----AVLQNDNP	199
Qy	114	ELLESARSGNEEKMMALLTPLNVNCHASDGRKS-----TPLHLAAGY	155
Db	200	DVL--SKTG-----FTPLHIAAHVENLVAQLLNRGASVNFPTQNGITPLHIAARR	249
Qy	156	NRVKIVOLLQHGADVHAKQGDVLVPLHNASCYGHYEVTLLVKHGACVNAWMLWQFTPL	215
Db	250	GNVIMVRLLDGRGAQIETKTKDELTPLHCAARNGHVRISETLLDHGADPIQAKTNGLSPI	309
Qy	216	HEAASKNRVFCVSLLSYGDAPDTLLNCHNSAIDLAPTPQLKERLAYEFKGHSLIQAARE	275
Db	310	HMAAQDHLDCVRLQLQYDAE-----ID-----	332
Qy	276	ADVTRIKGHLSELMVNFKHPOTHETALHCAAASYPFKKQICELLRRKGANINEKTEFL	335
Db	333	-DIT-----LDHLTPLHVAA---HCGHRRYAKVLLDKGAKPNSRALNGF	372
Qy	336	TPLHVASEKAHNDVVEVVKHEAKVNALDNLGQTSLHRAACVGHLCOTCRLLLSYGCDPNI	395
Db	373	TPLHIACKKHVRVWELLTKGASIDAVTESGLTPLHVASFWGHLPIVKNLLQRGASENV	432
Qy	396	ISLQGF TALQW-----NENVQQLQE-----GISLGNSEADQQLLE-	432
Db	433	SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKAQDQTPHLHCAARIGTHTNMVKLLLE	492
Qy	433	-----AAKAGDVETVKKLCVQ--SYNCRDIEGRQSTPLHFAAGYNEVS	474
Db	493	NANPNLATTAGHTPLHIAAREGHVETVLALEKEASQACMTKG--FTPLHVAAKYKVR	550
Qy	475	VVEYLLQHGADVHAKDGGVLPLHNASCYGHYEVAELLVKHGAVVNVADLWK--FTPLHEA	533
Db	551	VAELLERDAHNAAGKNGLTPLHAVVHHNLDIVKLLPRGGSFH--SPAMNGYTPLHIA	609
Qy	534	AAKGKYEI CKLLLOHGADPTKKNRDNTPDL--VKDGTDIQDLRGDAALLDRAKKGCL	592
Db	610	AKQNVARSRLLYGGSANAESVQGVTPHLAAQEGHAEVALL-----	654
Qy	593	ARVKLSSPDNVNCRDTGGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHN	652
Db	655	-----LSQANGNLGNKSG--LTPHLHVQSGHPVPADVLIKHGVWDATTTMGYTPLHV	707
Qy	653	AASYGHVDVAALLIKYNA CVNATDKWAFTPLHEAAQKGTQLCALLLAHGADPTLKNQEG	712
Db	708	ASHYGNIKLVKFLLOHQADVNAKTKLGYSPHQAAQQGHTDITVTLILKNGASPNVEVSDG	767
Qy	713	QTPLDL-----VSADVSAALLTAAMPSPALPSC-----	740
Db	768	TTPLAIAKRIGYISVTDVLKVVTDTETSPVUSDKHRMSFFETVDEILDVSDGDELLISF	827
Qy	741	-----YKQVNLNGVRSPGATADALSSGSPSSLSL--AASSLDN	777

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Db      828 KAERDRSRDVEDKEKLLDFPKLDQVVESPAI-----PRIPCAMPETVVIKSESEQ 879
Qy      778 LSGSFSLSVSSSGTTEGASSLKKKEVPGVDFPSITQFVRNMLGLEHLMDFIFEREQITLDV 837
Db      880 ASKEYDEDSLIPSPATETSDNISPVASPVHTGFLVSFM----- 918
Qy      838 LVEMGHKELKEIGINAYGHRHKLIKGYE-----RLISGOOGLNPYLTLNTSG 884
Db      919 -----VDARGSGMRGSRHGLRVVIPRTCAAPTRITCRLVKPKLSTPPPLAEEG 970
Qy      885 SGTLLIDLSP-----DKEFOSVEEEMQSTVREHRDGGHAGGIF 923
Db      971 LASRIIALGTGAQFLSPVIVEIPHFASHGRGORELVLRSENGSVWKEHR----- 1021
Qy      924 NRYNLIKQVCN 936
Db      1022 SRYGESYLDQILN 1034

RESULT 4
US-11-293-697-4122
; Sequence 4122, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4122
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4122

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Query Match	12.1%;	Score 678;	DB 7;	Length 919;
Best Local Similarity	28.5%;	Pred. No. 3.7e-35;		
Matches	235;	Conservative 109;	Mismatches 304;	Indels 178; Gaps 24;
QY	11	LLQNGASVQARDGGGLIPLHNACSFSGHAEVVNLLLRHGADPNARDNNYNTPLHEAAIKGK	70	
DB	2	LIHKTEDVNTLDSEKRTPLHVAAPLGDAEIIELLISGARVNACDNMWLTPLHRAVASRS	61	
QY	71	IDVCIVLLQGAEPFTINTDGRALTADIADPSAKAVLTGEYKKBELLESARGNEEKWAL	130	
DB	62	EEAVQVLIKESADVARNADKQWOTPLHVA-AANKAV-----KCAEV	100	
QY	131	LTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLIHQGDVHAKDKGDLVPLHNACSYGH	190	
DB	101	IIPLLSSVNSDRGRTALHHAALNGHEVMVNLILAKGANINAFDKDRRALHWAAYMGH	160	
QY	191	YEVTELVAKHGACVAMDLMOFTPLHEAASKRVEVCSLLLSYGADPTPLNCHNKSAIDL	250	
DB	161	LDVVALLINEGAETVCKDKKGYTPLHAASNGQINVVVKHLINLNGVEIDEINVYNGTALHI	220	
QY	251	APTQPKERLAYEFKGSLLQAREADVTRIKHLSLEWMVNFHKPQTHE-TALHCAASP	309	
DB	221	A-----CYN-----GDAVVNELIDY-----GANVNOPNNGFTPLHFAAAS	258	
QY	310	YPKRKQIC-ELLARKGANINEKTEFTPLHFAASEKAHNDVVEVVVXHEAKVAMDLNLQG	368	
DB	259	H---GALCELLLVNNGADVNIQSKDGKSPLHMTAVHGRFTRSQTLIQNGGEIDCVDKGN	315	
QY	369	TSLHRAAYCGHLQTCRLLLSVCGDPNIIISLGFTALQMGNEVQQLQEGISLGNSEADR	428	
DB	316	TPLHVAARYGHELLINTLRTSGADATCKGIHSMFPPLHAAIN-----AHSOCCR	364	
QY	429	QLLEAAKAGADVETVKCLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHA	488	

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Db 365 KLL--SSGFEIDTPDKF-----GR--TCLHAAAGGNVECIKLOSSADPHK 408
Qy 489 KDKGLVPLHNACSYGHEVEAEVLVKGAVNVADLWKFPLHEAAA-----535
Db 409 KDKCGRTPLHYAAANCHFCIETLTTGANVNETDDWGTALHYAAASMDRKNKTLGNA 468
Qy 536 -----KGKYEIC-KULLQHGADPTKKNRDG-----559
Db 469 HDNSEELERARELKEATCLCLEFLLQNDANPSIRDKEGYNSIHVAAAYGHRQCLELLE 528
Qy 560 -----NTPLDLVK-DG-----DTDIQDLRGDAALLDAKGC 591
Db 529 RTNSGFEBSDSGATKSPHLHAYNGHQALEVLLQSLVDLDIRD-EKGTALDLAFAFKGH 587
Qy 592 LARVKKGSSP-----DNVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGAD-----VN 640
Db 588 TECVEALINPGASIFVKONVTKR-----TPLH-ASVINGHTLCRLLELLEIADNPEAVD 639
Qy 641 AODKGGGLPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGTOLCALLLA 700
Db 640 VKDAGQTPPLMAVAYGHIDAVSLLEKEANVDTVDILGCTALHRTGIMTGHEECVQMLLE 699
Qy 701 HGADPTLKNQSGOTPLDLVSADD-----VSALI-TAAMPSPALPSCYK 742
Db 700 QEVSLCKDSRGTPLHYAARGHATWLSLQMAL--SEEDCCFK 743

RESULT 5
US-11-371-354-56501
; Sequence 56501, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; TITLE OF INVENTION: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 56501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-56501

Query Match 9.4%; Score 527; DB 7; Length 743;
Best Local Similarity 24.0%; Pred. No. 1.3e-25;
Matches 201; Conservative 98; Mismatches 238; Indels 302; Gaps 19;

Qy 3 GRKDVVEYLLQNGASVQARDGGGLIPLHNA-----CSFGHAEVNVNLLRHGADPNARDNW 57
Db 2 GHREIVEVLLDHGAEVNHEDVDGRTALSAALCVPAKSGHASVSLLDIRGAEVDHCDKD 61
Qy 58 NVTPLHEAAIKGKIDVCTVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKXDELLE 117
Db 62 GMTPLLVAAEGHVDDVLLLEGGAD--VDHTD-----92
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Qy 118 SARSNGEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKG 177
Db 93 -----NNGR--TPLLAASASMGHASVVNTLLFWGAADVDSIDSE 127
Qy 178 DLVPLHNACSYGHEVEATELLVKGACVNAWDLWQFTPLHEAAKSNRVEVCSSLISYGADP 237
Db 128 GRTVLSIASAQGNVEVVRTLLORGLDENHRDDAGWTPLHMAA-----169
Qy 238 TLLNCHINKSAIDLAPTPQLKERLAYEFKGHSLLOQAAREADVTRIKKHLSEMVNFKHPQT 297
Db 170 -----FEGHRL-----175
Qy 298 HETALHCAASAPYPRKQICELLRLKGANINEKTEFLPLHVASEKAKHNDVVVVVKHE 357
Db 176 -----ICEALIEQGARTNEIDNGRIPFILASQEGHYDCVQILLLENK 217
Qy 358 AKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFALTQMGNENVQOLLQE 417
Db 218 SNIDQGYDGRNALRVAALLEGHRDIVELLFSGAD-----252
Qy 418 GISLGNSEADRLQLEAAKAGDVETVKLCTVOSVNCRDIEGROSTPLHFAAGYNNRVSVVE 477
Db 253 -----VNCKDADGRPT--LYILALENQLTMAE 277
Qy 478 YLLQHGADVHAKDKGLVPLHNACSYGHEVEAEVLVKGAVNVADLWKFPLHEAAKAG 537
Db 278 YFLENGANYEASDAEGRTALHVSQMGHMEMVQVLIAYHADVNAADNEKRSALQSAAWQG 337
Qy 538 KYEICKLLQHGADPTKKNRDGNTPLDLVKOGDTDIQDLRLGDAALLDAKGCCLARVKK 597
Db 338 HVKVQOLLIEHG-----AVVD-----353
Qy 598 LSSPDVNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYG 657
Db 354 -----HTCNOGATALCIAAQSGHIDVQVLLLEGADPNHAQDQGRMTRVAAKNG 403
Qy 658 HVDVAALLIKYNACVNATDKWAFTPLHEAAQKGTOLCALLLAHGADPTLK-NOEGQTPL 716
Db 404 HSGIILKLEKYGA--SSLNGCSPSPVHTMEQKPLQSLSKV-----QSLTIKSNSSGST--455
Qy 717 DLVSADDDVSALLTAAMPSPALPSCYKPVNLGVRSFGATADALSSGSPSSSL--SAASS 774
Db 456 ---GGGD-----MQPS-----LRGL--PNGTHAFSSPSESFDSIVDRQKSS 492
Qy 775 LDNLGSGFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQI 833
Db 493 LSNNSLKSSKSNLSLRTSSTAQT-----VPIDSPHNLSFTEQIQHSLPRSRSRQSI 546

RESULT 6
US-10-533-519-1308
; Sequence 1308, Application US/10533519
; Publication No. US20060263774A1
; GENERAL INFORMATION:
; APPLICANT: CLARK, HILARY
; APPLICANT: SCHOENFELD, JILL
; APPLICANT: VANLOOKEREN, MENNO
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF OR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1984R1 US
; CURRENT APPLICATION NUMBER: US/10/533,519
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/34312
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/423,394
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2517
; SEQ ID NO 1308
; LENGTH: 685
```

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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-519-1308

Query Match      8.7%; Score 483.5; DB 6; Length 685;
Best Local Similarity 25.4%; Pred. No. 7.1e-23;
Matches 196; Conservative 93; Mismatches 259; Indels 225; Gaps 22;

QY 3 GRKDVVYLQNGASVQARDGGLIPLHNACSFHAEVUNLLRHGADPNARDNNYTP 62
Db 7 GHLELVKLLASGANVHATTATGDTALTACBNGHTDVADVLLQAGADKQGE----- 59
QY 63 HAAIKGKIDVICVILQHGAEPTIRNTDGTALDLPSPAKAVLTGEYKQDELLESARS 122
Db 60 -----DMKTILEGIDPA-----KHQE----- 75
QY 123 NEEKWALLTPLNVNCHASDRKSTPLHLAAGYNRKIVQLLLQHGADVH-AKQKGDLPV 181
Db 76 -----HESEGR-TPLMKAARAGHLCTVQFLISKGANVNVRATANDHTV 118
QY 182 LHNACSYGHEVTELLVKGHCNVAMDLWQFTPLH-----EAASKNRVEVCSTLL 231
Db 119 VSLACAGHLAVELLALHGA-----DPTRLKDGSTMLTEAAKGHTNVVSYLL 168
QY 232 SYGADPTLLNCHNKSAIDLAPT-----QLKERLAYEFKSHSLLOAAREADVTRIK--KH 284
Db 169 DY---PNNVLSVPTTDVSQLPPPSQDSQEPDRTSQE--NSPALLGVQKAVSTRVPTGSN 223
QY 285 LSEMVNFKHPQT-----HETALHCAAAASPYPKPKQ 315
Db 224 SSSQTECLTPBESCQTTSNVASQSMPPVYPSVDVDAHTESNHDALTALACAGGH---EE 280
QY 316 ICELLLRKGANINEKTEFLPLHVAASEKANDNVVVVVKHAKVNA-LDNLGQTSLHRA 374
Db 281 LVSVLIAARDAKIEHRDKGFTPLILAAATAGHVGVVEIILLDKGDIQAQSERKDTPLSLA 340
QY 375 AVCGHLOTCLRLLSYGCDPNIISLQGFALQW-----GNENVQOLL-----QEGISL 421
Db 341 CSGGQEVVDLLLAGANKEHRNVSDYTPLSLAASGGYVNIKIILLNAGAEINSTGSKL 400
QY 422 GNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQ 481
Db 401 GIS-----PLMLAAMNGHPVAPVKLLDMGSDINAQIETNRNTALTALACFGRAEVVSLLD 456
QY 482 HGADVHAKDKGLVPLHNACSYGHEVVAELLVKHGAVNVADL---WKFTPLHAAAKGY 539
Db 457 RKANVEHRAKTGLTPLMEAASGGYAEVGRVLLDKGADVNAPEVPSRDTALTIAADKGYH 516
QY 540 EICKLLQHGADPTKKNRDNTPDLVKDGDITDIDLLRGDAALLDAAKKGCLARVKKLS 599
Db 517 KPCELLIHRGAHIDVRNKKGNTPMLASNG----- 546
QY 600 SPDVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHV 659
Db 547 -----GHFVQVLLVQAGADVDAADRNRKITPLMSAFKRGHV 582
QY 660 DVAALLIK-----YNACVNATDKWAFPLHAAQ---KGRTOICA 696
Db 583 KVVQVLVKEVNPFPSPDIECMRYIATI--TDKELLKKCHQCVETIVKAKDQQA 633

RESULT 7
US-11-317-329-3
; Sequence 34, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 34
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-34

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

QY 245 KSAIDLAP-----TPQLKERLAYEFKSHSLLOAAREADVTRIKHLSLEMVNFKHPQTHET 300
Db 338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
QY 301 ALHCAAAASPYPKPKQICELLRLKGANINEKTEFLPLHVAASEKANDNVVVVVKHAKV 360
Db 387 DVDQCOTASGY-----TPLLIAAQDQPPDLCALLLAHGADA 421
QY 361 NALDNLGQTSLHRAAYCCHLOTCLRLLSYGCDPNIISLQGFALQMGNNVQOLLQEGIS 420
Db 422 NRVEDGWPALHFAAQNGDDRTARLLLDHGCACVDAQEREGETPLHLAAQN----- 471
QY 421 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 472 --NFENVARLLVSQA-----DPLREAEKG--TPLHVAAYFGHVSIVKLLT 514
QY 481 QHGADVHAKDKGLVPLHNACSYGHEVVAELLVKHGAVNVADLWKFTPLHAAAKGYE 540
Db 515 SOGAELDAQQRNLTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYL 574
QY 541 ICKLLQHGADPTKKNRDNTPDLVKDGDITDIDLLRGDAALLDAAKKGCLARVKKLS 600
Db 575 ICKMLRYGASLELPTHQGTPLHL-----AAYKGHL-EIHLILA 613
QY 601 PDNVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPPLHLAARHGEEAVVSALQCGADPNAAEQSGWTPHLAVQSRSTFL 673
QY 661 VAALLIKYCNATDKWAFPLHAAQKGRTOICALLLAHGADPTLKNQSGQTPDL 718
Db 674 SVINLEHHANVHARNKVGWTPAHLAALKGNITAILKVLVEAGAQLVDQGVSCPTPLQ 731

RESULT 8
US-11-317-329-34
; Sequence 34, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 34
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-34

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

QY 245 KSAIDLAP-----TPQLKERLAYEFKSHSLLOAAREADVTRIKHLSLEMVNFKHPQTHET 300
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-519-1308

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

QY 245 KSAIDLAP-----TPQLKERLAYEFKSHSLLOAAREADVTRIKHLSLEMVNFKHPQTHET 300
Db 338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
QY 301 ALHCAAAASPYPKPKQICELLRLKGANINEKTEFLPLHVAASEKANDNVVVVVKHAKV 360
Db 387 DVDQCOTASGY-----TPLLIAAQDQPPDLCALLLAHGADA 421
QY 361 NALDNLGQTSLHRAAYCCHLOTCLRLLSYGCDPNIISLQGFALQMGNNVQOLLQEGIS 420
Db 422 NRVEDGWPALHFAAQNGDDRTARLLLDHGCACVDAQEREGETPLHLAAQN----- 471
QY 421 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 472 --NFENVARLLVSQA-----DPLREAEKG--TPLHVAAYFGHVSIVKLLT 514
QY 481 QHGADVHAKDKGLVPLHNACSYGHEVVAELLVKHGAVNVADLWKFTPLHAAAKGYE 540
Db 515 SOGAELDAQQRNLTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYL 574
QY 541 ICKLLQHGADPTKKNRDNTPDLVKDGDITDIDLLRGDAALLDAAKKGCLARVKKLS 600
Db 575 ICKMLRYGASLELPTHQGTPLHL-----AAYKGHL-EIHLILA 613
QY 601 PDNVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPPLHLAARHGEEAVVSALQCGADPNAAEQSGWTPHLAVQSRSTFL 673
QY 661 VAALLIKYCNATDKWAFPLHAAQKGRTOICALLLAHGADPTLKNQSGQTPDL 718
Db 674 SVINLEHHANVHARNKVGWTPAHLAALKGNITAILKVLVEAGAQLVDQGVSCPTPLQ 731

RESULT 8
US-11-317-329-34
; Sequence 34, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 34
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-34

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

QY 245 KSAIDLAP-----TPQLKERLAYEFKSHSLLOAAREADVTRIKHLSLEMVNFKHPQTHET 300
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Db 338 KRALQLSDRKNLVRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 301 ALHCAAAAPYKPKRQICELLRLKKGANINEKTEFTPLHVAEKAHNDVVEVVVKEAKV 360
Db 387 DVDCCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLQGTALONGNENVQQLQEGIS 420
Db 422 NRVDGDMAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSADRLQLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DPNLRREAGK--TPLHVAAYFGHVSIVKLIT 514
Qy 481 OHGADVHAKDKGGLVPLHNACSYGHYEVAELLYKHGAVNVNADLWKFTPLHEAAAKGYE 540
Db 515 SGAEALDAQORNLRTPLHLAVERGKVAIQHLLKSGAVDPALDQSGYGLPHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLILA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 472 --NFENVARLLVSRQA-----DPNLRREAGK--TPLHVAAYFGHVSIVKLIT 514
Qy 481 OHGADVHAKDKGGLVPLHNACSYGHYEVAELLYKHGAVNVNADLWKFTPLHEAAAKGYE 540
Db 515 SGAEALDAQORNLRTPLHLAVERGKVAIQHLLKSGAVDPALDQSGYGLPHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLILA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPHLHAAHGEAVVSALLQCGADPNAAEQSGWTPHLAVQORSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL 718
Db 674 SVINLLEHHANVHARNKVGWTPAHLAALKGNNTAILKVLVEAQAQLDVQDGVSTCTPLQL 731

RESULT 9
US-11-317-329-35
; Sequence 35, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-35

Query Match 8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 245 KSAIDLAP----TPOLKERLAYEFKSHLLQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db 338 KRALQLSDRKNLVRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 301 ALHCAAAAPYKPKRQICELLRLKKGANINEKTEFTPLHVAEKAHNDVVEVVVKEAKV 360
Db 387 DVDCCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLQGTALONGNENVQQLQEGIS 420
Db 422 NRVDGDMAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSADRLQLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DPNLRREAGK--TPLHVAAYFGHVSIVKLIT 514
Qy 481 OHGADVHAKDKGGLVPLHNACSYGHYEVAELLYKHGAVNVNADLWKFTPLHEAAAKGYE 540
Db 515 SGAEALDAQORNLRTPLHLAVERGKVAIQHLLKSGAVDPALDQSGYGLPHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLILA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPHLHAAHGEAVVSALLQCGADPNAAEQSGWTPHLAVQORSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL 718
Db 674 SVINLLEHHANVHARNKVGWTPAHLAALKGNNTAILKVLVEAQAQLDVQDGVSTCTPLQL 731

Db 515 SGAEALDAQORNLRTPLHLAVERGKVAIQHLLKSGAVDPALDQSGYGLPHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLILA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPHLHAAHGEAVVSALLQCGADPNAAEQSGWTPHLAVQORSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL 718
Db 674 SVINLLEHHANVHARNKVGWTPAHLAALKGNNTAILKVLVEAQAQLDVQDGVSTCTPLQL 731

RESULT 10
US-11-317-329-36
; Sequence 36, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-36

Query Match 8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 245 KSAIDLAP----TPOLKERLAYEFKSHLLQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db 338 KRALQLSDRKNLVRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 301 ALHCAAAAPYKPKRQICELLRLKKGANINEKTEFTPLHVAEKAHNDVVEVVVKEAKV 360
Db 387 DVDCCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLQGTALONGNENVQQLQEGIS 420
Db 422 NRVDGDMAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSADRLQLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DPNLRREAGK--TPLHVAAYFGHVSIVKLIT 514
Qy 481 OHGADVHAKDKGGLVPLHNACSYGHYEVAELLYKHGAVNVNADLWKFTPLHEAAAKGYE 540
Db 515 SGAEALDAQORNLRTPLHLAVERGKVAIQHLLKSGAVDPALDQSGYGLPHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLILA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPHLHAAHGEAVVSALLQCGADPNAAEQSGWTPHLAVQORSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL 718
Db 674 SVINLLEHHANVHARNKVGWTPAHLAALKGNNTAILKVLVEAQAQLDVQDGVSTCTPLQL 731

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RESULT 11
US-11-317-329-37
; Sequence 37, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-37

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy      245 KSAIDLAP-----TPOLKERLAYEFKGHSLQQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db      338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386

Qy      301 ALHCAASPYPRKQKICELLARKGANINEKTEFTPLHVASAKAHNDVVEVVKHEAKV 360
Db      387 DVDCQTASGY-----TPLLIAAQDQDPLCALLAHGADA 421

Qy      361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQMGNEVQQLLQEGIS 420
Db      422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN-----471

Qy      421 LGNSEADRLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db      472 --NFENVARLLVSRQA-----DPLREAEKG--TPLHVAAYFGHVSIVKLLT 514

Qy      481 OHGADVHAKRGGLVPLHNACSYGHYEVAELLVKHGAVNVVADLWKFTPLHEAAKGYE 540
Db      515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGLPHTAAARGKYL 574

Qy      541 ICKLLQHAGDPTKQRDGNTPDLVKDGTDTIQDLLRGDAALDAAKKGCLARVKKLSS 600
Db      575 ICKMLLYGASLELPTHQGWTPHL-----AYKGHL-EIHLA 613

Qy      601 PDVNCRTDQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db      614 ESHANMGALGAVNWTPLHLAARGHEAVVSALLQCGADPNAAEQSGWTPHLHVAQVSTFL 673

Qy      661 VAALLIKYNACVNATDKWAFPLHEAAQKGTQLCALLAHGADPTLKNQSGQTPDL 718
Db      674 SVINLLEHANVHARNKVGWTPFAHLAALKGNATILKVLVEAGAQLDVQDGVSCPTPLQ 731

RESULT 12
US-11-317-329-38
; Sequence 38, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-38

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy      245 KSAIDLAP-----TPOLKERLAYEFKGHSLQQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db      338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386

Qy      301 ALHCAASPYPRKQKICELLARKGANINEKTEFTPLHVASAKAHNDVVEVVKHEAKV 360
Db      387 DVDCQTASGY-----TPLLIAAQDQDPLCALLAHGADA 421

Qy      361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQMGNEVQQLLQEGIS 420
Db      422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN-----471

Qy      421 LGNSEADRLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db      472 --NFENVARLLVSRQA-----DPLREAEKG--TPLHVAAYFGHVSIVKLLT 514

Qy      481 OHGADVHAKRGGLVPLHNACSYGHYEVAELLVKHGAVNVVADLWKFTPLHEAAKGYE 540
Db      515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGLPHTAAARGKYL 574

Qy      541 ICKLLQHAGDPTKQRDGNTPDLVKDGTDTIQDLLRGDAALDAAKKGCLARVKKLSS 600
Db      575 ICKMLLYGASLELPTHQGWTPHL-----AYKGHL-EIHLA 613

Qy      601 PDVNCRTDQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db      614 ESHANMGALGAVNWTPLHLAARGHEAVVSALLQCGADPNAAEQSGWTPHLHVAQVSTFL 673

Qy      661 VAALLIKYNACVNATDKWAFPLHEAAQKGTQLCALLAHGADPTLKNQSGQTPDL 718
Db      674 SVINLLEHANVHARNKVGWTPFAHLAALKGNATILKVLVEAGAQLDVQDGVSCPTPLQ 731
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Qy 301 ALHCAASPYPKQICELLRKANINEKTEFLTPLVASEKAKNDVVEVVVKEAKV 360
Db 387 DVDCQTASGY-----TPLLIAAQOQPDLCALLAHGADA 421
Qy 361 NALDNLGQTSIHRAAYCGHLQTCRLLSYGCDPNIIISLQGFALQMGNNVQQLQEGIS 420
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DNLREAEKG--TPLHVAAYFGHVSLLVLLT 514
Qy 481 OHGADVHAKOGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAKGYE 540
Db 515 SQGAELDAQORNLRTPHLAVERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGYL 574
Qy 541 ICKLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGAALDAAKKGCLARVKKLSS 600
Db 575 ICKMLLYGASLELPTHQGTPLHL-----AAYKGHL-EIIHLLA 613
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGAVNWTPLHLAARHGEAEVVSALLQCGADPNAAEQSGWTPHLAVQVSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFTPLEHAQKGTQICALLAHGADPTLKNQEGQTPDL 718
Db 674 SVINLEHHANVHARNKVGWTPAHLAALKGNATLKVLEAGAQLDVQDQVGSCTPLQL 731

RESULT 14
US-11-317-329-40
; Sequence 40, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; PRIORITY FILING DATE: 2005-12-22
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-40

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 245 KSAIDLAP----TPQKERLAYEFKSHLSLQAAREADVTRIKKHLSEMNFKHPQTHET 300
Db 338 KRALQSDRKNLVRDEELCTIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
Qy 301 ALHCAASPYPKQICELLRKANINEKTEFLTPLVASEKAKNDVVEVVVKEAKV 360
Db 387 DVDCQTASGY-----TPLLIAAQOQPDLCALLAHGADA 421
Qy 361 NALDNLGQTSIHRAAYCGHLQTCRLLSYGCDPNIIISLQGFALQMGNNVQQLQEGIS 420
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DNLREAEKG--TPLHVAAYFGHVSLLVLLT 514
Qy 481 OHGADVHAKOGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAKGYE 540
Db 515 SQGAELDAQORNLRTPHLAVERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGYL 574
Qy 541 ICKLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGAALDAAKKGCLARVKKLSS 600
Db 575 ICKMLLYGASLELPTHQGTPLHL-----AAYKGHL-EIIHLLA 613
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 674 SVINLEHHANVHARNKVGWTPAHLAALKGNATLKVLEAGAQLDVQDQVGSCTPLQL 731

RESULT 15
US-11-317-329-41
; Sequence 41, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; PRIORITY FILING DATE: 2005-12-22
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-41

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 245 KSAIDLAP----TPQKERLAYEFKSHLSLQAAREADVTRIKKHLSEMNFKHPQTHET 300
Db 338 KRALQSDRKNLVRDEELCTIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
Qy 301 ALHCAASPYPKQICELLRKANINEKTEFLTPLVASEKAKNDVVEVVVKEAKV 360
Db 387 DVDCQTASGY-----TPLLIAAQOQPDLCALLAHGADA 421
Qy 361 NALDNLGQTSIHRAAYCGHLQTCRLLSYGCDPNIIISLQGFALQMGNNVQQLQEGIS 420
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DNLREAEKG--TPLHVAAYFGHVSLLVLLT 514
Qy 481 OHGADVHAKOGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAKGYE 540
Db 515 SQGAELDAQORNLRTPHLAVERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGYL 574
Qy 541 ICKLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGAALDAAKKGCLARVKKLSS 600
Db 575 ICKMLLYGASLELPTHQGTPLHL-----AAYKGHL-EIIHLLA 613
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 674 SVINLEHHANVHARNKVGWTPAHLAALKGNATLKVLEAGAQLDVQDQVGSCTPLQL 731

```

Search completed: December 18, 2006, 18:01:20

Job time : 39.6529 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:21:00 ; Search time 162.464 Seconds
(without alignments)
3489.682 Million cell updates/sec

Title: US-10-616-101-4
Perfect score: 6464
Sequence: 1 RCSARRGAAGGQAGRGARV.....AYPEYLITYQIMRPGMVDG 1240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6464	100.0	1240	4 AAY97749	Aay97749 Tankyrase
2	6464	100.0	1240	6 ABG73731	Abg73731 Tankyrase
3	6464	100.0	1240	7 ADH69406	Adh69406 Human tan
4	6464	100.0	1240	9 ADY97762	Ady97762 Human tan
5	6375.5	98.6	1262	4 AAB66290	Aab66290 Human tan
6	6375.5	98.6	1287	8 ADR66429	Adr66429 Human pro
7	6375.5	98.6	1287	8 ADR66087	Adr66087 Human pro
8	6375.5	98.6	1385	4 AAB66294	Aab66294 Human tan
9	6121	94.7	1169	4 AAB66288	Aab66288 Human tan
10	6121	94.7	1169	4 AAB66278	Aab66278 Human tan
11	6108	94.5	1166	4 AAB66295	Aab66295 Human tan
12	6108	94.5	1166	8 ADR14792	Adr14792 Amino aci
13	6092	94.2	1166	3 ADR27211	Adr27211 Human tan
14	6088	94.2	1166	5 ABP69457	Abp69457 Human pol
15	6053	93.6	1166	4 AAY72589	Aay72589 Human tan
16	5766	89.2	1100	4 AAY97748	Aay97748 Tankyrase
17	5766	89.2	1100	6 ABG73732	Abg73732 Tankyrase
18	5766	89.2	1100	6 ABG73730	Abg73730 Tankyrase
19	5766	89.2	1100	7 ADH69405	Adh69405 Human tan
20	5766	89.2	1100	9 ADY97766	Ady97766 Human tan
21	5760	89.1	1100	6 ABG73735	Abg73735 Tankyrase
22	5760	89.1	1100	9 ADY97769	Ady97769 Human tan
23	5658	87.5	1084	6 ABG73736	Abg73736 Tankyrase

24	5656	87.5	1083	9	ADY97770	Ady97770 Human tan
25	5605	86.7	1074	2	AAV05734	Aay05734 Human Grb
26	5582	86.4	1065	9	ADY97761	Ady97761 Human tan
27	5543	85.8	1166	4	AAB47022	Aab47022 Human SPA
28	5474	84.7	1431	3	AAB27210	Aab27210 Human tan
29	5303.5	82.0	1083	6	AAE35352	Aae35352 Human col
30	5103.5	79.0	1327	3	AAV44402	Aay44402 Human tan
31	5103.5	79.0	1327	3	AAV44402	Aay44402 Human tan
32	5103.5	79.0	1327	4	AAB66279	Aab66279 Human tan
33	5103.5	79.0	1327	5	AAU79537	Aau79537 Human tan
34	5103.5	79.0	1327	8	ADR14791	Adr14791 Amino aci
35	5040.5	78.0	1333	3	AAB27209	Aab27209 Human tan
36	5038.5	77.9	991	4	AAB47023	Aab47023 Mouse SPA
37	4624.5	71.5	907	4	AAB48574	Aab48574 Human bre
38	4102	63.5	784	4	AAB66285	Aab66285 Human tan
39	4005	62.0	1181	4	ABB60894	Abb60894 Drosophil
40	3997	61.8	1181	4	AAB66297	Aab66297 Drosophil
41	3959	61.2	756	4	AAB66286	Aab66286 Human tan
42	3938	60.9	802	5	AAO20512	Aao20512 Protein o
43	3307	51.2	949	3	RAY44404	Aay44404 Human tru
44	3307	51.2	949	5	AAU79539	Aau79539 Truncated
45	2913	45.1	583	9	ADY97768	Ady97768 Human tan

ALIGNMENTS

RESULT 1
AAY97749
ID AAY97749 standard; protein; 1240 AA.
XX
AC AAY97749;
XX
DT 06-AUG-2001 (first entry)
XX
DE Tankyrase homologue. isotype 2 protein sequence.

XX Tankyrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation;
KW cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
KW chromosome mapping; gene therapy; vaccine.
XX Unidentified.
XX WO200130987-A2.
XX PD 03-MAY-2001.
XX PF 25-OCT-2000; 2000WO-US041528.
XX PR 25-OCT-1999; 99US-00427154.
XX (RIGE-) RIGEL PHARM INC.

XX Luo Y, Chan E, Xu X, Huang B;
WPI; 2001-300503/31.
XX N-PSDB; AA91488.

XX Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing
or preventing cell proliferation in cells, and for diagnosing, treating
or preventing cell cycle associated disorders such as cancer.

XX Claim 22; Fig 4; 63pp; English.

XX This sequence is the Tankyrase homologue isotype 2 (TaHo-2) protein of
the invention. The invention also relates to the TaHo-2 protein. The TaHo
proteins are useful for inducing or preventing cell proliferation in
cells, and in the study or treatment of conditions mediated by the cell
cycle proteins, such as to diagnose, treat or prevent cell cycle
associated disorders, preferably cancer. The TaHo coding sequences are
useful as hybridisation probes, in chromosome and gene mapping and in the
generation of anti-sense DNA and RNA. The coding sequences are also
useful for the preparation of TaHo, for generating either transgenic

CC	animals or knock out animals which, in turn, are useful in a development
CC	and screening of therapeutically useful agents, in gene therapy, as
CC	vaccine, and for construction of hybridisation probes for mapping the
CC	gene which encodes TaHo and for the genetic analysis of individuals with
CC	genetic disorders. The TaHo proteins, and their coding sequences are
CC	useful in screening assays
XX	
XX	
SQ	Sequence 1240 AA;
	Query Match
	Best Local Similarity 100.0%; Score 6464; DB 4; Length 1240;
	Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RCSARRGAGCGAQRGARVGAAGHTAPDPVTAGQAARALASASSPGGLALLAGPGLLL 60
DB	1 RCSARRGAGCGAQRGARVGAAGHTAPDPVTAGQAARALASASSPGGLALLAGPGLLL 60
QY	61 RLLALLLAAVAARIMSGRCAGGGAACAASAAEAVEPAARELFEACRNGDVERVRLVTP 120
DB	61 RLLALLLAAVAARIMSGRCAGGGAACAASAAEAVEPAARELFEACRNGDVERVRLVTP 120
QY	121 EKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFGEAEV 180
DB	121 EKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFGEAEV 180
QY	181 VNLLRHGADPNARDNWNYPPLHEAAIKGKIDVCIVLLOHGAEPTRINTDGTALDLADP 240
DB	181 VNLLRHGADPNARDNWNYPPLHEAAIKGKIDVCIVLLOHGAEPTRINTDGTALDLADP 240
QY	241 SAKAVLTGEYKDELESARSNGEKMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKI 300
DB	241 SAKAVLTGEYKDELESARSNGEKMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKI 300
QY	301 VQLLQHGADVHAKDGLVPLHNACSYGHYEVTELLVKHGACVNMALMQPTPLHEAAS 360
DB	301 VQLLQHGADVHAKDGLVPLHNACSYGHYEVTELLVKHGACVNMALMQPTPLHEAAS 360
QY	361 KNRVECSLLSYGADPTLLNCHNKSADLAPTPQIKERLAYEFKGHSLLOQAREADVTR 420
DB	361 KNRVECSLLSYGADPTLLNCHNKSADLAPTPQIKERLAYEFKGHSLLOQAREADVTR 420
QY	421 IKKHLSLEWVNFKHPQTHETALHCAASAPYPRKQICELLRLKGANINEKTEFTPLHV 480
DB	421 IKKHLSLEWVNFKHPQTHETALHCAASAPYPRKQICELLRLKGANINEKTEFTPLHV 480
QY	481 ASEKAHNDVVEVVVKEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQ 540
DB	481 ASEKAHNDVVEVVVKEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQ 540
QY	541 FTALQNGHENVQQLLOEGISLGNSEADROLLEAAKAGDVETVKCLCTVQSVNCRDIEGRQ 600
DB	541 FTALQNGHENVQQLLOEGISLGNSEADROLLEAAKAGDVETVKCLCTVQSVNCRDIEGRQ 600
QY	601 STPLHFAAGYNNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHVEVAELLVKGAANN 660
DB	601 STPLHFAAGYNNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHVEVAELLVKGAANN 660
QY	661 VADLWKFTPLHEAAAKGYEICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGD 720
DB	661 VADLWKFTPLHEAAAKGYEICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGD 720
QY	721 AALLDAAKGCCLARVKLSPPNVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADYN 780
DB	721 AALLDAAKGCCLARVKLSPPNVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADYN 780
QY	781 AQDKGGLIPLHNAASVGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRQLCALLLA 840
DB	781 AQDKGGLIPLHNAASVGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRQLCALLLA 840
QY	841 HGADPTLKNQEGQTPDLVLSADVSALLTAAMPSPALPSCYKPOVLNVRSPGATADALS 900
DB	841 HGADPTLKNQEGQTPDLVLSADVSALLTAAMPSPALPSCYKPOVLNVRSPGATADALS 900

QY	901 SGPSPSSLSAASSLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLG 960
DB	901 SGPSPSSLSAASSLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLG 960
QY	961 LEHLMDFERSQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLLISGQOGLNPYLT 1020
DB	961 LEHLMDFERSQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLLISGQOGLNPYLT 1020
QY	1021 NTSGSGTILIDLSPDDKEFQSVVEEEMQSTVRHRDGHAGGIFNRYNLIKIKVCNKKLW 1080
DB	1021 NTSGSGTILIDLSPDDKEFQSVVEEEMQSTVRHRDGHAGGIFNRYNLIKIKVCNKKLW 1080
QY	1081 ERYTHRRKEVSEENHNHANERMLFHGSPFVNAI IHKGFDERHAYIGCMFGAGIYFAENSS 1140
DB	1081 ERYTHRRKEVSEENHNHANERMLFHGSPFVNAI IHKGFDERHAYIGCMFGAGIYFAENSS 1140
QY	1141 KSNQVYVIGGGTGPCVHKDRSCYI CHROLLPFCRVTLGKSFLOFSAMKMAHSPPGHHSVT 1200
DB	1141 KSNQVYVIGGGTGPCVHKDRSCYI CHROLLPFCRVTLGKSFLOFSAMKMAHSPPGHHSVT 1200
QY	1201 GRPSVNGLALAEYVYIRGEQAYPEYLITYQIMRPEGMVDG 1240
DB	1201 GRPSVNGLALAEYVYIRGEQAYPEYLITYQIMRPEGMVDG 1240
RESULT 2	
ID	ABG73731 standard; protein; 1240 AA.
XX	ABG73731;
XX	08-APR-2003 (first entry)
DE	Tankyrase H isotype 2 TaHo-2 fragment from clone K23.
KW	Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2;
KW	TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
KW	cell cycle related disorder; poly ADP-ribose polymerase; PARP.
OS	Unidentified.
XX	WO200286170-A1.
PN	31-OCT-2002.
PD	
XX	25-APR-2002; 2002WO-US013185.
PF	
XX	25-APR-2001; 2001US-00843159.
PR	(RIGE-) RIGEL PHARM INC.
PA	
XX	Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
PI	
XX	WPI; 2003-093158/08.
DR	N-PSDB; ABQ77067.
XX	
PT	New recombinant nucleic acid encoding a cell cycle protein, useful for
PT	diagnosing and treating a cell cycle related disorder, e.g. cancer.
XX	
PS	Claim 14; Fig 4; 90pp; English.
XX	
CC	This invention describes a novel recombinant nucleic acid encoding the
CC	cell cycle protein TaHo, a tankyrase H isoform. The products of the
CC	invention have cytostatic and immunostimulant activity and can be used
CC	for gene therapy and in vaccines. The cell cycle protein TaHo and the
CC	nucleic acid encoding the protein are useful for diagnosing and treating
CC	a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
CC	tumour cell. The methods are useful for screening for a bioactive agent
CC	capable of binding to a cell cycle protein tankyrase H, or a bioactive
CC	agent capable of modulating a cell cycle protein tankyrase H or PARP
CC	(poly ADP-ribose polymerase) activity. The antibodies are useful for
CC	inducing an immune response against the cell cycle proteins. This
CC	sequence represents the tankyrase H isoform 2, TaHo-2, isolated from

CC clone K23 which is described in the disclosure of the invention

XX SQ Sequence 1240 AA;

Query Match 100.0%; Score 6464; DB 6; Length 1240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCSARRGAAGGCGAORGARVGAAGTADPDVVTAGSQAARALSSASPGGLALLAGPGLLL 60
DB 1 RCSARRGAAGGCGAORGARVGAAGTADPDVVTAGSQAARALSSASPGGLALLAGPGLLL 60
QY 61 RLLALLAVAAARIMSGRRCCAGGACASAAAEVPAARELFACRNGDVERVRLVTP 120
DB 61 RLLALLAVAAARIMSGRRCCAGGACASAAAEVPAARELFACRNGDVERVRLVTP 120
QY 121 EKVSRRDTAGRKSTPLHFAAGFRKDVVEYLLQNGANVOARDGGLIPLHNACSFHAEV 180
DB 121 EKVSRRDTAGRKSTPLHFAAGFRKDVVEYLLQNGANVOARDGGLIPLHNACSFHAEV 180
QY 181 VNLRLRHGADPNARDNNWYTPLHAAIKGKIDVICIVLQHGAEPTIRNTDGR TALDLADP 240
DB 181 VNLRLRHGADPNARDNNWYTPLHAAIKGKIDVICIVLQHGAEPTIRNTDGR TALDLADP 240
QY 241 SAKAVLTGEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHAAAGYNNVKI 300
DB 241 SAKAVLTGEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHAAAGYNNVKI 300
QY 301 VOLLLQHGDVHAKDKGDLVPLHNACSYGHEVTELLVKGHCACVNMADLQFTPLHEAAS 360
DB 301 VOLLLQHGDVHAKDKGDLVPLHNACSYGHEVTELLVKGHCACVNMADLQFTPLHEAAS 360
QY 361 KNRVEVCSLLSYGADPTLLNCHNSAIDLAPTPOLKERLAYEFKHSILQAAAREADVTR 420
DB 361 KNRVEVCSLLSYGADPTLLNCHNSAIDLAPTPOLKERLAYEFKHSILQAAAREADVTR 420
QY 421 IKKHLSEWVNFKHPQTHETALHCAAAPYKPKQICELLRLKGANINEKTEFETPLHV 480
DB 421 IKKHLSEWVNFKHPQTHETALHCAAAPYKPKQICELLRLKGANINEKTEFETPLHV 480
QY 481 ASEKAHNDVVEVVKHAKVNALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIISLQ 540
DB 481 ASEKAHNDVVEVVKHAKVNALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIISLQ 540
QY 541 FTALQMGNEVQQLLOEGISLGNSEADQLLEAKAGDVETVKKLTCTVQVNCRDIEGRQ 600
DB 541 FTALQMGNEVQQLLOEGISLGNSEADQLLEAKAGDVETVKKLTCTVQVNCRDIEGRQ 600
QY 601 STPLHFAAGYNNRVSVEVYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVN 660
DB 601 STPLHFAAGYNNRVSVEVYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVN 660
QY 661 VADLWKFTPLHAAAKGYEICKLLQHGADPTKKNRGDNTPLDVKDGDITDIDLLRGD 720
DB 661 VADLWKFTPLHAAAKGYEICKLLQHGADPTKKNRGDNTPLDVKDGDITDIDLLRGD 720
QY 721 AALLDAKKGCLARVKKLSPPDNVNCRTQGRHSTPLHAAAGYNNLEVAEYLLQHGADV 780
DB 721 AALLDAKKGCLARVKKLSPPDNVNCRTQGRHSTPLHAAAGYNNLEVAEYLLQHGADV 780
QY 781 AQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHAAAKGRTQLCALLA 840
DB 781 AQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHAAAKGRTQLCALLA 840
QY 841 HGADPTLKNQEGQTPDLVSDADDVSALLTAAMPSPALPSCKYKQVNLGVRSPGATADALS 900
DB 841 HGADPTLKNQEGQTPDLVSDADDVSALLTAAMPSPALPSCKYKQVNLGVRSPGATADALS 900
QY 901 SGPSPSSLSAASSLDNLSGFSFSELSVSVSSGTEGASLEKEVPGVDFSTQVRLNG 960
DB 901 SGPSPSSLSAASSLDNLSGFSFSELSVSVSSGTEGASLEKEVPGVDFSTQVRLNG 960
QY 961 LEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTL 1020

DB 961 LEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTL 1020
QY 1021 NTSGSGTILIDLSDDKEFQSVBEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLW 1080
DB 1021 NTSGSGTILIDLSDDKEFQSVBEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLW 1080
QY 1081 ERYTHRRKEVSEENHNHANERMLPHGSPFVNAIHKGFDERHAYIGGMFGAGIYFAENSS 1140
DB 1081 ERYTHRRKEVSEENHNHANERMLPHGSPFVNAIHKGFDERHAYIGGMFGAGIYFAENSS 1140
QY 1141 KSNQVYVIGGGTGPCVHKDRSCYICHRQLLFCRVTLTKSFLQFSAMQVAHSPPGHHSVT 1200
DB 1141 KSNQVYVIGGGTGPCVHKDRSCYICHRQLLFCRVTLTKSFLQFSAMQVAHSPPGHHSVT 1200
QY 1201 GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGMVDG 1240
DB 1201 GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGMVDG 1240

RESULT 3
ADH69406

ID ADH69406 standard; protein; 1240 AA.

XX AC ADH69406;

XX DT 25-MAR-2004 (first entry)

XX DE Human tankyrase homologue isotype 2 (TaHo-2).

XX KW Tankyrase H cell cycle protein; p21; gene therapy;

XX KW bioactive agent screening; cancer; cytostatic; human.

XX OS Homo sapiens.

XX PN US6617102-B1.

XX PD 09-SEP-2003.

XX PF 25-OCT-2000; 2000US-00696668.

XX PR 25-OCT-1999; 99US-00427154.

XX PA (RIGE-) RIGEL PHARM INC.

XX PI Luo Y, Chan E, Xu X, Huang B, Ososovskaya V;

XX DR WPI; 2003-895391/82.

XX DR N-PSDB; ADH69415.

XX PT Screening for a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21 for diagnosing or treating cancer by combining a tankyrase H cell cycle protein, a candidate bioactive agent and p21.

XX PS Claim 1; SEQ ID NO 4; 39pp; English.

XX CC The invention relates to a method for screening a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21. The invention is useful in gene therapy. The method is useful for screening for a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21 for preparing a composition for diagnosing or treating cancer. the present sequence is human tankyrase homologue isotype 2 (TaHo-2).

XX SQ Sequence 1240 AA;

Query Match 100.0%; Score 6464; DB 7; Length 1240;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCSARRGAAGGCGAORGARVGAAGTADPDVVTAGSQAARALSSASPGGLALLAGPGLLL 60

Db 1 RCSARRGAGGQAGQAGARVGAAGTAPDPVTVTAGSQAARALSSAPGGALLALLGPGGLLL 60
Qy 61 RLALLLAVAAARIMSGRCAGGGAA CASAAAEAVEPAARELFEACRNGDVERVKRLVTP 120
Db 61 RLALLLAVAAARIMSGRCAGGGAA CASAAAEAVEPAARELFEACRNGDVERVKRLVTP 120
Qy 121 EKNSRDTAGRKSTPLHFAAGGRKDVVEYLLONGANVOARDGGGLIPLHNACSPGHAEV 180
Db 121 EKNSRDTAGRKSTPLHFAAGGRKDVVEYLLONGANVOARDGGGLIPLHNACSPGHAEV 180
Qy 181 VNLLRHGADPNARDNWNVTPLHEAAIKGIDVICIVLLQHGAEPTIRNTDGR TALDLADP 240
Db 181 VNLLRHGADPNARDNWNVTPLHEAAIKGIDVICIVLLQHGAEPTIRNTDGR TALDLADP 240
Qy 241 SAKAVLTGYKKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 300
Db 241 SAKAVLTGYKKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 300
Qy 301 VOLLQHGADVHAKDKGDLVPLHNACSYGHYEVTPELLVKGACVNMMDLWQFTPLHEAAS 360
Db 301 VOLLQHGADVHAKDKGDLVPLHNACSYGHYEVTPELLVKGACVNMMDLWQFTPLHEAAS 360
Qy 361 KNRVECSLLLSYGADPTLLNCHNKSAIDLPTPOLKERLAYEFKGHSLLOAAREADVTR 420
Db 361 KNRVECSLLLSYGADPTLLNCHNKSAIDLPTPOLKERLAYEFKGHSLLOAAREADVTR 420
Qy 421 IKKHLSELMVNFKQPTHETALHCAAAAPYKPKQICELLLRKGANINKEFTPLPHV 480
Db 421 IKKHLSELMVNFKQPTHETALHCAAAAPYKPKQICELLLRKGANINKEFTPLPHV 480
Qy 481 ASEKAHNDVVEVVKHEAKVNALDNLGQTSLSHRAAYCGHLQTCRLLLSYGCDDPNTISLQ 540
Db 481 ASEKAHNDVVEVVKHEAKVNALDNLGQTSLSHRAAYCGHLQTCRLLLSYGCDDPNTISLQ 540
Qy 541 FTALQMGNEVVOQLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
Db 541 FTALQMGNEVVOQLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
Qy 601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAVVN 660
Db 601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAVVN 660
Qy 661 VADLWKFTPLHEAAAKGKYEICKLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLRGD 720
Db 661 VADLWKFTPLHEAAAKGKYEICKLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLRGD 720
Qy 721 AALLDAAKKGCLARVKKLSPPDNVNCRDQTGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
Db 721 AALLDAAKKGCLARVKKLSPPDNVNCRDQTGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
Qy 781 AQDKGGLIPLHNAASYGHVDVAALLIKYNACVNAIDKWAFTPLHEAAQKGRTOCALLLA 840
Db 781 AQDKGGLIPLHNAASYGHVDVAALLIKYNACVNAIDKWAFTPLHEAAQKGRTOCALLLA 840
Qy 841 HGADPTLKNQEGOTPLDLVSADVDVSAALLTAAMPSPALPCYKPOVLNGVRSFGATADALS 900
Db 841 HGADPTLKNQEGOTPLDLVSADVDVSAALLTAAMPSPALPCYKPOVLNGVRSFGATADALS 900
Qy 901 SQPSPSSLSAASLDNLGSGFSELSSVSSVSSGTEGASLEKKEVPGVDFSTQFVRNLG 960
Db 901 SQPSPSSLSAASLDNLGSGFSELSSVSSVSSGTEGASLEKKEVPGVDFSTQFVRNLG 960
Qy 961 LEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTL 1020
Db 961 LEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTL 1020
Qy 1021 NTSGSGTLLIDLSPPDKERQSVSEEMQSVREHRCGGHAGGIFNRYNLIKIQKVCNKKLW 1080
Db 1021 NTSGSGTLLIDLSPPDKERQSVSEEMQSVREHRCGGHAGGIFNRYNLIKIQKVCNKKLW 1080
Qy 1081 ERYTHRRKEVSENNHANERMLFHGSPFNVAIIHKGFDERHAYIGGMFGAGIYFAENSS 1140
Db 1081 ERYTHRRKEVSENNHANERMLFHGSPFNVAIIHKGFDERHAYIGGMFGAGIYFAENSS 1140

Qy 1141 KSNQYVYIGGGTGGCPVHKDRSCYICHRQLLCFVRTLIGKSFLOFSAMKMAHSPGHHSVT 1200
Db 1141 KSNQYVYIGGGTGGCPVHKDRSCYICHRQLLCFVRTLIGKSFLOFSAMKMAHSPGHHSVT 1200
Qy 1201 GRPSVNLALAEVYIYRGEOAYPEYLITYQIMRPEGMDVG 1240
Db 1201 GRPSVNLALAEVYIYRGEOAYPEYLITYQIMRPEGMDVG 1240

RESULT 4

ADY97762
ID ADY97762 standard; protein; 1240 AA.

XX ADY97762;

XX AC ADY97762;

XX DT 16-JUN-2005 (first entry)

XX DE Human tankyrase homologue isotype 2 protein SEQ ID NO:4.

XX KW cell cycle; cancer; cytostatic; tankyrase homologue isotype 2.

XX OS Homo sapiens.

XX PN US2005074825-A1.

XX PD 07-APR-2005.

XX PF 08-JUL-2003; 2003US-00616101.

XX PR 25-OCT-1999; 99US-00427154.

XX PR 25-OCT-2000; 2000US-00696668.

XX PR 25-APR-2001; 2001US-00843159.

XX PA (LUOY/) LUO Y.

XX PA (CHAN/) CHAN E.

XX PA (XUX/) XU X.

XX PA (HUAN/) HUANG B.

XX PA (OSSO/) OSSOVSKAYA V.

XX PI Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;

XX WPI; 2005-294737/30.

XX N-PSDB; ADY97760.

XX PT Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase

XX PS homolog, useful for screening its modulator.

XX PS Claim 21; SEQ ID NO 4; 75pp; English.

XX CC The invention relates to a recombinant polypeptide (I) such as cell cycle protein e.g. tankyrase homologue (TaHo), comprising an amino acid sequence having 85% or more sequence identity to the 1065 amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also described: (1) diagnosing cancer, which involves determining the activity of (I) from a test sample of an individual and comparing the level with a control with a control; (2) treating (M1) an individual with a cell cycle related disorder, which involves administering to the individual an inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I), comprising a nucleic acid that hybridizes under high stringent conditions to a sequence complementary to the 3797 base pair sequence of ADY97760, or a nucleic acid having 85% or more sequence identity to ADY97759 or ADY97760; (4) an expression vector (III) comprising (II) operably linked to regulatory sequences recognized by a host cell (IV) transformed with the nucleic acid; (5) a host cell comprising (II) or (III); (6) producing (I); (7) a polypeptide that specifically binds to (I); and (8) inhibiting (M2) growth of a tumor cell, involves contacting the tumor with a bioactive agent capable of inhibiting TaHo activity. (I) is useful for screening a bioactive agent capable of modulating (I), or screening for agents capable of interfering with the binding of (I) and P21. (M1) is useful for treating an individual with a cell cycle related disorder. (M2) is useful for inhibiting growth of a tumor cell by a bioactive agent e.g. antisense

CC	oligonucleotide. The present sequence represents the human tankyrase	
CC	homologue isotype 2.	
XX		
Sequence 1240 AA;		
Query Match	100.0%; Score 6464; DB 9; Length 1240;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1240; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	RCSARRGAAGCGGAGRGARVGAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLL 60
Db	1	RCSARRGAAGCGGAGRGARVGAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLL 60
Qy	61	RLALLAVAAARIMSGRRRCAGGGAACASAAAEVPAARELFACRNGDVERVKRLVTP 120
Db	61	RLALLAVAAARIMSGRRRCAGGGAACASAAAEVPAARELFACRNGDVERVKRLVTP 120
Qy	121	EKNSRDTAGRKSTPLHPAAGFGKDVVYLLQNGANVQARDGGLIPLHNACSFHAEV 180
Db	121	EKNSRDTAGRKSTPLHPAAGFGKDVVYLLQNGANVQARDGGLIPLHNACSFHAEV 180
Qy	181	VNLLRHGADPNARDNNYTPLHAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDLADP 240
Db	181	VNLLRHGADPNARDNNYTPLHAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDLADP 240
Qy	241	SAKAVLTGEYKDELLSARGSEKEMWALLTPNVNCHASDGRKSTPLHLAGVNRVKI 300
Db	241	SAKAVLTGEYKDELLSARGSEKEMWALLTPNVNCHASDGRKSTPLHLAGVNRVKI 300
Qy	301	VQLLQHGADVHAKDGDVPLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAAS 360
Db	301	VQLLQHGADVHAKDGDVPLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAAS 360
Qy	361	KNRVECSLLSYGADPTLLCHNKSADIDAPTQLKERLAYEPKSHLSLQAAEADVTR 420
Db	361	KNRVECSLLSYGADPTLLCHNKSADIDAPTQLKERLAYEPKSHLSLQAAEADVTR 420
Qy	421	IKHLSLEWVNFHPOTHETALHCAASPYPKRKQICELLURKGANINEKTEFLTPHV 480
Db	421	IKHLSLEWVNFHPOTHETALHCAASPYPKRKQICELLURKGANINEKTEFLTPHV 480
Qy	481	ASEKAHNDVVEVVKHAKVNALNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQ 540
Db	481	ASEKAHNDVVEVVKHAKVNALNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQ 540
Qy	541	FTALQMGNEVQQLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
Db	541	FTALQMGNEVQQLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
Qy	601	STPLHFAAGVNRVSVVEYLLQHGADVHAKDGGVPLHNACSYGHEVVAELLVKHGAVN 660
Db	601	STPLHFAAGVNRVSVVEYLLQHGADVHAKDGGVPLHNACSYGHEVVAELLVKHGAVN 660
Qy	661	VADLWKTPLHEAAKGYEICKLLQHGADPTKKNRDGNTPDLVKDGDITDIQLLRGD 720
Db	661	VADLWKTPLHEAAKGYEICKLLQHGADPTKKNRDGNTPDLVKDGDITDIQLLRGD 720
Qy	721	AALLDAKKGCLARVKLSSPDNNVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADV 780
Db	721	AALLDAKKGCLARVKLSSPDNNVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADV 780
Qy	781	AQDKGGLIPLHNAAGYHVDVAALLIKYNACVNATDKWAFPLHEAAKQGTQICALLA 840
Db	781	AQDKGGLIPLHNAAGYHVDVAALLIKYNACVNATDKWAFPLHEAAKQGTQICALLA 840
Qy	841	HGADPTLKNQEGQTPDLVSDADDVALLTAAMPSPALPSCYKQVNLGVRSPGATADALS 900
Db	841	HGADPTLKNQEGQTPDLVSDADDVALLTAAMPSPALPSCYKQVNLGVRSPGATADALS 900
Qy	901	SGPSSPSLSAASLDNLGSGFSLSVSSSGTEGASSLEKKEVPVDFSIQFVRNLG 960
Db	901	SGPSSPSLSAASLDNLGSGFSLSVSSSGTEGASSLEKKEVPVDFSIQFVRNLG 960

Qy	961	LEHLMDFIEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTL 1020
Db	961	LEHLMDFIEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTL 1020
Qy	1021	NTSGSGTILDLSPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTIKTKQVCNKKLW 1080
Db	1021	NTSGSGTILDLSPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTIKTKQVCNKKLW 1080
Qy	1081	ERYTHRRKEVSEENHNHANERMLPHGSPFVNAIITHKGFDERHAYIGMGFAGIYFAENSS 1140
Db	1081	ERYTHRRKEVSEENHNHANERMLPHGSPFVNAIITHKGFDERHAYIGMGFAGIYFAENSS 1140
Qy	1141	KSNQYVYGIGGGTGCPCVHKDRSCYICHRQLLFCRVTLGKSLQFSAMMAHSPPGHHSVT 1200
Db	1141	KSNQYVYGIGGGTGCPCVHKDRSCYICHRQLLFCRVTLGKSLQFSAMMAHSPPGHHSVT 1200
Qy	1201	GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGWVDG 1240
Db	1201	GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGWVDG 1240
RESULT 5		
AAB66290		
ID	AAB66290	standard; protein; 1262 AA.
XX	AC	AAB66290;
XX	AC	AAB66290;
DT	05-APR-2001	(first entry)
XX		
DE		Human tankyrase2 clone consensus protein SEQ ID NO: 107.
XX		
KW		Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
KW		inflammatory disorder.
OS		Homo sapiens.
PN	WO200100849-A1.	
XX		
PD	04-JAN-2001.	
XX		
PF	28-JUN-2000; 2000WO-US017827.	
XX		
PR	29-JUN-1999; 99US-0141582P.	
XX		
PA	(ICOS-) ICOS CORP.	
XX		
PI	Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;	
XX		
DR	WPI; 2001-102896/11.	
XX	N-PSDB; AAF63930.	
DR		
XX		
PT	New tankyrase2 polypeptides, useful for treating conditions mediated by	
PT	poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,	
PT	inflammatory and autoimmune disorders.	
XX		
PS	Example 2; Page 173-176; 242pp; English.	
XX		
CC	The present invention provides the protein and coding sequence for the	
CC	human tankyrase2 protein. This is found in two different versions,	
CC	designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-	
CC	ribosylation activity and is involved in the modification of TRF1, which	
CC	is a telomere-specific binding protein. The regulation of telomere	
CC	length, in which TRF1 has a role, is linked to ageing and cancer. The	
CC	sequences are useful in the treatment of cancers and inflammatory	
CC	disorders	
XX		
SQ	Sequence 1262 AA;	
Query Match	98.6%; Score 6375.5; DB 4; Length 1262;	
Best Local Similarity	99.2%; Pred. No. 0;	
Matches 1225; Conservative	1; Mismatches 8; Indels 1; Gaps 1;	
Qy	6	RGAAGGAGRGARVGAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLLRLAL 65

Db 29 RGRGAGSPARGAR-GRGHGTAPDPVTAGSQARALASSPGGLALLAGFGLLRLLAL 87
Qy 66 LLAAVAARIMSGRRGAGGAAACASAAABEPAARELFEACRNGDVERKRLVTPKYNs 125
Db 88 LLAAVAARIMSGRRGAGGAAACASAAABEPAARELFEACRNGDVERKRLVTPKYNs 147
Qy 126 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGVQARDGGGLPLHNACSPGHAEVNNLL 185
Db 148 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGVQARDGGGLPLHNACSPGHAEVNNLL 207
Qy 186 RHGADPNARDNNWYTPLEAAIKGKIDVICIVLLQHGAEPTIRNTDERTALDOLADPSAKAV 245
Db 208 RHGADPNARDNNWYTPLEAAIKGKIDVICIVLLQHGAEPTIRNTDERTALDOLADPSAKAV 267
Qy 246 LTGEYKDDLEESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 305
Db 268 LTGEYKDDLEESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 327
Qy 306 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNAWMDLWQFTPLHEAASKNRVE 365
Db 328 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNAWMDLWQFTPLHEAASKNRVE 387
Qy 366 VCSLLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEFKGHSLLQAAAREADVTRIKKHL 425
Db 388 VCSLLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEFKGHSLLQAAAREADVTRIKKHL 447
Qy 426 SLEMYNFKHPOTHETALHCAAASPYPRKQICELELLRKGANINEKTEFLTPLHVASEKA 485
Db 448 SLEMYNFKHPOTHETALHCAAASPYPRKQICELELLRKGANINEKTEFLTPLHVASEKA 507
Qy 486 HNDVVEVVVKGHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQFTALQ 545
Db 508 HNDVVEVVVKGHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQFTALQ 567
Qy 546 MGENNVQQLQEGISLGENSEADROLLEAAKAGDVETVKLCVQSVNCRDIEGRSTPLH 605
Db 568 MGENNVQQLQEGISLGENSEADROLLEAAKAGDVETVKLCVQSVNCRDIEGRSTPLH 627
Qy 606 FAAGYNRVSVVEYLLQHGADVHAKDGGVLPLHNACSYGHEVTELLVKGAGVAVNVADLW 665
Db 628 FAAGYNRVSVVEYLLQHGADVHAKDGGVLPLHNACSYGHEVTELLVKGAGVAVNVADLW 687
Qy 666 KFTPLHEAAAGKYEIKCLLQHGADPTKKNRDGNTPLDLVKDGTDTQDLLRGDAALLD 725
Db 688 KFTPLHEAAAGKYEIKCLLQHGADPTKKNRDGNTPLDLVKDGTDTQDLLRGDAALLD 747
Qy 726 AAKGCLARVKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785
Db 748 AAKGCLARVKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 807
Qy 786 GLIPLHNAASGHVDVAALLIKYNACVNAATKWAFTPLHEAAQKGRTOQLCALLAHGADP 845
Db 808 GLIPLHNAASGHVDVAALLIKYNACVNAATKWAFTPLHEAAQKGRTOQLCALLAHGADP 867
Qy 846 TLKNOEGTDLVADDDVALLTAMPSPALPCYKQVNLNVGRSPGNATDALSPPSS 905
Db 868 TLKNOEGTDLVADDDVALLTAMPSPALPCYKQVNLNVGRSPGNATDALSPPSS 927
Qy 906 PSSLSAASLNLGSGFSELSSVSSSGTEGASSLEKKEVPGVDFSITQFVNLGLHELM 965
Db 928 PSSLSAASLNLGSGFSELSSVSSSGTEGASSLEKKEVPGVDFSITQFVNLGLHELM 987
Qy 966 DIFEREQITDLVIVMGHKLKEIGINAYGHRHKLIKGVERLISQOQGLNPLYTLNTSGS 1025
Db 988 DIFEREQITDLVIVMGHKLKEIGINAYGHRHKLIKGVERLISQOQGLNPLYTLNTSGS 1047
Qy 1026 GTILIDLSPDDKEFOSVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCKNKLWERYTH 1085
Db 1048 GTILIDLSPDDKEFOSVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCKNKLWERYTH 1107
Qy 1086 RRKEYSEENHNHNERMLPHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSCKSNQY 1145

Db 1108 RRKEYSEENHNHNERMLPHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSCKSNQY 1167
Qy 1146 VYIGGGTGCPCPHKDRSCYICHRQLLCFVYTLGKFLQFSAMKMAHSPGHHSVTGRPSV 1205
Db 1168 VYIGGGTGCPCPHKDRSCYICHRQLLCFVYTLGKFLQFSAMKMAHSPGHHSVTGRPSV 1227
Qy 1206 NGLALAEVYVYRGEQAYPEYLYTYQIMRPEGMVDG 1240
Db 1228 NGLALAEVYVYRGEQAYPEYLYTYQIMRPEGMVDG 1262
RESULT 6
ADR66429
ID ADR66429 standard; protein; 1287 AA.
XX ADR66429;
XX
DT 02-DEC-2004 (first entry)
XX Human prostatic carcinoma derived protein SEQ ID 283 #2.
DE human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.
XX Homo sapiens.
XX
PN WO2004076614-A2.
XX 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
XX (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
agents.
XX
PS Claim 2; Page 1266; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from

CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of a
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR5803-ADR6954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.

XX Sequence 1287 AA;

Query Match 38.6%; Score 6375.5; DB 8; Length 1287;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 6 RGAAGGGGAGRGVGAAGTADPVTAGSQARALSSAPGGGLALLLAGPGLLLALL 65
DB 54 RGRGAGSPARGAR-GRGHGTADPVTAGSQARALSSAPGGGLALLLAGPGLLLALL 112

QY 66 LLAVAAARIMSGRRACGGGAACASAAAEVPAARELFACRNGDVERVRLVTPKVN 125
DB 113 LLAVAAARIMSGRRACGGGAACASAAAEVPAARELFACRNGDVERVRLVTPKVN 172

QY 126 RDTAGRKSTPLHPFAAGGRKDVVEYLLQNGANVOARDGGLIPLHNACSGFHAENVNLL 185
DB 173 RDTAGRKSTPLHPFAAGGRKDVVEYLLQNGANVOARDGGLIPLHNACSGFHAENVNLL 232

QY 186 RHGADPNARDNNYTPLHEAAIKGIDVCTVLLQHGAEPTIRNDGRTALDLDADPSAKAV 245
DB 233 RHGADPNARDNNYTPLHEAAIKGIDVCTVLLQHGAEPTIRNDGRTALDLDADPSAKAV 292

QY 246 LTGEYKDKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 305
DB 293 LTGEYKDKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 352

QY 306 QHGADVHAKDGLVPLHNACSGHYEVTELLVKGHCACVNMADLWQFTPLHBAASKRVE 365
DB 353 QHGADVHAKDGLVPLHNACSGHYEVTELLVKGHCACVNMADLWQFTPLHBAASKRVE 412

QY 366 VCSLLSYGADPTLLNCHNSASDIDLATPQKRLAYEPKGSLLQAREADVTRIKKHL 425
DB 413 VCSLLSYGADPTLLNCHNSASDIDLATPQKRLAYEPKGSLLQAREADVTRIKKHL 472

QY 426 SLEWVNFKIPQTHETALHCAAAAPYPRKQICELLFRKGANINEKTEFLTPLHVASEKA 485
DB 473 SLEWVNFKIPQTHETALHCAAAAPYPRKQICELLFRKGANINEKTEFLTPLHVASEKA 532

QY 486 HNDVVEVVKHAKVNDLNGQTSLSHRAAYCGHLQTCRLLLSYGCDDPNIISLGFTALQ 545
DB 533 HNDVVEVVKHAKVNDLNGQTSLSHRAAYCGHLQTCRLLLSYGCDDPNIISLGFTALQ 592

QY 546 MGNENVQQLLEQGISLGNSEADQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 605
DB 605 MGNENVQQLLEQGISLGNSEADQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 652

DB 593 MGNENVQQLLEQGISLGNSEADQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 652
QY 606 FAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSGHYEVAELLVKHGA VNVNADLW 665
DB 653 FAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSGHYEVAELLVKHGA VNVNADLW 712
QY 666 KFTPLHEAAKGYEICKLLQHGADPTKKNRDGNTPLDLVKDGDITDIQDLLRGDAALLD 725
DB 713 KFTPLHEAAKGYEICKLLQHGADPTKKNRDGNTPLDLVKDGDITDIQDLLRGDAALLD 772
QY 726 AAKKGCLARVKKLSLSSPDNVNCRDTQGRHSTPLHLAAGYNLNLEVAEYLLQHGADVNAQDKG 785
DB 773 AAKKGCLARVKKLSLSSPDNVNCRDTQGRHSTPLHLAAGYNLNLEVAEYLLQHGADVNAQDKG 832
QY 786 GLIPLHNAASGYHVDVAALLIKYNACVNATDKWAFPLHEAAKGRGTQCALLLAHGA DP 845
DB 833 GLIPLHNAASGYHVDVAALLIKYNACVNATDKWAFPLHEAAKGRGTQCALLLAHGA DP 892
QY 846 TLKNQSGOTPLDLVSAADDVSALLTAAMPSPALSCYKQVLNGVRSPGATADALSSG PSS 905
DB 893 TLKNQSGOTPLDLVSAADDVSALLTAAMPSPALSCYKQVLNGVRSPGATADALSSG PSS 952
QY 906 PSSLSAASSLDNLSSGSELSVSSSGTEGASSLEKKEVPVDFSIQTFVRNLGLEHLM 965
DB 953 PSSLSAASSLDNLSSGSELSVSSSGTEGASSLEKKEVPVDFSIQTFVRNLGLEHLM 1012
QY 966 DIPERSOITLDVLVEMGHKELKEIGINAYGHRHKLKGVBERLISGQGLNPYLTNTSGS 1025
DB 1013 DIPERSOITLDVLVEMGHKELKEIGINAYGHRHKLKGVBERLISGQGLNPYLTNTSGS 1072
QY 1026 GTTILIDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTH 1085
DB 1073 GTTILIDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTH 1132
QY 1086 RRKEVSEENHNHANERMLFHGSPFVNALIHKGFDERHAYITGGMFGAGIYFAENSSKSNQY 1145
DB 1133 RRKEVSEENHNHANERMLFHGSPFVNALIHKGFDERHAYITGGMFGAGIYFAENSSKSNQY 1192
QY 1146 VYIGGGTGCVPVHKRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205
DB 1193 VYIGGGTGCVPVHKRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1252
QY 1206 NGLALAEYVIYRGEQAYPEYLIITYQIMRPEGMDG 1240
DB 1253 NGLALAEYVIYRGEQAYPEYLIITYQIMRPEGMDG 1287

RESULT 8
AAB66294
ID AAB66294 standard; protein; 1385 AA.
XX AAB66294;
XX AC
XX XX
DT 05-APR-2001 (first entry)
XX
DB Human tankyrase2 TANK2-LONG SEQ ID NO: 133.
XX
KW Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
KW inflammatory disorder.
XX
OS Homo sapiens.
XX
FN WO200100849-A1.
XX
PD 04-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US017827.
XX
PR 29-JUN-1999; 99US-0141582P.
XX
PA (ICOS-) ICOS CORP.
PI Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;

XX WPI; 2001-102896/11.
DR N-PSDB; AAF63952.
XX
PT New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX
PS Claim 2; Page 191-194; 242pp; English.
XX
CC The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
XX
SQ Sequence 1385 AA;

Query Match 98.6%; Score 6375.5; DB 4; Length 1385;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

6 RGAAGGGAQAGARVGAAGHTAPDPVVTAGSQAARALSASSPGGLALLAGPGLLLRLIAL 65
152 RGSRGAGSPARGAR-GRGHTGATPDPVTAGSQAARALSASSPGGLALLAGPGLLLRLIAL 210

66 LLAVAAARIMSGRCAGGAAACASAAAEVPAARELFEACRNGDVERVKRLVTPKVN 125
211 LLAVAAARIMSGRCAGGAAACASAAAEVPAARELFEACRNGDVERVKRLVTPKVN 270

126 RDTAGRKSTPLHFAAGFRKDWVEYLLQNGANVQARDGGGLPLHNACSPGHAEVNNLLL 185
271 RDTAGRKSTPLHFAAGFRKDWVEYLLQNGANVQARDGGGLPLHNACSPGHAEVNNLLL 330

186 RHGADPNARDNWNTPPLHEAAIKGIDVICVILQHGAEPTIRNTDGRALTALDADPSAKAV 245
331 RHGADPNARDNWNTPPLHEAAIKGIDVICVILQHGAEPTIRNTDGRALTALDADPSAKAV 390

246 LTGEYKDKDELLESARSNGNEERKMALLTPLNVNCHASDGRKSTPLHLAGYNRKIVQLLL 305
391 LTGEYKDKDELLESARSNGNEERKMALLTPLNVNCHASDGRKSTPLHLAGYNRKIVQLLL 450

306 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKRVE 365
451 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKRVE 510

366 VCSLLLSYGADPTLLNCHNKAIDLAPTPOLKERLAYEFKSHLLQAREADVTRIKKHL 425
511 VCSLLLSYGADPTLLNCHNKAIDLAPTPOLKERLAYEFKSHLLQAREADVTRIKKHL 570

426 SLEWNVFKHPQTHETALHCAASPYPKKQICELLRRKGANINEKTEFLTPLHVASEKA 485
571 SLEWNVFKHPQTHETALHCAASPYPKKQICELLRRKGANINEKTEFLTPLHVASEKA 630

486 HNDVVVVVHKAENALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQGFALQ 545
631 HNDVVVVVHKAENALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQGFALQ 690

546 MGENVVOQLLOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLH 605
691 MGENVVOQLLOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLH 750

606 FAAGYNRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVKGAVNVNADLW 665
751 FAAGYNRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVKGAVNVNADLW 810

666 KFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDITDQLLRGDAALLD 725
811 KFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDITDQLLRGDAALLD 870

QY 726 AAKGCLARVKLSSPDNVNCRDTQGRHSSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785
DB 871 AAKGCLARVKLSSPDNVNCRDTQGRHSSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 930

QY 786 GLIPLHNAASYGHVDVAALLIKYNACVNDKWAFTPLHHAQAQKRTQLCALLAHGADP 845
DB 931 GLIPLHNAASYGHVDVAALLIKYNACVNDKWAFTPLHHAQAQKRTQLCALLAHGADP 990

QY 846 TLKNOEGQTPLDLVSADDDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSS 905
DB 991 TLKNOEGQTPLDLVSADDDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSS 1050

QY 906 PSSLSAASSLDNLGSGSFSELSVVSSSGTEGASLEKEVPGVDFSIQTFVRNLGLEHLM 965
DB 1051 PSSLSAASSLDNLGSGSFSELSVVSSSGTEGASLEKEVPGVDFSIQTFVRNLGLEHLM 1110

QY 966 DIFEREQITDLVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGS 1025
DB 1111 DIFEREQITDLVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGS 1170

QY 1026 GTLILDLSPDDKBFQSVVEEMOSTVREHRDGHAGGIFNRVNIKIQKCNKKLWERYTH 1085
DB 1171 GTLILDLSPDDKBFQSVVEEMOSTVREHRDGHAGGIFNRVNIKIQKCNKKLWERYTH 1230

QY 1086 RRKEVSEENHNANERMLFHGSPFVNAIIHKGFDERHAYIGMFGAGIYFAENSCKSNQY 1145
DB 1231 RRKEVSEENHNANERMLFHGSPFVNAIIHKGFDERHAYIGMFGAGIYFAENSCKSNQY 1290

QY 1146 VYGGTGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205
DB 1291 VYGGTGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1350

QY 1206 NGLALAEVLYRGEOAYPEVLYITQIMRPSGMDG 1240
DB 1351 NGLALAEVLYRGEOAYPEVLYITQIMRPSGMDG 1385

RESULT 9
AAB66288
ID AAB66288 standard; protein; 1169 AA.
XX AAB66288;
AC
XX
DT 05-APR-2001 (first entry)
XX
DE Human tankyrase2 clone consensus protein SEQ ID NO: 101.
XX
XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
KW inflammatory disorder.
XX
XX Homo sapiens.
XX
XX WO200100849-A1.
XX
XX 04-JAN-2001.
XX
XX 28-JUN-2000; 2000WO-US017827.
XX
XX 29-JUN-1999; 99US-0141582P.
XX
XX (ICOS-) ICOS CORP.
XX
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
XX WPI; 2001-102896/11.
DR N-PSDB; AAF63952.
XX
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX
XX Example 1; Page 162-1665; 242pp; English.
XX

CC The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
XX
SQ Sequence 1169 AA;
Query Match 94.7%; Score 6121; DB 4; Length 1169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 72 ARMSGRRRCAGGGAACASAAAEVPAARELFELACRNGDVERVKRLVTPKVNSTRDTAGR 131
Db 1 ARMSGRRRCAGGGAACASAAAEVPAARELFELACRNGDVERVKRLVTPKVNSTRDTAGR 60
Qy 132 KSTPLHPAAGFGRKDVVEYLLONGANVQARDGGGLIPLHNACSFHAEVNVNLLRHGADP 191
Db 61 KSTPLHPAAGFGRKDVVEYLLONGANVQARDGGGLIPLHNACSFHAEVNVNLLRHGADP 120
Qy 192 NARDNNWYTPLHEAAIKGKIDVCITVLLQHGAEPTIRNTDGTALDPSAKAVLTGEYK 251
Db 121 NARDNNWYTPLHEAAIKGKIDVCITVLLQHGAEPTIRNTDGTALDPSAKAVLTGEYK 180
Qy 252 KDELLSARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADV 311
Db 181 KDELLSARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADV 240
Qy 312 HAKDKGLVPLHNACSYGHVEVTELLVKGACVNAMDWFOTPLHAEASKNRVEVCSSL 371
Db 241 HAKDKGLVPLHNACSYGHVEVTELLVKGACVNAMDWFOTPLHAEASKNRVEVCSSL 300
Qy 372 SYGADPTLLNCHNKSADLAPTPOKLERLAYEFKSHLQAAAREADVTRIKKHLSEMVN 431
Db 301 SYGADPTLLNCHNKSADLAPTPOKLERLAYEFKSHLQAAAREADVTRIKKHLSEMVN 360
Qy 432 FKHPQTHETALHCAAAAPYPRKRKQICELLRLKGANINEKTEFLTPLHVASERAHNDVVE 491
Db 361 FKHPQTHETALHCAAAAPYPRKRKQICELLRLKGANINEKTEFLTPLHVASERAHNDVVE 420
Qy 492 VVYHKAQNALDNLGQTSLHRAAYCCHLOTCTRLLLSYGCDPNIISLQGTALOMGNENV 551
Db 421 VVYHKAQNALDNLGQTSLHRAAYCCHLOTCTRLLLSYGCDPNIISLQGTALOMGNENV 480
Qy 552 QQLAQEGISLGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYN 611
Db 481 QQLAQEGISLGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYN 540
Qy 612 RVSVEYLLQHGADVHAKDKGLVPLHNACSYGHVEVAELLVKGAVNVNADLWKFTPLH 671
Db 541 RVSVEYLLQHGADVHAKDKGLVPLHNACSYGHVEVAELLVKGAVNVNADLWKFTPLH 600
Qy 672 EAAAKGYEICKLLQHGADPTKKNRGNTPLDLVKGDDTDIDQLLRGDAALLDAKKGC 731
Db 601 EAAAKGYEICKLLQHGADPTKKNRGNTPLDLVKGDDTDIDQLLRGDAALLDAKKGC 660
Qy 732 LARVKLSSPDNVNCRDTQGHSTPLHLAAGYNLEVAEYLLQHGADVNAQDGGLIPLH 791
Db 661 LARVKLSSPDNVNCRDTQGHSTPLHLAAGYNLEVAEYLLQHGADVNAQDGGLIPLH 720
Qy 792 NAASGYHVDVAALLIKYNACVNAQDKWAFPLHAEAAQKRTQLCALLLHAGADPTLKNQE 851
Db 721 NAASGYHVDVAALLIKYNACVNAQDKWAFPLHAEAAQKRTQLCALLLHAGADPTLKNQE 780
Qy 852 GQTPDLVSDADVSAALLTAAMPSPALSCYKQPVNGVRSPGATADALSSGPPSPSSLSA 911
Db 781 GQTPDLVSDADVSAALLTAAMPSPALSCYKQPVNGVRSPGATADALSSGPPSPSSLSA 840
Qy 912 ASSLDNLGSGSFSELSSVSSSGTEGASLEKKEKVPVDFPSITQPVRLNGLHLMDFERE 971

Db 841 ASSLDNLGSGSFSELSSVSSSGTEGASLEKKEKVPVDFPSITQPVRLNGLHLMDFERE 900
Qy 972 QITLDVLVEMGHKELKEIGINAYGHRHKLKGVVERLISGOOGLNPYLTNTSGSGTILID 1031
Db 901 QITLDVLVEMGHKELKEIGINAYGHRHKLKGVVERLISGOOGLNPYLTNTSGSGTILID 960
Qy 1032 LSPDDKEFQSVSEEMOSTVREHRDGGHAGGIPNRYNLIKIQKVCNKKLWERYTHRRKEVS 1091
Db 961 LSPDDKEFQSVSEEMOSTVREHRDGGHAGGIPNRYNLIKIQKVCNKKLWERYTHRRKEVS 1020
Qy 1092 EENHNHANERMLPHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGG 1151
Db 1021 EENHNHANERMLPHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGG 1080
Qy 1152 GTGCPVHKORSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPFGHHSVTGRPSVNGLALA 1211
Db 1081 GTGCPVHKORSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPFGHHSVTGRPSVNGLALA 1140
Qy 1212 EYVIYRGEQAYPEYLITYQIMRPEGWVDG 1240
Db 1141 EYVIYRGEQAYPEYLITYQIMRPEGWVDG 1169
RESULT 10
AAB66278
ID AAB66278 standard; protein; 1169 AA.
XX AAB66278;
DT AC
DT 05-APR-2001 (first entry)
XX Human tankyrase2 related protein sequence SEQ ID NO: 2.
DE Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
KW inflammatory disorder.
XX Homo sapiens.
OS WO200100849-A1.
PN 04-JAN-2001.
XX 28-JUN-2000; 2000WO-US017827.
XX 29-JUN-1999; 99US-0141582P.
PR (ICOS-) ICOS CORP.
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
PI WPI; 2001-102896/11.
DR N-PSDB; AAF63837.
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX Disclosure; Page 109-113; 242pp; English.
PS The present invention provides the protein and coding sequence for the
XX human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
SQ Sequence 1169 AA;
Query Match 94.7%; Score 6121; DB 4; Length 1169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ARIMSGRCAGGAAACASAAAAEVEPAARELFEACRNGDVERVKRLVTPPEKNSRDTAGR 131
DB 1 ARIMSGRCAGGAAACASAAAAEVEPAARELFEACRNGDVERVKRLVTPPEKNSRDTAGR 60
QY 132 KSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHGAHVNNLLRHGADP 191
DB 61 KSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHGAHVNNLLRHGADP 120
QY 192 NARDNMYTTPHAAIKGKIDVICVILLOHGAEPTRINTDGRALDADPSAKAVLTGEYK 251
DB 121 NARDNMYTTPHAAIKGKIDVICVILLOHGAEPTRINTDGRALDADPSAKAVLTGEYK 180
QY 252 KDELLESARSNGEENKWMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADV 311
DB 181 KDELLESARSNGEENKWMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADV 240
QY 312 HAKOKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLL 371
DB 241 HAKOKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLL 300
QY 372 SYGADPTLLNCHNSAIDLPTPOLKERLAYEFKGSLLQAREADVTRI KKHLSLEWVN 431
DB 301 SYGADPTLLNCHNSAIDLPTPOLKERLAYEFKGSLLQAREADVTRI KKHLSLEWVN 360
QY 432 FKHPQTHETALHCAASPYPKRKQICELLRRKGANINEKTEFLTPLVHASEKAHNDVVE 491
DB 361 FKHPQTHETALHCAASPYPKRKQICELLRRKGANINEKTEFLTPLVHASEKAHNDVVE 420
QY 492 VVVKHEAKVNDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLQGTALQNGENV 551
DB 421 VVVKHEAKVNDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLQGTALQNGENV 480
QY 552 QOLLOEGISLGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGROSTPLHFAAGYN 611
DB 481 QOLLOEGISLGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGROSTPLHFAAGYN 540
QY 612 RVSVEYLLQHGADVHAKDGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLH 671
DB 541 RVSVEYLLQHGADVHAKDGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLH 600
QY 672 EAAAKGKYEICKLLQHGADPTKNGRDNPTPLDLVKDGDPTDQLLRGDAALLDAKKGC 731
DB 601 EAAAKGKYEICKLLQHGADPTKNGRDNPTPLDLVKDGDPTDQLLRGDAALLDAKKGC 660
QY 732 LARVKLSSPDVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLH 791
DB 661 LARVKLSSPDVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLH 720
QY 792 NAASGYHVDVAALLIKYNACVNAATDKWFTPLHAAQKGRTOLCALLAHGADPTLKNQE 851
DB 721 NAASGYHVDVAALLIKYNACVNAATDKWFTPLHAAQKGRTOLCALLAHGADPTLKNQE 780
QY 852 GQTPDLVSDVADVSALLTAAMPSPALPCYKQVINGVRSPCATADALSSGSPSPSLSA 911
DB 781 GQTPDLVSDVADVSALLTAAMPSPALPCYKQVINGVRSPCATADALSSGSPSPSLSA 840
QY 912 ASSLDNLSSGSPSELSSVSSGTEGASLEKEVEGVDFSTQFVRNIGLHLMIDIPERE 971
DB 841 ASSLDNLSSGSPSELSSVSSGTEGASLEKEVEGVDFSTQFVRNIGLHLMIDIPERE 900
QY 972 QITLDLVEMGHKELKEIGINAYGHRHLIKGVBERLISGQOGLNPYLTLNTSGSTILID 1031
DB 901 QITLDLVEMGHKELKEIGINAYGHRHLIKGVBERLISGQOGLNPYLTLNTSGSTILID 960
QY 1032 LSPDDKEFQSVSEEMQSVREHRDGGHAGGIFNRYNLIKIKVCKKMLWERYTHRRKEVS 1091
DB 961 LSPDDKEFQSVSEEMQSVREHRDGGHAGGIFNRYNLIKIKVCKKMLWERYTHRRKEVS 1020
QY 1092 BENHNHANERMLFHGSPFNVAIIHKGFDERHAYTGMFGAGIYFPAENSSKNQYVYIGG 1151
DB 1021 BENHNHANERMLFHGSPFNVAIIHKGFDERHAYTGMFGAGIYFPAENSSKNQYVYIGG 1080

QY 1152 GTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALA 1211
DB 1081 GTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALA 1140
QY 1212 EYVIYRGEQAYPEYLLITYQIMRPEGWVG 1240
DB 1141 EYVIYRGEQAYPEYLLITYQIMRPEGWVG 1169
RESULT 11
AAB66295
ID AAB66295 standard; protein; 1166 AA.
XX AAB66295;
AC XX
XX XX
DT 05-APR-2001 (first entry)
XX Human tankyrase2 TANK2-SHORT SEQ ID NO: 135.
DE Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasia; aging;
KW inflammatory disorder.
KW Homo sapiens.
XX OS
XX WO200100849-A1.
XX PN
XX 04-JAN-2001.
XX PD
XX XX
XX 28-JUN-2000; 2000WO-US017827.
XX PF
XX 29-JUN-1999; 99US-0141582P.
XX PR
XX (ICOS-) ICOS CORP.
XX PA
XX Christenson E, Denaggio AJ, Goldman PS, Mcelligott DL;
PI WPI; 2001-102896/11.
XX DR N-PSDB; AAF63953.
XX DR
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX PS
PS Claim 3; Page 200-203; 242pp; English.
XX CC
CC The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the regulation of telomere
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
SQ Sequence 1166 AA;
Query Match 94.5%; Score 6108; DB 4; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 75 MSGRCAGGGAACASAAAAEVEPAARELFEACRNGDVERVKRLVTPPEKNSRDTAGRKST 134
DB 1 MSGRCAGGGAACASAAAAEVEPAARELFEACRNGDVERVKRLVTPPEKNSRDTAGRKST 60
QY 135 PLHPAAGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHGAHVNNLLRHGADPNAR 194
DB 61 PLHPAAGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHGAHVNNLLRHGADPNAR 120
QY 195 DNMYTTPHAAIKGKIDVICVILLOHGAEPTRINTDGRALDADPSAKAVLTGEYKDE 254
DB 121 DNMYTTPHAAIKGKIDVICVILLOHGAEPTRINTDGRALDADPSAKAVLTGEYKDE 180
QY 255 LLESARSNGEENKWMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAK 314

Db 181 LLESARSGNEBEKMMALLITPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 240
Qy 315 DKGLDVLPHNACSYGHEVTELLVKHGACVAMDLWQFTPLHEAASKNRVEVCSSLISYG 374
Db 241 DKGLDVLPHNACSYGHEVTELLVKHGACVAMDLWQFTPLHEAASKNRVEVCSSLISYG 300
Qy 375 ADPTLLCHNKSAIDLAPTOLKRLAYEFKGHSLLQAAREADVTRIKGHSLEWNVFKH 434
Db 301 ADPTLLCHNKSAIDLAPTOLKRLAYEFKGHSLLQAAREADVTRIKGHSLEWNVFKH 360
Qy 435 POTHETALHCAASAPYPRKQICELLRLKGNINKEKTEPLTLHVASEKAHNDVVEVV 494
Db 361 POTHETALHCAASAPYPRKQICELLRLKGNINKEKTEPLTLHVASEKAHNDVVEVV 420
Qy 495 KHEAKVNALDNLGQTSLHRAAYCCHLOTICRLLLSYGCDPNIIISLQGTALQMGNEVQOL 554
Db 421 KHEAKVNALDNLGQTSLHRAAYCCHLOTICRLLLSYGCDPNIIISLQGTALQMGNEVQOL 480
Qy 555 LQEGISLGNSEADQLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRV 614
Db 481 LQEGISLGNSEADQLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRV 540
Qy 615 VVEYLLQHGADVHAKDGGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAA 674
Db 541 VVEYLLQHGADVHAKDGGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAA 600
Qy 675 AKGYEICKLLQHGADPTKKNRDGNTPLDILVKDGDIDQLLRGDAALLDAKKGCLAR 734
Db 601 AKGYEICKLLQHGADPTKKNRDGNTPLDILVKDGDIDQLLRGDAALLDAKKGCLAR 660
Qy 735 VKLSSPDNVNCRDTQGRHSTPLHAGYNNLEVAEYLLQHGADVNAQDGGGLIPLHNA 794
Db 661 VKLSSPDNVNCRDTQGRHSTPLHAGYNNLEVAEYLLQHGADVNAQDGGGLIPLHNA 720
Qy 795 SYGHVDVAALLIKYNACVNATDKAFTPLHAAQKGRTOLCALLAHGADPTLKNQSGQT 854
Db 721 SYGHVDVAALLIKYNACVNATDKAFTPLHAAQKGRTOLCALLAHGADPTLKNQSGQT 780
Qy 855 PLDLSADDDVSALLTAAMPSPALPCYKQVINGVRSPGATADALSSGSPSSLSAASS 914
Db 781 PLDLSADDDVSALLTAAMPSPALPCYKQVINGVRSPGATADALSSGSPSSLSAASS 840
Qy 915 LDNLSSGFSSELSVSSSGTGAASLEKKEVPGVDFSIQTVRNGLGLEHLMIDIFERSQIT 974
Db 841 LDNLSSGFSSELSVSSSGTGAASLEKKEVPGVDFSIQTVRNGLGLEHLMIDIFERSQIT 900
Qy 975 LDVLVEMGHKELKEIGINAYGHRHKLKGVRLISGQGLNPYLTLNTSGSTLIDLSP 1034
Db 901 LDVLVEMGHKELKEIGINAYGHRHKLKGVRLISGQGLNPYLTLNTSGSTLIDLSP 960
Qy 1035 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKQKCNKCLWERYTHRRKEVSEEN 1094
Db 961 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKQKCNKCLWERYTHRRKEVSEEN 1020
Qy 1095 HNANERMLFHGSPFVNAILHKGDERHAYITGFMFGAGIYPAENSXSNQVYIGGGTG 1154
Db 1021 HNANERMLFHGSPFVNAILHKGDERHAYITGFMFGAGIYPAENSXSNQVYIGGGTG 1080
Qy 1155 CPVHKDRSCYICHRQLLFCRVTLGKSFLOPSAMKWAHSPRGHHSVTGRPSVNGLALAEYV 1214
Db 1081 CPVHKDRSCYICHRQLLFCRVTLGKSFLOPSAMKWAHSPRGHHSVTGRPSVNGLALAEYV 1140
Qy 1215 IYRGEQAYPEYLITYQIMRPEGVDG 1240
Db 1141 IYRGEQAYPEYLITYQIMRPEGVDG 1166

RESULT 12
ADRI4792
ID ADRI4792 standard; protein; 1166 AA.
XX
AC ADRI4792;

XX DT 04-NOV-2004 (first entry)
XX DE Amino acid sequence of human MAPCAX orthologue #24.
XX KW adenomatous polyposis coli protein; APC; axin pathway;
XX KW modifier of APC and axin; MAPCAX; cancer; human.
XX OS Homo sapiens.
XX PN WO2004066948-A2.
XX PD 12-AUG-2004.
XX PF 28-JAN-2004; 2004WO-US002338.
XX PR 29-JAN-2003; 2003US-0443484P.
XX PR 11-FEB-2003; 2003US-0447358P.
XX PR 10-APR-2003; 2003US-0461789P.
XX PR 14-MAY-2003; 2003US-0470684P.
XX PR 19-JUN-2003; 2003US-0479650P.
XX PA (EXEL-) EXELIXIS INC.
XX PI Gendreau SB, Morabianco EL, Lickteig K, Zhang H;
XX DR WPI; 2004-580849/56.
XX DR N-PSDB; ADRI4766.
XX PT Identifying a candidate adenomatous polyposis coli protein (APC) and axin
XX PT pathways modulating agent for treating cancer by contacting an assay
XX PT system comprising a modifier of APC and axin polypeptide or nucleic acid
XX PT with a test agent.
XX PS Example 1; SEQ ID NO 50; 199pp; English.
XX CC The specification describes a method for identifying a candidate
XX CC adenomatous polyposis coli protein (APC) and axin pathways modulating
XX CC agents. The method comprises providing an assay system comprising a
XX CC modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting
XX CC the assay system with a test agent under conditions where, except for the
XX CC presence of the test agent, the system provides a reference activity, and
XX CC detecting a test agent-biased activity of the assay system, where a
XX CC difference between the test agent-biased activity and the reference
XX CC activity identifies the test agent as a candidate APC and axin pathways
XX CC modulating agent. The method is useful in identifying a candidate
XX CC adenomatous polyposis coli protein (APC) and a pathways modulating agent,
XX CC which are useful for preparing a composition for diagnosing or treating
XX CC cancer. The present sequence represents a human orthologue of a
XX CC Caenorhabditis elegans MAPCAX polypeptide. The sequence was identified
XX CC using BLAST analysis.
XX SQ Sequence 1166 AA;
Query Match 94.5%; Score 6108; DB 8; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 75 MSGRRACAGGGAACASAAAEEVEPAARELFEACRNGDVERVKRLVTPKVNSRDTRGRKST 134
Db 1 MSGRRACAGGGAACASAAAEEVEPAARELFEACRNGDVERVKRLVTPKVNSRDTRGRKST 60
Qy 135 PLHPAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVLLLRHGADPNAR 194
Db 61 PLHPAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVLLLRHGADPNAR 120
Qy 195 DNNYITPLHEAAIKGKIDVCIVLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDE 254
Db 121 DNNYITPLHEAAIKGKIDVCIVLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDE 180
Qy 255 LLESARSGNEBEKMMALLITPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 314
Db 181 LLESARSGNEBEKMMALLITPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 240

QY 315 DKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 374
DB 241 DKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 300
QY 375 ADPTLLCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKKHLSELMVNFKH 434
DB 301 ADPTLLCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKKHLSELMVNFKH 360
QY 435 PQTHETALHCAASPYPRKQICELLARPGANINEKTEFLTPLVASEKAHNDVVEVV 494
DB 361 PQTHETALHCAASPYPRKQICELLARPGANINEKTEFLTPLVASEKAHNDVVEVV 420
QY 495 KHEAKVNADNLGQTSLEHAAVCGHLCRLLSYGCDPNIIISLQGTALQMGNEVQOL 554
DB 421 KHEAKVNADNLGQTSLEHAAVCGHLCRLLSYGCDPNIIISLQGTALQMGNEVQOL 480
QY 555 LOEGISLGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRV 614
DB 481 LOEGISLGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRV 540
QY 615 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAEILLVKHGVNVDLWKFTPLHEAA 674
DB 541 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAEILLVKHGVNVDLWKFTPLHEAA 600
QY 675 AKGYEICKLLQHGADPTKKNRDGNTPLDLVKOGDTDIQDLRGDAALLDAKKGCLAR 734
DB 601 AKGYEICKLLQHGADPTKKNRDGNTPLDLVKOGDTDIQDLRGDAALLDAKKGCLAR 660
QY 735 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNLLEVAEYLLQHGADVNAQDKGLIPLHNA 794
DB 661 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNLLEVAEYLLQHGADVNAQDKGLIPLHNA 720
QY 795 SYGHVDVNAALLIKNACVNAATDKWFTPLHEAAQKGRTOICALLLAHGAADPTLKNOEGQT 854
DB 721 SYGHVDVNAALLIKNACVNAATDKWFTPLHEAAQKGRTOICALLLAHGAADPTLKNOEGQT 780
QY 855 PLDLVSADVVSAALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSPSSLSAASS 914
DB 781 PLDLVSADVVSAALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSPSSLSAASS 840
QY 915 LDNLGSFSELSVVSSSGTEGASLEKEVPGVDFSTITQFVRNLGLEHMDIFEREQIT 974
DB 841 LDNLGSFSELSVVSSSGTEGASLEKEVPGVDFSTITQFVRNLGLEHMDIFEREQIT 900
QY 975 LDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQLNPYLTLNTSGSTLIDLSL 1034
DB 901 LDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQLNPYLTLNTSGSTLIDLSL 960
QY 1035 DDKFQSVSEEMQSVREHRDGHAGGIFNRVNIILKIOKVCNKKLWERYTHRRKEVSEEN 1094
DB 961 DDKFQSVSEEMQSVREHRDGHAGGIFNRVNIILKIOKVCNKKLWERYTHRRKEVSEEN 1020
QY 1095 HNHNEMRLFHGSPFVNAIILHKGFDERHAYIGGMFAGIYFAENSSKSNQYVYIGGGTG 1154
DB 1021 HNHNEMRLFHGSPFVNAIILHKGFDERHAYIGGMFAGIYFAENSSKSNQYVYIGGGTG 1080
QY 1155 CPVHKDRSCYICHRQLLCRVTLGKSFLOFSAMKMAHSPPGHSHSVTGRPSVNGLALBYV 1214
DB 1081 CPVHKDRSCYICHRQLLCRVTLGKSFLOFSAMKMAHSPPGHSHSVTGRPSVNGLALBYV 1140
QY 1215 IYRGEQAYPEVILTYQIMRPGWVDG 1240
DB 1141 IYRGEQAYPEVILTYQIMRPGWVDG 1166

RESULT 13
ID AAB27211 standard; protein; 1166 AA.
XX
AC AAB27211;
XX
DT 27-FEB-2001 (first entry)

XX Human tankyrase II protein sequence SEQ ID NO: 6.
DE Human; tankyrase II; telomere length; signal transduction.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Misc-difference 124 /note= "encoded by TTA"
FT Misc-difference 125 /note= "encoded by TAC"
FT
XX WO200061813-A1.
PN 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-US009558.
XX
XX 09-APR-1999; 99US-0128577P.
XX 13-APR-1999; 99US-0129123P.
XX (GERO-) GERON CORP.
XX
XX Morin GB, Funk WD, Piatyszek MA;
PI
XX WPI; 2000-679503/66.
XX N-PSDB; AAC66825.
XX
XX Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding the polypeptide useful for modulating or maintaining telomere length, replicative capacity, apoptosis, chromosome packing or gene expression.
XX
XX Claim 4; Fig 4; 52pp; English.
XX
XX The present sequence is a version of the human tankyrase II protein sequence. The protein is thought to be involved in signal transduction in the cell, and to have binding activity for other telomere-associated proteins. It is possible that it plays a role in the regulation of telomere length, thus affecting the replicative ability of the cell. The protein is useful for ribosylating target proteins, for determining tankyrase II binding activity in a sample, and for modulating telomere length in a cell
XX
SQ Sequence 1166 AA;

Query Match 94.2%; Score 6092; DB 3; Length 1166;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 75 MSGRRCCAGGGAACASAAAEVPAARELFEACRNGDVERVKRLVTPKVNSRDTAGRKST 134
DB 1 MSGRRCCAGGGAACASAAAEVPAARELFEACRNGDVERVKRLVTPKVNSRDTAGRKST 60
QY 135 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNAR 194
DB 61 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNAR 120
QY 195 DNWNTYPLHEAAIKGKIDVCIVLLQHGAEPIRNTDGRALTDLADPSKAVLTGEYKDE 254
DB 121 DNWNTYPLHEAAIKGKIDVCIVLLQHGAEPIRNTDGRALTDLADPSKAVLTGEYKDE 180
QY 255 LLESARSGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 314
DB 181 LLESARSGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 240
QY 315 DKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 374
DB 241 DKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 300
QY 375 ADPTLLCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKKHLSELMVNFKH 434
DB 301 ADPTLLCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKKHLSELMVNFKH 360

Qy 435 POTHETALHCAAAAPYPRKQKQICELLIRKKGANINEKTEKFEFTPLHVASAKAHNDVVEVV 494
Db 361 POTHETALHCAAAAPYPRKQKQICELLIRKKGANINEKTEKFEFTPLHVASAKAHNDVVEVV 420
Qy 495 KHEAKVALDNLGOTSLHRAAYCCHLOTCLLLSYGCDPNIIISLOGFTALQMGHENVQOL 554
Db 421 KHEAKVALDNLGOTSLHRAAYCCHLOTCLLLSYGCDPNIIISLOGFTALQMGHENVQOL 480
Qy 555 LQEGISLGNSEADRLLEAAKAGDVETVKLCITQVSNCRDIEGRQSTPLHFAAGYNNRV 614
Db 481 LQEGISLGNSEADRLLEAAKAGDVETVKLCITQVSNCRDIEGRQSTPLHFAAGYNNRV 540
Qy 615 VVEYLQHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAA 674
Db 541 VWEYLQHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAA 600
Qy 675 AKGKYEICKLLOHGADPTKQNRDGTPLDVLKDGDDTDIOLLRGDAALLDAKGGCLAR 734
Db 601 AKGKYEICKLLOHGADPTKQNRDGTPLDVLKDGDDTDIOLLRGDAALLDAKGGCLAR 660
Qy 735 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNA 794
Db 661 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNA 720
Qy 795 SYGHVDVAALLIKYNACVNDKWAFTPLHEAAQKGRTOICALLLAHGAFTPLKQBGQT 854
Db 721 SYGHVDVAALLIKYNACVNDKWAFTPLHEAAQKGRTOICALLLAHGAFTPLKQBGQT 780
Qy 855 PLDLVSADDDVSALLTAAMPSPALPSYKQVINGVSPGATADALSSGSPSSLSAASS 914
Db 781 PLDLVSADDDVSALLTAAMPSPALPSYKQVINGVSPGATADALSSGSPSSLSAASS 840
Qy 915 LDNLSGSFSELSVVSSSGTGASLSKEKVPVDFSTTQVRNLGLEHLMIDIFEREQIT 974
Db 841 LDNLSGSFSELSVVSSSGTGASLSKEKVPVDFSTTQVRNLGLEHLMIDIFEREQIT 900
Qy 975 LDVLVEMGHKELKIGINAYGHRHKLKGVVERLISGQGLNPYTLTNTSGSTLIDLSP 1034
Db 901 LDVLVEMGHKELKIGINAYGHRHKLKGVVERLISGQGLNPYTLTNTSGSTLIDLSP 960
Qy 1035 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTILKQVCKKWLERYTHRRKEVSEEN 1094
Db 961 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTILKQVCKKWLERYTHRRKEVSEEN 1020
Qy 1095 HNANERMLFHGSPFVNAIHKGFDERHAYTIGGMFGAGIYPAENSCKSNQVYVYGGGTG 1154
Db 1021 HNANERMLFHGSPFVNAIHKGFDERHAYTIGGMFGAGIYPAENSCKSNQVYVYGGGTG 1080
Qy 1155 CPVHKDRSCYICHRQLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSVNGLALAEYV 1214
Db 1081 CPVHKDRSCYICHRQLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSVNGLALAEYV 1140
Qy 1215 IYRGEQAYPEYLITYQIMRPEGVDG 1240
Db 1141 IYRGEQAYPEYLITYQIMRPEGVDG 1166

ESULT 14
BP69457
X ABP69457 standard; protein; 1166 AA.
C ABP69457;
X
T 20-JAN-2003 (first entry)
E Human polypeptide SEQ ID NO 1504.
X
W Human; genome mapping; gene therapy; food supplement; virus; fungus;
W cell-proliferative disorder; neurodegenerative disease; bacterial;
W Parkinson's disease; Alzheimer's disease; autoimmune disease;
W multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
W arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;

KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
OS Homo sapiens.
PN W0200270539-A2.
XX 12-SEP-2002.
XX 05-MAR-2002; 2002MO-US005095.
XX 05-MAR-2001; 2001US-00799451.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Zhou P, Goodrich RW, Auundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX WPI; 2002-759812/82.
DR N-PSDB; ABZ11674.
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative, or platelet
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX Claim 9; SEQ ID NO 1504; 1012pp + Sequence Listing; English.
PS The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burn, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1166 AA;

Query Match 94.2%; Score 6088; DB 5; Length 1166;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 75 MSGRRCAGGAGCAACAAAAEVEPAARELFEACRNGDVERVKRLVTPEKNSRDTAGRKST 134
Db 1 MSGRRCAGGAGCAACAAAAEVEPAARELFEACRNGDVERVKRLVTPEKNSRDTAGRKIH 60
Qy 135 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAENVNLLLRHGDAPNAR 194
Db 61 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAENVNLLLRHGDAPNAR 120
Qy 195 DNWNYTFLHEAAIKGKIDVICVILLOHGAETIRNTDGTALDPSAKAVLTGEYKDE 254
Db 121 DNWNYTFLHEAAIKGKIDVICVILLOHGAETIRNTDGTALDPSAKAVLTGEYKDE 180
Qy 255 LLESARSNGEKKMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKI VOLLLOHGADVHAK 314
Db 181 LLESARSNGEKKMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKI VOLLLOHGADVHAK 240
Qy 315 DKGDLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKRVEVCILLSYSG 374
Db 241 DKGDLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKRVEVCILLSYSG 300

QY 255 LLESARSGNEBKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIYQLLQHGADVHAK 314
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 LLESARSGNEBKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIYQLLQHGADVHAK 240
QY 315 DKGDVPLHNACS YGHEVTELLVKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYG 374
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 DKGDVPLHNACS YGHEVTELLVKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYG 300
QY 375 ADPTLLNCHNKAIDLAPTQLKERLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKH 434
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 ADPTLLNCHNKAIDLAPTQLKERLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKH 360
QY 435 POTHETALHCAASPYPKRQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVV 494
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 POTHETAXHCAASPYPKRQICELLRLKGAAXINEKTEFLTPLHVASEKAHNDXVEVVV 420
QY 495 KHEAKVNALNLGOTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQMGNEVQQL 554
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 KHEAKVNALNLGOTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQMGNEVQQL 480
QY 555 LQEGISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV 614
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 LQEGISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV 540
QY 615 VVEYLLQHGADVHAKDKGGLVPLHNACS YGHEVVAELLVKHGAVNVADLWKFTPLHEAA 674
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 VVEYLLQHGADVHAKDKKXLVPLHNACS YGHEVVAELLVKHGAVNVADLWKFTPLHEAA 600
QY 675 AKGYEICKLLLOHGADPTKKNRDGNTPLDVKDGDTDIQLLGRDAALLDAKKGCLAR 734
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AKGYEICKLLLOHGADPTKKNRDGNTPLDVKDGDTDIQLLGRDAALLDAKKGCLAR 660
QY 735 VKKLSSPDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNA 794
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 VKKLSSPDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNA 720
QY 795 SYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKGRTOQLCALLAHGADPTLKNQEGOT 854
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 SYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKGRTOQLCALLAHGADPTLKNQEGOT 780
QY 855 PLDLVSADDDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 914
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 PLDLVSADDDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 840
QY 915 LDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIITQFVRNLGLEHLMDFEREQIT 974
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 LDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIITQFVRNLGLEHLMDFEREQIT 900
QY 975 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTNTSGSGTILIDLSP 1034
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTNTSGSGTILIDLSP 960
QY 1035 DDKEFQSVEEEMOSTVREHRDGGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEEN 1094
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
961 DDKEFQSVEEEMOSTVREHRDGGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEEN 1020
QY 1095 HNHANERMLFHGSPFVNAILHKGFDERHAYTGGMFGAGIYPAENSSKSNQYVYIGGGTG 1154
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 HNHANERMLFHGSPFVNAILHKGFDERHAYTGGMFGAGIYPAENSSKSNQYVYIGGGTG 1080
QY 1155 CPVHKDRSCVYICHRQLLFCRVTLTKSFLQFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1214
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 CPVHKDRSCVYICHRQLLFCRVTLTKSFLQFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1140
QY 1215 IYRGEQAYPEYLITYQIMRPEGWVDG 1240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1141 IYRGEQAYPEYLITYQIMRPEGWVDG 1166

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:51:56 ; Search time 153.857 Seconds
(without alignments)
3733.253 Million cell updates/sec

Title: US-10-616-101-4

Perfect score: 6464

Sequence: 1 RCSARRGAAGGQAGRGARV.....AYPEYLITYQIMRPGMVDG 1240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6464	100.0	1240	5	US-10-616-101-4
2	6375.5	98.6	1262	4	US-10-199-937-107
3	6375.5	98.6	1385	4	US-10-199-937-133
4	6121	94.7	1169	4	US-10-199-937-2
5	6121	94.7	1169	4	US-10-199-937-101
6	6108	94.5	1166	3	US-09-972-115A-6
7	6108	94.5	1166	4	US-10-163-587A-15
8	6108	94.5	1166	4	US-10-199-937-135
9	5877	90.9	1227	3	US-09-849-602-26
10	5766	89.2	1100	5	US-10-616-101-8
11	5760	89.1	1100	5	US-10-616-101-11
12	5656	87.5	1083	5	US-10-616-101-12
13	5602	86.7	1074	3	US-09-509-196A-2
14	5582	86.4	1065	5	US-10-616-101-3
15	5452	84.3	1267	3	US-09-972-115A-4
16	5103.5	79.0	1327	3	US-09-841-835-2
17	5103.5	79.0	1327	3	US-09-972-115A-8
18	5103.5	79.0	1327	4	US-10-199-937-4
19	5031.5	77.8	1333	3	US-09-972-115A-2
20	4102	63.5	784	4	US-10-199-937-89
21	4005	62.0	1181	6	US-11-097-143-9474
22	3997	61.8	1181	4	US-10-199-937-139
23	3959	61.2	756	4	US-10-199-937-91
24	3938	60.9	802	3	US-09-964-899-41
25	3938	60.9	802	5	US-10-975-523-41
26	3307	51.2	949	3	US-09-841-835-10
27	2913	45.1	583	5	US-10-616-101-10

28	2722	42.1	522	4	US-10-199-937-99	Sequence 99, Appl
29	2165	33.5	415	4	US-10-276-774-1690	Sequence 1690, Ap
30	2132.5	33.0	673	3	US-09-841-835-8	Sequence 8, Appli
31	2056.5	21.8	1099	4	US-10-199-937-178	Sequence 178, App
32	1895	29.3	362	4	US-10-199-937-160	Sequence 160, App
33	1736	26.9	338	5	US-10-616-101-9	Sequence 9, Appli
34	895	13.8	1765	5	US-10-055-877-140	Sequence 140, App
35	892.5	13.8	4274	5	US-10-450-763-31331	Sequence 31331, A
36	892.5	13.8	4377	5	US-10-756-149-4917	Sequence 4917, Ap
37	892.5	13.8	4384	5	US-10-821-234-1120	Sequence 1120, Ap
38	892.5	13.8	4386	5	US-10-450-763-37734	Sequence 37734, A
39	889	13.7	1940	5	US-10-055-877-141	Sequence 141, App
40	888.5	13.7	1762	4	US-10-205-194-117	Sequence 117, App
41	886.5	13.7	215	4	US-10-199-937-105	Sequence 105, App
42	877	13.6	1330	4	US-10-108-260A-3237	Sequence 3237, Ap
43	874	13.5	160	3	US-09-972-115A-20	Sequence 20, Appl
44	874	13.5	160	4	US-10-199-937-46	Sequence 46, Appl
45	869.5	13.5	4397	5	US-10-450-763-52303	Sequence 52303, A

ALIGNMENTS

RESULT 1
US-10-616-101-4
; Sequence 4, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossoskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616.101
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-101-4

Query Match	100.0%	Score	6464;	DB	5;	Length	1240;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches	1240;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	RCSARRGAAGGQAGRGARVGAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLLL	60				
Db	1	RCSARRGAAGGQAGRGARVGAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLLL	60				
Qy	61	RLALLLAVAAARIMSGRRCCAGGGAACASAAAEEAVEPAARELFACRNGDVERVKRLVTP	120				
Db	61	RLALLLAVAAARIMSGRRCCAGGGAACASAAAEEAVEPAARELFACRNGDVERVKRLVTP	120				
Qy	121	EKVSRTAGKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSFGEAEV	180				
Db	121	EKVSRTAGKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSFGEAEV	180				
Qy	181	VNLLRHGADPNARDNNYTPPLHAAATKGKIDVCIVLQHGAEPTIRNTDGTALDLADP	240				
Db	181	VNLLRHGADPNARDNNYTPPLHAAATKGKIDVCIVLQHGAEPTIRNTDGTALDLADP	240				
Qy	241	SAKAVLTGEYKKDBLLSARSNGEKKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI	300				

Db 241 SAKAVITGEYKDELLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 300
Qy 301 VOLLQHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 360
Db 301 VOLLQHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 360
Qy 361 KNRVECSLLSYGADPTLLNCHNSAIDLAPTOLKERLAYEFKGHSLLOAREADVTR 420
Db 361 KNRVECSLLSYGADPTLLNCHNSAIDLAPTOLKERLAYEFKGHSLLOAREADVTR 420
Qy 421 IKGHLSEWVNFKHPQTHETALHCAASAPYPRKQICELLIRKGANINEKTEFTPLHV 480
Db 421 IKGHLSEWVNFKHPQTHETALHCAASAPYPRKQICELLIRKGANINEKTEFTPLHV 480
Qy 481 ASEKANDNVVVVKGHAKVNDLNGOTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQ 540
Db 481 ASEKANDNVVVVKGHAKVNDLNGOTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQ 540
Qy 541 FTALQMGHNVQOLLQEGISLGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGR 600
Db 541 FTALQMGHNVQOLLQEGISLGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGR 600
Qy 601 STPLHFAAGYNRVSVEYLLQHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNM 660
Db 601 STPLHFAAGYNRVSVEYLLQHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNM 660
Qy 661 VADLWKFPLHEAAKGYEIKLLQHGADPTKKNRDNLTPLVKGDDTDIQLLRGD 720
Db 661 VADLWKFPLHEAAKGYEIKLLQHGADPTKKNRDNLTPLVKGDDTDIQLLRGD 720
Qy 721 AALLDAKGGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
Db 721 AALLDAKGGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
Qy 781 AQDKGGLPLHNAASYGHVDVAALLIKYNACVNTDKWAFPLHEAAKGRQOLCALLIA 840
Db 781 AQDKGGLPLHNAASYGHVDVAALLIKYNACVNTDKWAFPLHEAAKGRQOLCALLIA 840
Qy 841 HGADPTLKNQEGTDLVSDVVSALITAMPSPALPSCYKQVNLGVRSPGATADALS 900
Db 841 HGADPTLKNQEGTDLVSDVVSALITAMPSPALPSCYKQVNLGVRSPGATADALS 900
Qy 901 SGSPSSLSAASLDNLGSPSELSSVSSSGTEGASLEKKEVPGVDFSTQFVRNLG 960
Db 901 SGSPSSLSAASLDNLGSPSELSSVSSSGTEGASLEKKEVPGVDFSTQFVRNLG 960
Qy 961 LEHLMDIFEREQITLDVLVEGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLT 1020
Db 961 LEHLMDIFEREQITLDVLVEGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLT 1020
Qy 1021 NTSGGTLLIDLSPPDKBFSQVEEMQSTVREHRRDGGHAGGIFNRYNLIKIQKVCNKKLW 1080
Db 1021 NTSGGTLLIDLSPPDKBFSQVEEMQSTVREHRRDGGHAGGIFNRYNLIKIQKVCNKKLW 1080
Qy 1081 ERYTHRRKEVSENNHANERMLFHGSPFVNAI IHKGFDERHAYIGMFGAGIYFAENSS 1140
Db 1081 ERYTHRRKEVSENNHANERMLFHGSPFVNAI IHKGFDERHAYIGMFGAGIYFAENSS 1140
Qy 1141 KSNQVYVIGGTCPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVT 1200
Db 1141 KSNQVYVIGGTCPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVT 1200
Qy 1201 GRPSVNGALAEYVIRGEQAYPEYLITYQIMRPEGVMDG 1240
Db 1201 GRPSVNGALAEYVIRGEQAYPEYLITYQIMRPEGVMDG 1240

RESULT 2

US-10-199-937-107

Sequence 107, Application US/10199937

Publication No. US20030190739A1

GENERAL INFORMATION:

APPLICANT: CHILKERSON, Erik

APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 107
LENGTH: 1262
TYPE: PRT
ORGANISM: Homo sapiens
US-10-199-937-107

Query Match 98.6%; Score 6375.5; DB 4; Length 1262;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 6 RGAAGGGAQGAQGAARVCAAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLRLLAL 65
Db 29 RGRGAGSPARGAR-GRGHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLRLLAL 87
Qy 66 LLAAVAAARIMSGRRRCAGGGAACASAAAAEVEPAARELFECACRNGDVERVKRLVTPKVS 125
Db 88 LLAAVAAARIMSGRRRCAGGGAACASAAAAEVEPAARELFECACRNGDVERVKRLVTPKVS 147
Qy 126 RTAGRKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSGHAEVNVNLL 185
Db 148 RDTAGRKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSGHAEVNVNLL 207
Qy 186 RRGADPNARNNNYTPLEHAAIKGIDVCILVLOHGAETPIRNTDGTALDADPSAKAV 245
Db 208 RRGADPNARNNNYTPLEHAAIKGIDVCILVLOHGAETPIRNTDGTALDADPSAKAV 267
Qy 246 LTGEYKDELLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 305
Db 268 LTGEYKDELLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 327
Qy 306 QHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKORVE 365
Db 328 QHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKORVE 387
Qy 366 VCSLLLSYGADPTLLNCHNSAIDLAPTOLKERLAYEFKGHSLLOAREADVTRIKKHL 425
Db 388 VCSLLLSYGADPTLLNCHNSAIDLAPTOLKERLAYEFKGHSLLOAREADVTRIKKHL 447
Qy 426 SLEWVNFKHPQTHETALHCAASAPYPRKQICELLIRKGANINEKTEFTPLHVAESEA 485
Db 448 SLEWVNFKHPQTHETALHCAASAPYPRKQICELLIRKGANINEKTEFTPLHVAESEA 507
Qy 486 HNDVVEVVVKGHAKVNDLNGOTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQ 545
Db 508 HNDVVEVVVKGHAKVNDLNGOTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQ 567
Qy 546 MGENVQOLLQEGISLGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLH 605
Db 568 MGENVQOLLQEGISLGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLH 627
Qy 606 FAAGYNRVSVEYLLQHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLW 665
Db 628 FAAGYNRVSVEYLLQHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLW 687
Qy 666 KFTPLHEAAKGYEIKLLQHGADPTKKNRDNLTPLVKGDDTDIQLLRGDAAALLD 725
Db 688 KFTPLHEAAKGYEIKLLQHGADPTKKNRDNLTPLVKGDDTDIQLLRGDAAALLD 747
Qy 726 AAKKGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785

Db 748 AAKGCLARVKLSSPDNVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 807
Qy 786 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOCALLLAHAGADP 845
Db 808 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOCALLLAHAGADP 867
Qy 846 TLKQEGQTPDLVSADDDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGPSS 905
Db 868 TLKQEGQTPDLVSADDDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGPSS 927
Qy 906 PSSLSAASLDNLSSPSELSSVSSSGTEGASSLEKKEVPQVDSITQFVRNGLGHELM 965
Db 928 PSSLSAASLDNLSSPSELSSVSSSGTEGASSLEKKEVPQVDSITQFVRNGLGHELM 987
Qy 966 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPLYTLNTSGS 1025
Db 988 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPLYTLNTSGS 1047
Qy 1026 GTILIDLPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERVTH 1085
Db 1048 GTILIDLPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERVTH 1107
Qy 1086 RRKEVSEENHNHANERMLFHGSPFVNAIHHKGFDERHAYIGGMFGAGIYFAENSSKSNOY 1145
Db 1108 RRKEVSEENHNHANERMLFHGSPFVNAIHHKGFDERHAYIGGMFGAGIYFAENSSKSNOY 1167
Qy 1146 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTRPSV 1205
Db 1168 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTRPSV 1227
Qy 1206 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGVMDG 1240
Db 1228 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGVMDG 1262

RESULT 3
US-10-199-937-133
; Sequence 133, Application US/10199937
; Publication No. US20030190749A1
GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: Damaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 133
; LENGTH: 1385
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-199-937-133

Query Match 98.6%; Score 6375.5; DB 4; Length 1385;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;
Qy 6 RGAAGGQAGRGARVGAHGTAPDPTVAGSQARALSSPGGLALLAGPGLLLRLAL 65
Db 152 RGSRGAGSPARGAR-GRGHTAPDPTVAGSQARALSSPGGLALLAGPGLLLRLAL 210
Qy 66 LLVAAAARIMSGRCGGGACASAAAEEAVEPAARELFEACNGDVERKRVTPKNS 125
Db 211 LLVAAAARIMSGRCGGGACASAAAEEAVEPAARELFEACNGDVERKRVTPKNS 270
Qy 126 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAEEVNNLL 185

Db 271 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAEEVNNLL 330
Qy 186 RHGADPNARDNNWNTPLHEAAIKGKIDVCI VLLQHGAEPTIRNTDGR TALDLADPSAKAV 245
Db 331 RHGADPNARDNNWNTPLHEAAIKGKIDVCI VLLQHGAEPTIRNTDGR TALDLADPSAKAV 390
Qy 246 LTGYKKDELLESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLL 305
Db 391 LTGYKKDELLESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLL 450
Qy 306 OHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNAWDLWQFTPLHEAASKNVE 365
Db 451 OHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNAWDLWQFTPLHEAASKNVE 510
Qy 366 VCSLLSYGADPTLLNCHNKSAIDLAPTPQKLERLAYEFKGHLSLQAAAREADVTRIKKHL 425
Db 511 VCSLLSYGADPTLLNCHNKSAIDLAPTPQKLERLAYEFKGHLSLQAAAREADVTRIKKHL 570
Qy 426 SLEWNVFKHPQTHETALHCAAASPYPKKQICEILLRKGANINEKTEFLTPLHVASEKA 485
Db 571 SLEWNVFKHPQTHETALHCAAASPYPKKQICEILLRKGANINEKTEFLTPLHVASEKA 630
Qy 486 HNDVVEVVKHAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYCCDPNIIISLQFTALQ 545
Db 631 HNDVVEVVKHAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYCCDPNIIISLQFTALQ 690
Qy 546 MGENVQQLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDTEGRQSTPLH 605
Db 691 MGENVQQLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDTEGRQSTPLH 750
Qy 606 FAAGYNRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVEALLVKHGA VNVADLM 665
Db 751 FAAGYNRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVEALLVKHGA VNVADLM 810
Qy 666 KFTPLHEAAAKGYEICKLLQHGADPTKORDGNTPLDLVKDGTDTODLLRGDAALLD 725
Db 811 KFTPLHEAAAKGYEICKLLQHGADPTKORDGNTPLDLVKDGTDTODLLRGDAALLD 870
Qy 726 AAKGCLARVKLSSPDNVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785
Db 871 AAKGCLARVKLSSPDNVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 930
Qy 786 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOCALLLAHAGADP 845
Db 931 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOCALLLAHAGADP 990
Qy 846 TLKQEGQTPDLVSADDDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGPSS 905
Db 991 TLKQEGQTPDLVSADDDVSALLTAAMPSPALPSYKPOVLNGVRSPGATADALSSGPSS 1050
Qy 906 PSSLSAASLDNLSSPSELSSVSSSGTEGASSLEKKEVPQVDSITQFVRNGLGHELM 965
Db 1051 PSSLSAASLDNLSSPSELSSVSSSGTEGASSLEKKEVPQVDSITQFVRNGLGHELM 1110
Qy 966 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPLYTLNTSGS 1025
Db 1111 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPLYTLNTSGS 1170
Qy 1026 GTILIDLPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERVTH 1085
Db 1171 GTILIDLPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERVTH 1230
Qy 1086 RRKEVSEENHNHANERMLFHGSPFVNAIHHKGFDERHAYIGGMFGAGIYFAENSSKSNOY 1145
Db 1231 RRKEVSEENHNHANERMLFHGSPFVNAIHHKGFDERHAYIGGMFGAGIYFAENSSKSNOY 1290
Qy 1146 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTRPSV 1205
Db 1291 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTRPSV 1350
Qy 1206 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGVMDG 1240

QY 132 KSTPLHFAAGFGKDVVEYLLQNGANVQARDGGIPLHNACSFGEAEVNVNLLLRHGADP 191
Db 61 KSTPLHFAAGFGKDVVEYLLQNGANVQARDGGIPLHNACSFGEAEVNVNLLLRHGADP 120
QY 192 NARDWNNTPLHAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGYK 251
Db 121 NARDWNNTPLHAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGYK 180
QY 252 KDELLESARSNGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVTIQLLQHGADV 311
Db 181 KDELLESARSNGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVTIQLLQHGADV 240
QY 312 HAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHAAASKNRVEVCSLL 371
Db 241 HAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHAAASKNRVEVCSLL 300
QY 372 SYGADPTLLCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKHLSLEWV 431
Db 301 SYGADPTLLCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKHLSLEWV 360
QY 432 FXHPOTHETALHCAASPYPRKQKQICELLRLKGANINEKTEFLPLHVASEKANDVVE 491
Db 361 FXHPOTHETALHCAASPYPRKQKQICELLRLKGANINEKTEFLPLHVASEKANDVVE 420
QY 492 VVVHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQNGENV 551
Db 421 VVVHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQNGENV 480
QY 552 QLLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYN 611
Db 481 QLLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYN 540
QY 612 RVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVEAELLVKGAVNVNADLWKFPLH 671
Db 541 RVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVEAELLVKGAVNVNADLWKFPLH 600
QY 672 EAAAGKYEICKLLQHGADPTKQNRDGNTPDLVKDGDITDQLLGRDGAALLDAKKG 731
Db 601 EAAAGKYEICKLLQHGADPTKQNRDGNTPDLVKDGDITDQLLGRDGAALLDAKKG 660
QY 732 LARVKLSGPDVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLH 791
Db 661 LARVKLSGPDVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLH 720
QY 792 NAASGHVDVVAALLIKYNACVNATDKWFTPLHAAQKQRTQICALLAHGADPTLKNQE 851
Db 721 NAASGHVDVVAALLIKYNACVNATDKWFTPLHAAQKQRTQICALLAHGADPTLKNQE 780
QY 852 GOTPLDVSADVSALLTAAMPSPALPCYKQVINGVRSPGATADALSSGSPSSLSA 911
Db 781 GOTPLDVSADVSALLTAAMPSPALPCYKQVINGVRSPGATADALSSGSPSSLSA 840
QY 912 ASSLONLGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMIDIFERE 971
Db 841 ASSLONLGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMIDIFERE 900
QY 972 QITLDVLMGHKELKEIGINAYGHRKLIKGVERLISQOQGLNPVTLTNTSGSGTILID 1031
Db 901 QITLDVLMGHKELKEIGINAYGHRKLIKGVERLISQOQGLNPVTLTNTSGSGTILID 960
QY 1032 LSPDDKEFOSVEEEMOSTVREHRDGHAGGIIFNRVNIKIQVCKNKLWERVTHRRKEYS 1091
Db 961 LSPDDKEFOSVEEEMOSTVREHRDGHAGGIIFNRVNIKIQVCKNKLWERVTHRRKEYS 1020
QY 1092 EENHNHANERMLFHGSPFVNAIIHKGFDRHAYIGGMFGAGIYFAENSCKSNQYVYIGG 1151
Db 1021 EENHNHANERMLFHGSPFVNAIIHKGFDRHAYIGGMFGAGIYFAENSCKSNQYVYIGG 1080
QY 1152 GTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOPSANKMAHSPGHHSVTGRFSVNGLALA 1211
Db 1081 GTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOPSANKMAHSPGHHSVTGRFSVNGLALA 1140
QY 1212 EYVIYRGEQAYPEYLITYQIMRPEGMDVG 1240

Db 1141 EYVIYRGEQAYPEYLITYQIMRPEGMDVG 1169
RESULT 6
US-09-972-115A-6
; Sequence 6, Application US/09972115A
; Publication No. US20030032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Miczyzlaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-6
Query Match 94.5%; Score 6108; DB 3; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 75 MSGRCAGGACGACASAAAEVPEARELFEACRNGDVERVKELVTPEKNSRDTAGRKST 134
Db 1 MSGRCAGGACGACASAAAEVPEARELFEACRNGDVERVKELVTPEKNSRDTAGRKST 60
QY 135 PLHFAAGFGKDVVEYLLQNGANVQARDGGIPLHNACSFGEAEVNVNLLLRHGADPNAR 194
Db 61 PLHFAAGFGKDVVEYLLQNGANVQARDGGIPLHNACSFGEAEVNVNLLLRHGADPNAR 120
QY 195 DNWNTYPLHAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGYKDE 254
Db 121 DNWNTYPLHAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGYKDE 180
QY 255 LLESARSNGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVTIQLLQHGADVNAK 314
Db 181 LLESARSNGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVTIQLLQHGADVNAK 240
QY 315 DKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHAAASKNRVEVCSLLLSYG 374
Db 241 DKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHAAASKNRVEVCSLLLSYG 300
QY 375 ADPTLLCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKHLSLEWVNFH 434
Db 301 ADPTLLCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVTRIKHLSLEWVNFH 360
QY 435 POTHETALHCAASPYPRKQKQICELLRLKGANINEKTEFLPLHVASEKANDVVEV 494
Db 361 POTHETALHCAASPYPRKQKQICELLRLKGANINEKTEFLPLHVASEKANDVVEV 420
QY 495 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQNGENVV 554
Db 421 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQNGENVV 480
QY 555 LOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNRV 614
Db 481 LOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNRV 540
QY 615 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVEAELLVKGAVNVNADLWKFPLHAA 674
Db 541 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVEAELLVKGAVNVNADLWKFPLHAA 600


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QY 675 AKGYEICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDILLRGDAALLDAAKKGCLAR 734
DB 601 AKGYEICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDILLRGDAALLDAAKKGCLAR 660
QY 735 VKKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGILPLHNA 794
DB 661 VKKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGILPLHNA 720
QY 795 SYGHVDAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 854
DB 721 SYGHVDAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 780
QY 855 PLDLVSADDSVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 914
DB 781 PLDLVSADDSVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 840
QY 915 LDNLGSFSELSSVSSSGTEGASSLEKKEVPGVDFPSITOFVRNLGLHLMDFEREQIT 974
DB 841 LDNLGSFSELSSVSSSGTEGASSLEKKEVPGVDFPSITOFVRNLGLHLMDFEREQIT 900
QY 975 LDVLEVMGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPLYTLNTSGSGTILDLSP 1034
DB 901 LDVLEVMGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPLYTLNTSGSGTILDLSP 960
QY 1035 DDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEEN 1094
DB 961 DDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEEN 1020
QY 1095 HNHANERMLPHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTG 1154
DB 1021 HNHANERMLPHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTG 1080
QY 1155 CPVHKDRSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1214
DB 1081 CPVHKDRSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1140
QY 1215 IYRGEQAYPEYLITYQIMRPEGWVDG 1240
DB 1141 IYRGEQAYPEYLITYQIMRPEGWVDG 1166

RESULT 7
US-10-163-587A-15
; Sequence 15, Application US/10163587A
; Publication No. US2003009263A1
; GENERAL INFORMATION:
; APPLICANT: Oliveira, Marcos
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CEMO/RADIO SENSITIZING
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10/163,587A
; PRIOR FILING DATE: 2003-01-10
; PRIOR FILING DATE: 2003-01-10
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-587A-15

Query Match 94.5%; Score 6108; DB 4; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 MSRRCCAGGAAACASAAAEVPAARELFACRNGDVERVKRLVTPKVNSRDTAGRKST 134
DB 1 MSRRCCAGGAAACASAAAEVPAARELFACRNGDVERVKRLVTPKVNSRDTAGRKST 60
QY 135 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVLLLRHGDPNAR 194
DB 61 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVLLLRHGDPNAR 120
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QY 195 DNWNVYPLHEAAIKGKIDVCIVLLOHGAEPITRNTDGTALDLPDSAKAVLTGEYKKDE 254
DB 121 DNWNVYPLHEAAIKGKIDVCIVLLOHGAEPITRNTDGTALDLPDSAKAVLTGEYKKDE 180
QY 255 LLESARSNGNEKMAWLLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAK 314
DB 181 LLESARSNGNEKMAWLLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAK 240
QY 315 DKGDVPLHNACSYGHEVTELLVKGGA CVNMDLWQFTPLHEAASKNRVEVCSLLLSYG 374
DB 241 DKGDVPLHNACSYGHEVTELLVKGGA CVNMDLWQFTPLHEAASKNRVEVCSLLLSYG 300
QY 375 ADPTLNCNKSADIDAPTOLKERLAYEFKSHLSLOAAREADVTRIKKHLSEMNVPKH 434
DB 301 ADPTLNCNKSADIDAPTOLKERLAYEFKSHLSLOAAREADVTRIKKHLSEMNVPKH 360
QY 435 POTHETALHCAASAPYKPKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVV 494
DB 361 POTHETALHCAASAPYKPKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVV 420
QY 495 KHEAKVNALDNLGQTSIHLRAAYCGHLQTCRLLLSYGCDPNIISLOGFTALQMGNEVQOL 554
DB 421 KHEAKVNALDNLGQTSIHLRAAYCGHLQTCRLLLSYGCDPNIISLOGFTALQMGNEVQOL 480
QY 555 LOEGISLGNSEADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRV 614
DB 481 LOEGISLGNSEADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRV 540
QY 615 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVTELLVKGGA CVNMDLWQFTPLHEAA 674
DB 541 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVTELLVKGGA CVNMDLWQFTPLHEAA 600
QY 675 AKGYEICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDILLRGDAALLDAAKKGCLAR 734
DB 601 AKGYEICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDILLRGDAALLDAAKKGCLAR 660
QY 735 VKKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGILPLHNA 794
DB 661 VKKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGILPLHNA 720
QY 795 SYGHVDAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 854
DB 721 SYGHVDAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 780
QY 855 PLDLVSADDSVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 914
DB 781 PLDLVSADDSVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 840
QY 915 LDNLGSFSELSSVSSSGTEGASSLEKKEVPGVDFPSITOFVRNLGLHLMDFEREQIT 974
DB 841 LDNLGSFSELSSVSSSGTEGASSLEKKEVPGVDFPSITOFVRNLGLHLMDFEREQIT 900
QY 975 LDVLEVMGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPLYTLNTSGSGTILDLSP 1034
DB 901 LDVLEVMGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPLYTLNTSGSGTILDLSP 960
QY 1035 DDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEEN 1094
DB 961 DDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEEN 1020
QY 1095 HNHANERMLPHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTG 1154
DB 1021 HNHANERMLPHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTG 1080
QY 1155 CPVHKDRSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1214
DB 1081 CPVHKDRSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1140
QY 1215 IYRGEQAYPEYLITYQIMRPEGWVDG 1240
DB 1141 IYRGEQAYPEYLITYQIMRPEGWVDG 1166
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RESULT 8
US-10-199-937-135
; Sequence 135, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-135

Query Match 94.5%; Score 6108; DB 4; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 MSRRCCGGGAACASAAAEVPEARELFACRNGDVERVKRLVTPKVNRSRDTAGRKST 134
Db 1 MSRRCCGGGAACASAAAEVPEARELFACRNGDVERVKRLVTPKVNRSRDTAGRKST 60

Qy 135 PLHPAAGFRKDVVEYLLQNGANVOARDGGGLPLHNACSGHAEVNVNLLRHGADPNAR 194
Db 61 PLHPAAGFRKDVVEYLLQNGANVOARDGGGLPLHNACSGHAEVNVNLLRHGADPNAR 120

Qy 195 DNWNYTPLHEAAIKGIDCVTLVLLQHGAEPTIRNTDGTALDLPDSKAVLTGEYKDE 254
Db 121 DNWNYTPLHEAAIKGIDCVTLVLLQHGAEPTIRNTDGTALDLPDSKAVLTGEYKDE 180

Qy 255 LLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIQVLLQHGADVHAK 314
Db 181 LLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIQVLLQHGADVHAK 240

Qy 315 DKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKRVEVCSLLSYG 374
Db 241 DKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKRVEVCSLLSYG 300

Qy 375 ADPTLLNCHNSAIDLAPTPQKRLAYEFKSHLSLQAREADVTRIKKHLSLEWVNFH 434
Db 301 ADPTLLNCHNSAIDLAPTPQKRLAYEFKSHLSLQAREADVTRIKKHLSLEWVNFH 360

Qy 435 PQTHETALHCAASYPYKPKQICELLRRKGANINEKTEKFEFLTPLHVASEKAHNDVVEVV 494
Db 361 PQTHETALHCAASYPYKPKQICELLRRKGANINEKTEKFEFLTPLHVASEKAHNDVVEVV 420

Qy 495 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISIQGFTALQNGENVOOL 554
Db 421 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISIQGFTALQNGENVOOL 480

Qy 555 LOEGISLGNSEADROLLEAAKAGDVETVKKLTQVSNCRDIEGROSTPLHFAAGYNRVS 614
Db 481 LOEGISLGNSEADROLLEAAKAGDVETVKKLTQVSNCRDIEGROSTPLHFAAGYNRVS 540

Qy 615 VVEYLLQHGADVHAKDGGVPLHNACSYGHEVTELLVKGACVNVNADLWKFTPLHEAA 674
Db 541 VVEYLLQHGADVHAKDGGVPLHNACSYGHEVTELLVKGACVNVNADLWKFTPLHEAA 600

Qy 675 AKGKYEICKLLQHGADPTKNGRDNPTPLDLVKOGDPTDIDLLRGDAALLDAKKGCLAR 734
Db 601 AKGKYEICKLLQHGADPTKNGRDNPTPLDLVKOGDPTDIDLLRGDAALLDAKKGCLAR 660

Qy 735 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAA 794
Db 661 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAA 720

Qy 795 SYGHVDVAALLIKYNACVNATDKWAFTPLHBAAGKRTQTCALLAHGADPTLKNQEGQT 854
Db 721 SYGHVDVAALLIKYNACVNATDKWAFTPLHBAAGKRTQTCALLAHGADPTLKNQEGQT 780

Qy 855 PLDLVSADDDVALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASS 914
Db 781 PLDLVSADDDVALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASS 840

Qy 915 LDNLSSGSELSVSSVSSGTEGASLEKKEVGVDFSIQTQVRNLGLEHLMDFEREQIT 974
Db 841 LDNLSSGSELSVSSVSSGTEGASLEKKEVGVDFSIQTQVRNLGLEHLMDFEREQIT 900

Qy 975 LDVLVENGHKLKEIGINAYCHRHKLKGVBERLISGQGLNPYLTANTSGSGTILIDLSP 1034
Db 901 LDVLVENGHKLKEIGINAYCHRHKLKGVBERLISGQGLNPYLTANTSGSGTILIDLSP 960

Qy 1035 DDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEEN 1094
Db 961 DDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEEN 1020

Qy 1095 HNANERMLFHGSPFVNAILHKGFDERHAYTGGMFGAGIYFAENSSKSNQVYVIGGGTG 1154
Db 1021 HNANERMLFHGSPFVNAILHKGFDERHAYTGGMFGAGIYFAENSSKSNQVYVIGGGTG 1080

Qy 1155 CPVKHRSYICHRQLLFCRVTLGKSLQFSAMKVAHSPPGHSHSVTGRPSVNGLALEYV 1214
Db 1081 CPVKHRSYICHRQLLFCRVTLGKSLQFSAMKVAHSPPGHSHSVTGRPSVNGLALEYV 1140

Qy 1215 IYRGEQAYPEYLLITYQIMRPEGMDG 1240
Db 1141 IYRGEQAYPEYLLITYQIMRPEGMDG 1166

RESULT 9
US-09-849-602-26
; Sequence 26, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-26

Query Match 90.9%; Score 5877; DB 3; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1148; Conservative 8; Mismatches 47; Indels 50; Gaps 5;

Qy 12 QGAQRGARVGAA-----HGTAPDPTVAGSQARALSASSPGCLALLLAGPGLL 59
Db 1 QGAQRGARVGAAAGLRRSGDSRPSGPGPVERVFGGPPRPPARGAGAPAPVAGAVAG---- 56

Qy 60 LRLALLLAVAAARIMSGRRCAAG-----CGGQDVGVSPLRRRSGGLRDAAAEVPEARELFACRN 108
Db 57 -----CGGQDVGVSPLRRRSGGLRDAAAEVPEARELFACRN 96

Qy 109 GDVERVKRLVTPKVNRSRDTAGRKSTPLHFAAGFRKDVVEYLLQNGANVOARDGGGLIP 168
Db 97 GDVERVKRLVTPKVNRSRDTAGRKSTPLHFAAGFRKDVVEYLLQNGANVOARDGGGLIP 156

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Qy	169	LHNACSFHAEVNVNLLRHGADPNARDNNYTPPLHEAAIKGKIDVCIVLLQHGASPTIRN	228
Db	157	LHNACSFHAEVNVNLLRHGADPNARDNNYTPPLHEAAIKGKIDVCIVLLQHGASPTIRN	216
Qy	229	TGRTALDADPSAKAVLTGTYKDELLESARGNEEKMMALLTPLNVNCHASDGRKSTP	288
Db	217	TGRTALDADPSAKAVLTGTYKDELLESARGNEEKMMALLTPLNVNCHASDGRKSTP	276
Qy	289	LHLAAGYNRVKIVQLLQHGADVHAKDGLVPLPHNACSYGHYEYVTELLVKGACVNAMD	348
Db	277	LHLAAGYNRVKIVQLLQHGADVHAKDGLVPLPHNACSYGHYEYVTELLVKGACVNAMD	336
Qy	349	LWQFTPLHEAASKNRVEVCSLLLSVGADPTLLNCHNKSAIDLAPTPQPKERLAYEFKGHS	408
Db	337	LWQFTPLHEAASKNRVEVCSLLLSVGADPTLLNCHNKSAIDLAPTPQPKERLAYEFKGHS	396
Qy	409	LLOAREADVTRIKKHLSELNWFPHQPTHETALHCAAAAPYPRKQICELLLRGANIN	468
Db	397	LLOAREADVTRIKKHLSELNWFPHQPTHETALHCAAAAPYPRKQICELLLRGANIN	456
Qy	469	EKTKEFLTPHVASEKAHNDVVVVVGHAEKYNALDNLGQTSLHRAAYCGHLQTCRLLLS	528
Db	457	EKTKEFLTPHVASEKAHNDVVVVVGHAEKYNALDNLGQTSLHRAAYCGHLQTCRLLLS	516
Qy	529	YGCDPNIIISLQFTALQMGNEVQQLQEGISLGNSEADRLLEAAKAGDVETVKKLCV	588
Db	517	YGCDPNIIISLQFTALQMGNEVQQLQEGISLGNSEADRLLEAAKAGDVETVKKLCV	576
Qy	589	QSVNCRDIEGROSTPLHFAAGYNRVVVEYLLQHGADVHAKDGLVPLPHNACSYGHYEV	648
Db	577	QSVNCRDIEGROSTPLHFAAGYNRVVVEYLLQHGADVHAKDGLVPLPHNACSYGHYEV	636
Qy	649	AELLVKGAVNVNADLWFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKD	708
Db	637	AELLVKGAVNVNADLWFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKD	696
Qy	709	GDTDIQDLRGGDAALLDAAKGCLARVKLSLSPDNVNCRDTOGRHSTPLHLAGYNNLEV	768
Db	697	GDTDIQDLRGGDAALLDAAKGCLARVKLSLSPDNVNCRDTOGRHSTPLHLAGYNNLEV	756
Qy	769	AEYLLQHGADVNAODKGGIPLHNAASVGHVDVAALLIKYNACVNATDKMAFTPLHEAAQ	828
Db	757	AEYLLQHGADVNAODKGGIPLHNAASVGHVDVAALLIKYNACVNATDKMAFTPLHEAAQ	816
Qy	829	KGRTQCALALLAHGADPTLKNQEGQTPDLVSADDSVALLTAAMPSPALPSCKPQVLNG	888
Db	817	KGRTQCALALLAHGADPTLKNQEGQTPDLVSADDSVALLTAAMPSPALPSCKPQVLNG	876
Qy	889	VRSPGATADALSSGSPSSLSAASLONLSGSFSELSSVSSSGTEGASSLEKKEVPGV	948
Db	877	VRSPGATADALSSGSPSSLSAASLONLSGSFSELSSVSSSGTEGASSLEKKEVPGV	936
Qy	949	DFSITQFVRNLGLEHLMIDIFEREQITLQVLMGHKELKEIGINAYGHRHKLIKGVERLI	1008
Db	937	DFSITQFVRNLGLEHLMIDIFEREQITLQVLMGHKELKEIGINAYGHRHKLIKGVERLI	996
Qy	1009	SGQOGLNPYLTLNTSGSGTILDLSPDKFQFOSVEEEMOSTVREHRDGHAGGIFNRYNI	1068
Db	997	SGQOGLNPYLTLNTSGSGTILDLSPDKFQFOSVEEEMOSTVREHRDGHAGGIFNRYNI	1056
Qy	1069	LKIQRKCNKWLWERTHRRKEVSEENHNANRMLFHGSPFFNAILIHKGFDRHAYIGGM	1128
Db	1057	LKIQRKCNKWLWERTHRRKEVSEENHNANRMLFHGSPFFNAILIHKGFDRHAYIGGM	1116
Qy	1129	FGAGIYFAENSCKSNQYVIGGGTGCPCVHK--DRSCYICHRQLLCFRVTLGKSLQFSAM	1187
Db	1117	FGAGIYFAENSCKSNQYVIGGGTGCPCVHK--DRSCYICHRQLLCFRVTLGKSLQFSAM	1174
Qy	1188	KWASHPPGHHSVTGRPSVNGLALAEYVIYVRGQAYPEYLITYQIMRPEGWVDG	1240
Db	1175	ENGTSPPGHHSVTGRPSVNGLALAEYVIYVRGQAYPEYLITYQIMRPEGWVDG	1227

RESULT 10
US-10-616-101-8
; Sequence 8, Application US/10616101
; Publication NO. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Osoovskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-101-8

Query Match	89.2%;	Score 5766;	DB 5;	Length 1100;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1099;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	141	GFRKDDVVEYLLQNGANVQARDGGLIPLHNACSFGHAEVNVNLLLRHGADPNARDNNYT	200	
Db	1	GFRKDDVVEYLLQNGASVQARDGGLIPLHNACSFGHAEVNVNLLLRHGADPNARDNNYT	60	
Qy	201	PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGSGYKDELLESAR	260	
Db	61	PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGSGYKDELLESAR	120	
Qy	261	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDKGDLV	320	
Db	121	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDKGDLV	180	
Qy	321	PLHNACSYGHYEYVTELLVKGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL	380	
Db	181	PLHNACSYGHYEYVTELLVKGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL	240	
Qy	381	NCHNKSALDIAPTPQPKERLAYEPKGSLLQAAAREADVTRIKKHLSEMNFKHPQTHET	440	
Db	241	NCHNKSALDIAPTPQPKERLAYEPKGSLLQAAAREADVTRIKKHLSEMNFKHPQTHET	300	
Qy	441	ALHCAAAAPYPRKQICELLLRGANINEKTFEPLHVASEKAHNDVVEVVVHKAHV	500	
Db	301	ALHCAAAAPYPRKQICELLLRGANINEKTFEPLHVASEKAHNDVVEVVVHKAHV	360	
Qy	501	NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQFTALQMGNEVQQLQEGIS	560	
Db	361	NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQFTALQMGNEVQQLQEGIS	420	
Qy	561	LGNSEADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL	620	
Db	421	LGNSEADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL	480	
Qy	621	QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAAGKYE	680	
Db	481	QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAAGKYE	540	
Qy	681	ICKLLQHGADPTKKNRDGNTPLDLVKDGDITQDLRLRGDAALLDAAKKGCLARVKLSS	740	
Db	541	ICKLLQHGADPTKKNRDGNTPLDLVKDGDITQDLRLRGDAALLDAAKKGCLARVKLSS	600	

QY 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800
DB 601 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
QY 801 VAALLIKYNACVNAATKWAFTPLHAAQKGRTOICALLAHGADPTLKNQEGOTPLDLVS 860
DB 661 VAALLIKYNACVNAATKWAFTPLHAAQKGRTOICALLAHGADPTLKNQEGOTPLDLVS 720
QY 861 ADDVSALLITAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 920
DB 721 ADDVSALLITAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
QY 921 SFSELSVSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFEREOITLDVLVE 980
DB 781 SFSELSVSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFEREOITLDVLVE 840
QY 981 MGKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 1040
DB 841 MGKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
QY 1041 SVEEEMQSTVREHRODGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 1100
DB 901 SVEEEMQSTVREHRODGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 1101 RMLFHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1160
DB 961 RMLFHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1020
QY 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVYIRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVYIRGEQ 1080
QY 1221 APPEYLITYQIMRPEGWVDG 1240
DB 1081 APPEYLITYQIMRPEGWVDG 1100

RESULT 11
US-10-616-101-11
; Sequence 11, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ososovskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; PRIORITY FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-10-616-101-11

Query Match 89.1%; Score 5760; DB 5; Length 1100;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1098; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 141 GFGKRDVVEYLLQNGASVQARDGGLIPLHNAACSFHAEVNNLLRLRHGADPNARDNNYTT 200
|||||

DB 1 GFGKRDVVEYLLQNGASVQARDGGLIPLHNAACSFHAEVNNLLRLRHGADPNARDNNYTT 60
QY 201 PLHAAAIKGIKDVCIIVLLOHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 260
DB 61 PLHAAAIKGIKDVCIIVLLOHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
QY 261 SGNEEKWALLTPLNVNCHASDGRKSTPLHAAAGYNNRVIKIVOLLQHGADVNAQDKGLD 320
DB 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHAAAGYNNRVIKIVOLLQHGADVNAQDKGLD 180
QY 321 PLHNACSYGHEVTELLVKGACVNAAMDLOFTPLHAAASKNRVEVCILLSYSGADPTLL 380
DB 181 PLHNACSYGHEVTELLVKGACVNAAMDLOFTPLHAAASKNRVEVCILLSYSGADPTLL 240
QY 381 NCHNKSALDLAPTQKRLAYEFKGHSLLOAAREADVTRIKCHLSLWVNFKHPQTHET 440
DB 241 NCHNKSALDLAPTQKRLAYEFKGHSLLOAAREADVTRIKCHLSLWVNFKHPQTHET 300
QY 441 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVHKAHV 500
DB 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVHKAHV 360
QY 501 NALDNLGQTSLHRAAYCGHLOTCRLLLSYSGCDPNIIISLOGFTALQMGHENVQOLLQEGIS 560
DB 361 NALDNLGQTSLHRAAYCGHLOTCRLLLSYSGCDPNIIISLOGFTALQMGHENVQOLLQEGIS 420
QY 561 LGNSEADRLLEAAKAGDVETVKKLCIVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 620
DB 421 LGNSEADRLLEAAKAGDVETVKKLCIVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
QY 621 QHGADVHAKQKGLVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHAAAKGYE 680
DB 481 QHGADVHAKQKGLVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHAAAKGYE 540
QY 681 ICKLLQHGADPTKKNRDGNTPLDLVKDQDPTDIOQLLEGDAALLDAAKKGCLARVKLSS 740
DB 541 ICKLLQHGADPTKKNRDGNTPLDLVKDQDPTDIOQLLEGDAALLDAAKKGCLARVKLSS 600
QY 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800
DB 601 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
QY 801 VAALLIKYNACVNAATKWAFTPLHAAQKGRTOICALLAHGADPTLKNQEGOTPLDLVS 860
DB 661 VAALLIKYNACVNAATKWAFTPLHAAQKGRTOICALLAHGADPTLKNQEGOTPLDLVS 720
QY 861 ADDVSALLITAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 920
DB 721 ADDVSALLITAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
QY 921 SFSELSVSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFEREOITLDVLVE 980
DB 781 SFSELSVSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFEREOITLDVLVE 840
QY 981 MGKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 1040
DB 841 MGKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
QY 1041 SVEEEMQSTVREHRODGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 1100
DB 901 SVEEEMQSTVREHRODGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 1101 RMLFHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1160
DB 961 RMLFHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1020
QY 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVYIRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVYIRGEQ 1080
QY 1221 APPEYLITYQIMRPEGWVDG 1240
DB 1081 APPEYLITYQIMRPEGWVDG 1100

RESULT 12

US-10-616-101-12
; Sequence 12, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Oesovekaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methode
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-10-616-101-12

Query Match 87.5%; Score 5656; DB 5; Length 1083;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1079; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 141 GGRKDVVEYLLQNGANVOARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNWT 200
DB 1 GGRKDVVEYLLQNGASVOARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNWT 60
QY 201 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDADPSAKAVLTGYKDELLESAR 260
DB 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDADPSAKAVLTGYKDELLESAR 120
QY 261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 320
DB 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 180
QY 321 PLHNACSYGHEVTELLVKGACVNMNDLWQFTPLHEAASKRVEVCSLLLSYGADPTLL 380
DB 181 PLHNACSYGHEVTELLVKGACVNMNDLWQFTPLHEAASKRVEVCSLLLSYGADPTLL 240
QY 381 NCHNSAIDLAPTQPKERLAYEFKGHSLQAAREADVTRIKHLSLEWVNFKHPOTHET 440
DB 241 NCHNSAIDLAPTQPKERLAYEFKGHSLQAAREADVTRIKHLSLEWVNFKHPOTHET 300
QY 441 ALHCAAAAPYKPKQICELLKRGANINKEFTPLPLHVASEKANDVVEVVVHKA 500
DB 301 ALHCAAAAPYKPKQICELLKRGANINKEFTPLPLHVASEKANDVVEVVVHKA 360
QY 501 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDDPNIIISLOGFTALQNGNENVOQLLEGIS 560
DB 361 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDDPNIIISLOGFTALQNGNENVOQLLEGIS 420
QY 561 LGNSEADROLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
DB 421 LGNSEADROLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
QY 621 QHGADVHAKDKGGLVPLHNACSYGHEVTELLVKGACVNMNDLWQFTPLHEAAAKGKYE 680
DB 481 QHGADVHAKDKGGLVPLHNACSYGHEVTELLVKGACVNMNDLWQFTPLHEAAAKGKYE 540
QY 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDTIQDLLRGDAALLDAAKKGCLARVKLSS 740

DB 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDTIQDLLRGDAALLDAAKKGCLARVKLSS 600
QY 741 PONVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
DB 601 PONVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
QY 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKQEGQTPLDLVS 860
DB 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKQEGQTPLDLVS 720
QY 861 ADDVSALLTAAMPSPALPCYKQVNLGVSPCATADALSSGSPSSSLAASSLDNLG 920
DB 721 ADDVSALLTAAMPSPALPCYKQVNLGVSPCATADALSSGSPSSSLAASSLDNLG 780
QY 921 SFSELSVVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE 980
DB 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE 840
QY 981 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILDLSPDDKEFQ 1040
DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILDLSPDDKEFQ 900
QY 1041 SVEEEMQSTVREHRDGHAGGIENRYNLIKQVCKKLEWERYTHRRKEYSEENHNANE 1100
DB 901 SVEEEMQSTVREHRDGHAGGIENRYNLIKQVCKKLEWERYTHRRKEYSEENHNANE 960
QY 1101 RMLFHGSPFVNAILHKGFDERHAYIGMGFAGIYFAENSCKSNQYVYIGGGTGCPVHKD 1160
DB 961 RMLFHGSPFVNAILHKGFDERHAYIGMGFAGIYFAENSCKSNQYVYIGGGTGCPVHKD 1020
QY 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSVNGLALAEYVYIRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSVNGLALAEYVYIRGEQ 1080
QY 1221 A 1221
DB 1081 A 1081

RESULT 13

US-09-509-196A-2
; Sequence 2, Application US/09509196A
; Patent No. US20020037582A1
; GENERAL INFORMATION:
; APPLICANT: DALY, Roger J.
; APPLICANT: SUTHERLAND, Robert L.
; TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling
; FILE REFERENCE: 1871-129
; CURRENT APPLICATION NUMBER: US/09/509,196A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: P09388
; PRIOR FILING DATE: 1997-09-23
; PRIOR APPLICATION NUMBER: PCT AU98/00795
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1074
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-509-196A-2

Query Match 86.7%; Score 5602; DB 3; Length 1074;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1068; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 167 IPLHNACSFHAEVNVNLLRHGADPNARDNWTPLHEAAIKGKIDVCIVLLQHGAEPTI 226
DB 1 IPLHNACSFHAEVNVNLLRHGADPNARDNWTPLHEAAIKGKIDVCIVLLQHGAEPTI 60
QY 227 RNTDGTALDADPSAKAVLTGYKDELLESARSGNEEKWALLTPLNVNCHASDGRKS 286


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Db 661 VAALLIKYNACVATDKWAFPLHEAAQKGRTOICALLAHGADPTLKNQEQTPDLVS 720
Qy 861 ADDVSALLTAAMPSPALPSCYKQVLNGVRSPGATADALSSGPPSPSLSAASLDNLG 920
Db 721 ADDVSALLTAAMPSPALPSCYKQVLNGVRSPGATADALSSGPPSPSLSAASLDNLG 780
Qy 921 SPSLSSVSSSGTEGASSLEKKVPVGDPSITQVRNLGLEHLMDFEREQITDLVIVE 980
Db 781 SPSLSSVSSSGTEGASSLEKKVPVGDPSITQVRNLGLEHLMDFEREQITDLVIVE 840
Qy 981 MGHKELKEIGNAGVHRHKLKIGVERLISGQGLNPVTLTNTSGSGTILDLSPDDKEFQ 1040
Db 841 MGHKELKEIGNAGVHRHKLKIGVERLISGQGLNPVTLTNTSGSGTILDLSPDDKEFQ 900
Qy 1041 SVEEMOSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNHANE 1100
Db 901 SVEEMOSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNHANE 960
Qy 1101 RMLFHGSPFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGIGGTGCPVHKD 1160
Db 961 RMLFHGSPFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGIGGTGCPVHKD 1020
Qy 1161 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGHHSVTGRPSV 1205
Db 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGHHSVTGRPSV 1065

RESULT 15
US-09-972-115A-4
; Sequence 4, Application US/09972115A
; Publication No. US20030032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972.115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1267
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: The 'Xaa' at location 1 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc_feature
; LOCATION: (42)..(42)
; OTHER INFORMATION: The 'Xaa' at location 42 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (98)..(98)
; OTHER INFORMATION: The 'Xaa' at location 98 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (110)..(110)
; OTHER INFORMATION: The 'Xaa' at location 110 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (114)..(114)
; OTHER INFORMATION: The 'Xaa' at location 114 stands for Asn, Ser, Thr, or Ile.
; NAME/KEY: misc feature
; LOCATION: (126)..(126)
; OTHER INFORMATION: The 'Xaa' at location 126 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (139)..(139)
; OTHER INFORMATION: The 'Xaa' at location 139 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc_feature
; LOCATION: (741)..(741)
; OTHER INFORMATION: The 'Xaa' at location 741 stands for Met, Val, or Leu.

; LOCATION: (144)..(144)
; OTHER INFORMATION: The 'Xaa' at location 144 stands for Thr.
; NAME/KEY: misc feature
; LOCATION: (153)..(153)
; OTHER INFORMATION: The 'Xaa' at location 153 stands for Thr.
; NAME/KEY: misc feature
; LOCATION: (166)..(166)
; OTHER INFORMATION: The 'Xaa' at location 166 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (173)..(173)
; OTHER INFORMATION: The 'Xaa' at location 173 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (174)..(174)
; OTHER INFORMATION: The 'Xaa' at location 174 stands for Glu, or Lys.
; NAME/KEY: misc feature
; LOCATION: (183)..(183)
; OTHER INFORMATION: The 'Xaa' at location 183 stands for Val.
; NAME/KEY: misc feature
; LOCATION: (185)..(185)
; OTHER INFORMATION: The 'Xaa' at location 185 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (188)..(188)
; OTHER INFORMATION: The 'Xaa' at location 188 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (202)..(202)
; OTHER INFORMATION: The 'Xaa' at location 202 stands for His, or Pro.
; NAME/KEY: misc feature
; LOCATION: (204)..(204)
; OTHER INFORMATION: The 'Xaa' at location 204 stands for Glu, or Lys.
; NAME/KEY: misc feature
; LOCATION: (205)..(205)
; OTHER INFORMATION: The 'Xaa' at location 205 stands for Asn, Ser, Thr, or Ile.
; NAME/KEY: misc feature
; LOCATION: (207)..(207)
; OTHER INFORMATION: The 'Xaa' at location 207 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (211)..(211)
; OTHER INFORMATION: The 'Xaa' at location 211 stands for Gln, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (213)..(213)
; OTHER INFORMATION: The 'Xaa' at location 213 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (215)..(215)
; OTHER INFORMATION: The 'Xaa' at location 215 stands for Lys, Asn, Glu, Asp, Gln, His,
; OTHER INFORMATION: , a stop codon, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: The 'Xaa' at location 227 stands for His, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (228)..(228)
; OTHER INFORMATION: The 'Xaa' at location 228 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (237)..(237)
; OTHER INFORMATION: The 'Xaa' at location 237 stands for Glu, or Asp.
; NAME/KEY: misc feature
; LOCATION: (238)..(238)
; OTHER INFORMATION: The 'Xaa' at location 238 stands for Asn, Ser, Thr, Ile, Asp, Gly
; OTHER INFORMATION: , Ala, Val, His, Arg, Pro, Leu, Tyr, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (667)..(667)
; OTHER INFORMATION: The 'Xaa' at location 667 stands for Tyr, Cys, Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (725)..(725)
; OTHER INFORMATION: The 'Xaa' at location 725 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (727)..(727)
; OTHER INFORMATION: The 'Xaa' at location 727 stands for His, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (735)..(735)
; OTHER INFORMATION: The 'Xaa' at location 735 stands for Glu, or Asp.
; NAME/KEY: misc feature
; LOCATION: (741)..(741)
; OTHER INFORMATION: The 'Xaa' at location 741 stands for Met, Val, or Leu.
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; NAME/KEY: misc feature
; LOCATION: (763)..(763)
; OTHER INFORMATION: The 'Xaa' at location 763 stands for Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (764)..(764)
; OTHER INFORMATION: The 'Xaa' at location 764 stands for Tyr, Cys, Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (787)..(787)
; OTHER INFORMATION: The 'Xaa' at location 787 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (789)..(789)
; OTHER INFORMATION: The 'Xaa' at location 789 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (790)..(790)
; OTHER INFORMATION: The 'Xaa' at location 790 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (791)..(791)
; OTHER INFORMATION: The 'Xaa' at location 791 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (792)..(792)
; OTHER INFORMATION: The 'Xaa' at location 792 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (793)..(793)
; OTHER INFORMATION: The 'Xaa' at location 793 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (794)..(794)
; OTHER INFORMATION: The 'Xaa' at location 794 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (795)..(795)
; OTHER INFORMATION: The 'Xaa' at location 795 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (796)..(796)
; OTHER INFORMATION: The 'Xaa' at location 796 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (797)..(797)
; OTHER INFORMATION: The 'Xaa' at location 797 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (798)..(798)
; OTHER INFORMATION: The 'Xaa' at location 798 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (799)..(799)
; OTHER INFORMATION: The 'Xaa' at location 799 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (800)..(800)

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; OTHER INFORMATION: The 'Xaa' at location 800 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (801)..(801)
; OTHER INFORMATION: The 'Xaa' at location 801 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: misc feature
; LOCATION: (802)..(802)

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Query Match      84.3%; Score 5452; DB 3; Length 1267;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1072; Conservative 6; Mismatches 161; Indels 4; Gaps 2;

```

```

QY 1 RCSARRGAGCGGARGARVGAHCTAPDPVTAGSQAARALSSASPGGLALLAGPGLLL 60
DB |||||||
QY 26 RCLRRRGAAGCGGARGHGXGARGRGHTAPDPVTAGSQAARALSSASPGGLALLAGPGLLL 85
DB |||||||
QY 61 RLLALLLAAVAARIMSGRRRCAGGGGACASAAAEVPAARELFACRNGDVERVRLVTP 120
DB |||||||
QY 86 RLLALLLAAVAAXINSGRRCAGGGGACAXAAAEVPAARXLFACRNGDVERXKLVYP 145
DB |||||||
QY 121 EKVNSRDTAGRKSTPLHPAAGFGRKDVVEYLLQNGANYQARDGGLIPLHNACSGHAEV 180
DB |||||||
QY 146 EKVNSRDYAGRKSTPLHPFPAXFGRKDLXXYLLTNGANXQXRDGGLIPLHNACSGFAXX 205
DB |||||||
QY 181 VNLLRHGADNADNWNNTPLHAAIKGKIDCVILLOHGAEPTRINDGTALDLADP 240
DB |||||||
QY 206 IXLXLLHXAXPNARDNWNNTYPXEAAIKGKIXCIVLLOHGAEPTRINDGTALDLADP 265
DB |||||||
QY 241 SAKAVLTGEYKDELLESARGNEBKMWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 300
DB |||||||
QY 266 SAKAVLTGEYKDELLESARGNEBKMWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 325
DB |||||||
QY 301 VOLLLQHGADVHAKDGLVPLHNACSYGHVEVTELLVKHGACVNAMDLMQWTPPLHEAAS 360
DB |||||||
QY 326 VOLLLQHGADVHAKDGLVPLHNACSYGHVEVTELLVKHGACVNAMDLMQWTPPLHEAAS 385
DB |||||||
QY 361 KNRVEVCSLLISYGADPTLNLCHNKSADLAPTPOLKERLAYEFKSHLSQOAREADVTR 420
DB |||||||
QY 386 KNRVEVCSLLISYGADPTLNLCHNKSADLAPTPOLKERLAYEFKSHLSQOAREADVTR 445
DB |||||||
QY 421 IKCHLSLBNWFKPQTHQTHALHCAASPYPKRKQICELLARKGANINEKTEFETPLHV 480
DB |||||||
QY 446 IKCHLSLBNWFKPQTHQTHALHCAASPYPKRKQICELLARKGANINEKTEFETPLHV 505
DB |||||||
QY 481 ASEKAHNDVVEVVKHEAKVNALDNLGQTSLHRAAYCGHLOTICRLLLSYGCDPNIISLQG 540
DB |||||||
QY 506 ASEKAHNDVVEVVKHEAKVNALDNLGQTSLHRAAYCGHLOTICRLLLSYGCDPNIISLQG 565
DB |||||||
QY 541 FTALQMGHENVQOLLOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
DB |||||||
QY 566 FTALQMGHENVQOLLOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 625
DB |||||||
QY 601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHVEVTELLVKHGACVN 660
DB |||||||
QY 626 STPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHVEVTELLVKHGACVN 685
DB |||||||
QY 661 VADLWKFTPLHEAAKAGKYEICKLLQHGADPTKQNRDGNTPDLVLQDGDITDIDLLRGD 720
DB |||||||
QY 686 VADLWKFTPLHEAAKAGKYEICKLLQHGADPTKQNRDGNTPDLVLQDGDITDIDLLRGD 745
DB |||||||
QY 721 AALLDAKKGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVN 780
DB |||||||
QY 746 AVLLDAKKGCLARVKXXKXFFPDNVNCRDTQGRHSTPLHL-AGXXXXXXXXXXXXXXXXXXXX 804
DB |||||||
QY 781 AQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAKQGRQTQCALLLA 840
DB |||||||
QY 805 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 864
DB |||||||
QY 841 HGADPTLNQEQOTPLDLVSDADVSAITAMPSPSALPCYKQVINGVRSPGATADALS 900
DB |||||||

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Db	865	XXXXXXXXXXXXXXXXXXXXXXXXXXXXTAAMPSPVLPSCNKPQVLNGVRSPGATADALS	924
Qy	901	SGPSSPSLSAASSLDNLSSGFSLSVSVSSSGTEGASSLEKKEVPQVDFSIITQFVRNLG	960
Db	925	SGPSSPSLSAASSLDNLSSGFSLSVSVSSSGTEGASSLEKKEVPQVDFSIITQFVRNLG	984
Qy	961	LEHLMDFEREQITLDVLVNGHKLKEIGINAYGHRHKLKIGVERLISGOQGLNPYTL	1020
Db	985	LEHLMDFXREQITLDVLVNGHKLKEIXINAYGHRHKLKISFERLISGOQGLNPYTL	1044
Qy	1021	NTSGSGTILDLSPDDKEFQSVVEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNK---	1077
Db	1045	NTSGSGTILDLSPDDKEFQSVVEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNRAKI	1104
Qy	1078	KLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAAIHKGFDERHAYIGMFGAGIYFAE	1137
Db	1105	RHEERYTHRRKEVSEENHNHANERMLFHGSPFVNAAIHKGFDERHAYIGMFGAGIYFAE	1164
Qy	1138	NSSKSNQYVYIGGGTQCPVHKDRSCYICHRQLLFCRVTILGKSELOFSAMKMAHSPGHH	1197
Db	1165	NSSKSNQYVYIGGGTQCPVHKDRSCYICHRQLLFCRVTILGKSELOFSAMKMAHSPGHH	1224
Qy	1198	SVTGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGWVDG	1240
Db	1225	SVTGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGWVDG	1267

Search completed: December 18, 2006, 17:59:55
Job time : 158.857 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2006, 17:27:10 ; Search time 38.1952 Seconds
(without alignments)
3123.657 Million cell updates/sec

Title: US-10-616-101-4
Perfect score: 6464
Sequence: 1 RCSARRGAAGGGAQRGARV.....AYPEYLITYQIMRPEGMVDG 1240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	895	13.8	1765	2 T42714	ankyrin 3, splice
2	895	13.8	1961	2 T42716	ankyrin 3, splice
3	892.5	13.8	4377	2 A55575	ankyrin 3, long sp
4	891	13.8	1943	2 T42713	ankyrin 3, splice
5	889	13.8	1940	2 T42715	ankyrin 3, splice
6	880.5	13.6	1856	2 B35049	ankyrin 1, erythro
7	880.5	13.6	1880	2 A35049	ankyrin 1, erythro
8	878.5	13.6	1881	1 SHUK	ankyrin 1, erythro
9	877	13.6	3924	2 S37431	ankyrin 2, neurona
10	876	13.6	1848	2 S37771	ankyrin, erythrocy
11	874	13.5	1862	2 T49502	ankyrin - mouse
12	866.5	13.4	1549	2 T13940	ankyrin - fruit fl
13	858	13.3	2039	2 T15347	ankyrin-related un
14	857	10.2	791	2 T42691	hypothetical prote
15	563.5	8.7	934	1 H71274	probable ankyrin -
16	552	8.5	1411	2 S30355	alpha-latroinsecto
17	507.5	7.9	1058	2 D82654	ankyrin-like prote
18	494.5	7.7	1062	2 T30255	inversin - mouse
19	489.5	7.6	1062	2 T14151	inv protein - mous
20	485	7.5	1401	2 S11527	alpha-latrotoxin p
21	463	7.2	1188	2 T19552	hypothetical prote
22	452.5	7.0	426	2 A52149	hypothetical prote
23	426	6.6	991	2 T00253	hypothetical prote
24	416.5	6.4	1184	2 T00253	gene Ankhzn protei
25	399	6.2	2584	2 T24158	hypothetical prote
26	399	6.2	2606	2 T24157	hypothetical prote
27	389.5	6.0	397	2 T46445	hypothetical prote
28	370	5.7	1031	2 T43458	hypothetical prote
29	350	5.4	557	2 T46507	hypothetical prote

30	348.5	5.4	606	2 AC2508	hypothetical prote
31	345	5.3	1423	1 I37275	death-associated p
32	343	5.3	1107	2 T21280	hypothetical prote
33	329.5	5.1	1435	2 T32930	hypothetical prote
34	321	5.0	1398	2 T21884	hypothetical prote
35	315.5	4.9	656	2 A34793	sex-determining pr
36	307	4.7	1004	2 A55142	myosin-light-chain
37	306	4.7	1016	2 T19006	ankyrin related pr
38	305	4.7	1322	2 A59288	myosin heavy chain
39	305	4.7	679	2 A54771	2-5A-dependent RNA
40	299.5	4.6	633	2 T27499	hypothetical prote
41	299	4.6	247	2 D84448	probable ankyrin l
42	297	4.6	1001	2 S30385	G9a protein - huma
43	297	4.6	1295	2 T21720	hypothetical prote
44	294.5	4.6	900	2 A42024	transcription fact
45	285.5	4.4	658	2 S68418	protein phosphatas

ALIGNMENTS

RESULT 1

T42714
ankyrin 3, splice form 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42714
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f
the repeat domain.
A:Reference number: 222237; MUID:95340633; PMID:7615634
A:Accession: T42714
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1765 <PET>
A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000029AB8; EMBL:L40632; NID:g710548; PID:
A:Experimental source: strain C57BL/6J, kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 1587/1
A:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match	13.8%	Score	895	DB	2	Length	1765
Best Local Similarity	30.3%	Pred. No.	2.8e-46				
Matches	294	Conservative	134	Mismatches	409	Indels	134
Gaps	25						
Qy	68	AVAAATMSGRGAGGGAACAAAEAVEPAARELFACRNGDVERVRLVTPKEVNSRD	127				
Db	10	AKPAHRRKKKKSDANASYLRAARAGHLEKA----	LDYIKNG-----VDVNICN	54			
Qy	128	TAGRKSTPLHPAAGRGKDVVEYLLQNGANYOARDGGLIPLHNACSGFHAFVNNLLRH	187				
Db	55	QNLGNA--LHLASKEGHVEVVSSELLQREANVDAATKKGNTALHIALAGQAEVVKVLVTN	112				
Qy	188	GADPNARDNWNYPPLHEAAIKGKIDVCIVLLOHGAETPIRNTDGTALDLA-----	DPSA	242			
Db	113	GANYNAOSQNGFTPLYMAAQENHLEVRFLDNGASQSLATEDGFTPLAVALQQGHQDV	172				
Qy	243	KAVLTGEVK---KDLESARSGNEEKWMLLTPLNVNCHASDGRKSTPLHLAAGYNRVK	299				
Db	173	SLLLENTKGKVRUPLHIAARKDDTKAALLQNDNADVESKSGFTPLHIAAHYGNIN	232				
Qy	300	IVQLLQHGADVHAKDGLVPLHNACSYGHYVTELLVKGACVNMADMLWQFTPLHEAA	359				
Db	233	VATLLNRAAAVDFTARNDIITFLHVASKRGNNANVKKLLDRGAKIDAKTRDGLTFLHCGA	292				
Qy	360	SKNRVVCSSLLSYGADPTLLNCHNKSAIDLAPTQPKERLAYEFKGHSLLQAAREADVT	419				
Db	293	RSQGEQVVMELLDRA-PILSKTKN-----	GLSLPHMATQGD--	328			

QY 541 FTALQM-----NENVOQLLQEGISLGENSEADRO--LLEAAKAGDVETVKKLCTV-OSVN 592
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 467 ETALHMAARSQAEBWRYLVQDGAQVEAKAKDDQTPLHISARLKGADI1VQOLLQQGASPN 526
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 593 CRDIEGRSQSTPLHEAAGYNRVSVVEYLLOHGADVHAOKGGGLVPLHNACSYGHYEVAELL 652
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 527 AATTSQ--YTPLHLUSAREGHEDVAFLDLHDGASLSITTKKGFTPLHVAAYKYGKLEVANLL 584
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 653 VHGAVNVNADLMKFPTPLHEAAAAGKYEICLLQLHQGDPTKKNRDGNTPLDL-VKDGD 711
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 585 LQKSASPDAAGKSGLTPLHVAHYDNQKVALLLLDQGASPHAAAKNGYTPLHIAAKKNQM 644
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 712 DIODLL-----RGDAALLDAAKKGCCLARVKKLSSPD-NVNCRDTOGRHSSTPLH 758
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 645 DIATTLLLEGADANAVENTRQGIASVHLAAQEAGHVDMVSLLLRNANVNLNKSG--LTLPL 702
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 759 LAAGYNNLEVAEYLLLOHGADVNAQDKGLIPLHNAASYCHVDVAALLIKYNACVNATDKW 818
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 703 LAAQEDRVNVAEVLVNGAHVDAQTMGYTFLHVGCHYGNIKI VNFLLQHSKAKVNARTKN 762
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 819 AFTPLHEAAQKGRGTOLCALILAHGADPTLKNOEGOTPLDL-----VSADDVSALLT-AA 871
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 763 GYTPLHQAAQOGHTHIINVLQNNASPNELTWNGNTALCIARRLGVISVVDTLKIVTEET 822
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 872 MPFSALPSCYK---POVLNGVRSPCATADALSSGPSFSSLSAASLDNLSSGSFSELSV 928
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 823 MTTTVTPEKHMNVPETMNEVL D-----MSDDEVKANAPEMLSDG----- 863
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 929 VSSSGTEGASSLEKKEVPGVDFSI TQFVRNLGLEHMDIFEREQ-ITLDVLVMGHKELK 987
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 864 -----EYISDVEGEDAMTGDTKYLGPQDLK 890
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 988 EIG 990
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 891 ELG 893
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||

RESULT 4
T42713
ankyrin 3, splice form 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42713
R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f
the repeat domain.
A;Reference number: Z22237; MUID:95340633; PMID:7615634
A;Accession: T42713
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1943 <PET>
A;Cross-references: UNIPROT.Q61307; UNIPARC.UPI0000028367; EMBL.L40632; NID:g710548; PID:
A;Experimental source: strain C57BL/6J; kidney
C;Genetics:
A;Gene: Ank3
A;Map position: 10
A;Intron: 855/1
C;Function:
A;Description: supposed to play an important role in the polarized distribution of many i
A;Note: major kidney ankyrin
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing

Query Match 13.8%; Score 891; DB 2; Length 1943;
Best Local Similarity 30.6%; Pred. No. 5.7e-46;
Matches 287; Conservative 127; Mismatches 380; Indels 144; Gaps 24;

QY 105 ACRRGVER----VKRLATYTEKNSRDTAGKSTPLHPAAGFGKDVVEYLLQNGANVOA 160
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 31 AAPAGHLEKALDYIKNGV---DVNNICNQNLNA--LHLASKGEHVVEYSSELLQREANVA 85
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||
QY 161 RDPGGHILPHNACSFGHAEVYVNLRLRHGADPNARDNNWNYPPLHFAAIKGIKIDVICVLLQH 220
Db |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||

Db 798 LKVVTEIMTTTTITEKHOMVPETMNEVLMDSDGDKCTWFKIPKQVQLVKSEDAIT 857
 Qy 901 S-----CP-----SSPSSLSAASSLNLGSGSFSELSSVWS-----SSGTEGASSL 940
 Db 858 GDTDKYLGPDQLKELGDDSLPAEGYVGSGLARSLSRFSDSRSTYTLNRSYARDSMMI 917
 Qy 941 EKKEVPGVDFISITQVRNLGLEHLMIDIFEREQITLDVL-----VEMGHKELKEIGINAY 994
 Db 918 BELLVPSKEOHLT-FTREFDSDSLRH-YSWAADTLDNVLNVSSPVHSGF--LVSFMDVAR 973
 Qy 995 G-----HRKLI-----KGVRLISGQGLANPLYTLNTSSGTHILDLSPDD 1036
 Db 974 GSGMRGSRHGMRIIIPRCKTAPTRICRLVGRKHLANPPMVEGEGLASRLVEMGPAG 1033
 Qy 1037 KEFQS-VEEEMQSTVREHGDGHAGGIFNRVNLKIQKCNKCLWE--RYTHRKEVSE- 1092
 Db 1034 AQFLGPVIVEIP-----HFGSMRGKRELIIVLRSENGETWKEHQPSKNEIDLAE 1083
 Qy 1093 ----ENNHNANERMLFHGSPFVNIIHKGFDERHAYIGMFGAGIYFAENS---SKSNQY 1145
 Db 1084 LMGDEELDSPEEL--GTKRICRIITKDFQ-----YFAVVSRIKQESNQ- 1126
 Qy 1146 VYGIQGG 1152
 Db 1127 -IGPEGG 1132

RESULT 6
 B35049
 ankyrin 1, erythrocyte splice form 3 - human
 N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 C;Species: Homo sapiens (man)
 C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
 C;Accession: B35049
 R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A;Title: cDNA sequence for human erythrocyte ankyrin.
 A;Reference number: A35049; MUID:90175370; PMID:1689849
 A;Accession: B35049
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1856 <LAM>
 A;Cross-references: UNIPARC:UPI0000177546
 C;Genetics:
 A;Gene: GDB:ANK1; ANK
 A;Cross-references: GDB:118737; OMIM:182900
 A;Map position: 8p11.2-9p11.2
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing
 F;2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
 F;2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F;77-109/Domain: ankyrin repeat homology <AN01>
 F;110-142/Domain: ankyrin repeat homology <AN02>
 F;143-171/Domain: ankyrin repeat homology <AN03>
 F;172-204/Domain: ankyrin repeat homology <AN04>
 F;205-237/Domain: ankyrin repeat homology <AN05>
 F;238-270/Domain: ankyrin repeat homology <AN06>
 F;271-303/Domain: ankyrin repeat homology <AN07>
 F;304-336/Domain: ankyrin repeat homology <AN08>
 F;337-369/Domain: ankyrin repeat homology <AN09>
 F;370-402/Domain: ankyrin repeat homology <AN10>
 F;403-435/Domain: ankyrin repeat homology <AN11>
 F;436-468/Domain: ankyrin repeat homology <AN12>
 F;469-501/Domain: ankyrin repeat homology <AN13>
 F;502-534/Domain: ankyrin repeat homology <AN14>
 F;535-567/Domain: ankyrin repeat homology <AN15>
 F;568-600/Domain: ankyrin repeat homology <AN16>
 F;601-633/Domain: ankyrin repeat homology <AN17>
 F;634-666/Domain: ankyrin repeat homology <AN18>
 F;667-699/Domain: ankyrin repeat homology <AN19>
 F;700-732/Domain: ankyrin repeat homology <AN20>
 F;733-765/Domain: ankyrin repeat homology <AN21>

F;733-765/Domain: ankyrin repeat homology <AN22>
 F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 13.6%; Score 880.5; DB 2; Length 1856;
 Best Local Similarity 26.0%; Pred. No. 2.3e-45;
 Matches 294; Conservative 156; Mismatches 374; Indels 307; Gaps 29;

Qy 105 ACRGNDVERKRLVTPKVNRSRDTAGRKSTPLHFAAGFGRKDVVVEYLQNGANVOARDG 164
 Db 52 ASKEGHVKNVVELLHKE-IILETTTKGNTALHIALAGQDEVRELVNNGANNVQSO 110
 Qy 165 GLIPLHNACSGHVAENVNLLRHGADPNARDNNMYTPLHAAIKGKIDVCIVLLOHGA 224
 Db 111 GFTEPLYMAAGBNHLEVVKFLLENGANQVATEDFTPLAVALQOQHCHENVVAHLIN 170
 Qy 225 TI-----RNTDGTALDLADPSAKAVLTGYKDELLESARSNGNEERKMALLT 275
 Db 171 KVRLLPALHIAARNDDTETA-----AVLLQNDPNPDVL--SKTG-----FTPLH 211
 Qy 276 VNCASD-----GRKS-----TPHLAAGYNRVKIVQLLLOHGDVHAKDKG 317
 Db 212 IAAHYENLVNAQLLNRGSSVNFPPQGITPLHIASRGNVIMVRLLLDRGAQIETKTKD 271
 Qy 318 DLVPLHNACSYGHVEVTELVKHGACVNMADLWQFTPLHAAASKNRVVEVCSLLSYGAD 377
 Db 272 ELTEPLHCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHLDCLVLLQYDAE- 330
 Qy 378 TLLNCHNKSAIDLAPTQLKERLAYEFKSHSLLOAAREADVTRIKKLSLEWVNFKHQ 437
 Db 331 -----ID-----DIT-----LD 337
 Qy 438 HETALHCAAAASPYPKQICELLRLKGNANTKEKFTPLHVASSEKANDNVVEVVKHE 497
 Db 338 HLTEPLHVA--HCGHHRVAKVLLDKGAKPNSRALNGFTPLHIAACKNHNVRMELLTKG 394
 Qy 498 AKVNALDNLGQTSILHRAAYCGHLQTCRLLSYCGDPNIIISLQGTALQMG-----NEN 552
 Db 395 ASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSVKVVETPLHMAARAGHTEVA 454
 Qy 553 QLLQE-----GISLGNSEADROLLE-----AAKAG 577
 Db 455 YLLQNKAKVNAKAKDDQTPHCAARIIGHTNNVKLLLENNANPNLATTAGTTPHIAAREG 514
 Qy 578 DVETVKKLCTVO--SVNCRDIEGRGSTPLHFAAGYNRVSVVEYLLOHGDVHAKDKGLVP 636
 Db 515 HVEIVLALLEKEASQACMTKKG--FTPLHVAATKGVKRVVAELLERDAHPNAAKNGITP 572
 Qy 637 LHNACSYGHVEVAELLVKHGAVNVNADLWK-FTPLHAAAAKGYEICKLLLOHGDPTKK 695
 Db 573 LHVAVHNNLDIVKLLLPGRGSPH-SPAWNGYTPHIAAKQNVQVEVARSLLQYGSANAE 631
 Qy 696 NRDGNTEPLDL-VKDGDTDIQDLRGDAALLDAKKGCLARVKKLSPPDNVNCRDTOGRHS 754
 Db 632 SVQGVTPHLAAQEGHAEMVALL-----LSKQANGNLKSG--L 669
 Qy 755 TPLHLAGYNNLEVAEYVLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNA 814
 Db 670 TPLHLVAQEGHVPADVLIKHGMVMDATTRMGYTPHVAISHYGNIKLVKFLLOHQA 729
 Qy 815 TDKWAFTPLHAAQKGTOLCALLLAHGADPTLKNOSGQTPDL-----VS 860
 Db 730 KTKLGYSPHLAAQOQHGDITVLLLNKGNASPNVSSDGTTPLAIAKRLGYISVTDVLKV 789
 Qy 861 ADDVSALLTAMPSPALPSC-----YKQP 884
 Db 790 TDETSFLVSDKHRMSPFETVDEILDVSEGEBELISFKAERRDRDVEDEKELLDVFPK 849
 Qy 885 VLNGVRSFGATADALSGSPSSLS-----AASLDNLGSGSFSELSSVSSSGTEGASS 939
 Db 850 LDQVWESPAL-----PRIPCAMPETVYIRSEEQASKEYDEDESLIPSSPATETSDN 901
 Qy 940 LEKKEVPGVDFSIQTFVRNLGLEHLMIDIFEREQITLDVLVEMGHKELKEIGINAYGHRHK 999

Db 902 ISPVASPVHTGFLVSM-----VDARGSGMRGSRHN 932

Qy 1000 LIKGVE-----RLISQOGLNPVLTNTSGSTILIDLP----- 1034

Db 933 GLRVVPIPTCAAPTRITCLRVKPKQLSTPPPLAEEGLASRIIALGPTGAQFLSPVIVE 992

Qy 1035 -----DDKEFQSVSEEMOSTVREHRDGGHAGGIFNRYNLIKIOKVCN 1076

Db 993 IPHFASHGRGDRELVLVRSENGSVWKEHR-----SRYGESYLDQILN 1034

RESULT 7

A35049

ankyrin 1, erythrocyte splice form 2 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

C;Species: Homo sapiens (man)

C;Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004

C;Accession: A35049

R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A;Title: cDNA sequence for human erythrocyte ankyrin.

A;Reference number: A35049; MUID:90175370; PMID:1689849

A;Accession: A35049

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1880 <LAM>

A;Cross-references: UNIPROT:P16157; UNIPARC:UPI0000177545; GB:M28880

C;Genetics:

A;Gene: GDB:ANK1; ANK

A;Cross-references: GDB:118737; OMIM:182900

A;Map position: 9p11.2-9p11.2

C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing; cytoskeleton

F;2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>

F;2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

F;44-76/Domain: ankyrin repeat homology <AN01>

F;77-109/Domain: ankyrin repeat homology <AN02>

F;110-142/Domain: ankyrin repeat homology <AN03>

F;143-171/Domain: ankyrin repeat homology <AN04>

F;172-204/Domain: ankyrin repeat homology <AN05>

F;205-237/Domain: ankyrin repeat homology <AN06>

F;238-270/Domain: ankyrin repeat homology <AN07>

F;271-303/Domain: ankyrin repeat homology <AN08>

F;304-336/Domain: ankyrin repeat homology <AN09>

F;337-369/Domain: ankyrin repeat homology <AN10>

F;370-402/Domain: ankyrin repeat homology <AN11>

F;403-435/Domain: ankyrin repeat homology <AN12>

F;436-468/Domain: ankyrin repeat homology <AN13>

F;469-501/Domain: ankyrin repeat homology <AN14>

F;502-534/Domain: ankyrin repeat homology <AN15>

F;535-567/Domain: ankyrin repeat homology <AN16>

F;568-600/Domain: ankyrin repeat homology <AN17>

F;601-633/Domain: ankyrin repeat homology <AN18>

F;634-666/Domain: ankyrin repeat homology <AN19>

F;667-699/Domain: ankyrin repeat homology <AN20>

F;700-732/Domain: ankyrin repeat homology <AN21>

F;733-765/Domain: ankyrin repeat homology <AN22>

F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 13.6%; Score 880.5; DB 2; Length 1880;

Best Local Similarity 26.0%; Pred. No. 2.4e-45;

Matches 294; Conservative 156; Mismatches 374; Indels 307; Gaps 29;

Qy 105 ACRNGDVERVKRLVTPPEKNSRDTAGKSTPLPHFAAGFGKDVVBYLLQNGANVOARDG 164

Db 52 ASKEGHVKNVVELLHKE-IILLETTKGNTALHIALAGQDEVRELVYNGANVNAQSQK 110

Qy 165 GLIPLHNACSGFHAEVFNLLLRHGDADPNARDNNVTPPLHEAAIKGIDKIDVICVILLQHGAP 224

Db 111 GFTPLVMAAQENHLEVVVKFLLNGANQNVATEDGFTPLAVALQQGHENVAHLINYGTKG 170

Qy 225 TI-----RNTDGRALDLADPSAKAVLTGTYKDBELLESARGNEEKWALLTPLN 275

Db 171 KVLPLALHIAARNDDTRTA-----AVLLQNDPNPDVL--SKTG-----FTPLH 211

Qy 276 VNCASD-----GRKS-----TPLHLAAGYNRVKIVQLLQHQGADVHAKDKG 317

Db 212 IAAHYENLNVACLNLNRSSVNFPTQNGITPLHIASRGNVIMVRLLLDRGAQIETKTCD 271

Qy 318 DLVPLHNACSYGHVEVTELLVKHGACVAMDLWQFTPLHEAASKNRVVECSLLLSYGADP 377

Db 272 ELTPLHCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHLDVRLLLQYDAE- 330

Qy 378 TLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLOAAREADVTRIKKLSLESMVNFKHPQT 437

Db 331 -----ID-----DIT-----LD 337

Qy 438 HETALHCAASPYPKRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVKE 497

Db 338 HLTPLHVA--HCGHHRVAKVLLDKGAKPNRSLNGFTPLHIACKKNHVRVMEILLKTG 394

Qy 498 AKVNALDNLGOTSLHRAAYCGHLQTCRLLSYGCDDPNIISLOGFTALOMG-----NENVQ 552

Db 395 ASIDAVTESGLTPLHVASFMGHLPIVKNLLQRCASPNVSNVKETPLHMAARAGHTEVAK 454

Qy 553 QLLQE-----GISLGNSEADROLLE-----AAKAG 577

Db 455 YLLQNKAKVNAKAKDDQTPHCAARIGHTNMVYKLLLENNANPNLATTAGHTPLHIAAREG 514

Qy 578 DVETVKLCITVQ--SYNCDDIEGRQSTPLHFAAGYNRVSVVEYLLQHQGADVHAKDKGLVP 636

Db 515 HVETVLALLEKEASQACMTKKG--FTPLHVAAYKGVRAELLERDAHPNAAAGKNGLTP 572

Qy 637 LHNACSYGHYEVAELLVKHGAVVNVADLWK--FTPLHEAAAKGYEICKLLLOHGADPTKK 695

Db 573 LHVAVHNNLDIVKLLPRGSGPH--SPAWNGYTPHLIAAKQKQVEVARSELLQYGGANAE 631

Qy 696 NRDGNTPIDL--VKQGDGTDIQDLRGAALLDAKKGCLARVKLSPDNVNCRDTOGRHS 754

Db 632 SVQGVTPHLAAQEGHAEMVALL-----LSQANGNLGNKSG--L 669

Qy 755 TPLHLAAGYNNLEVAEYLLQHQGADYNAQDKGLIPLHNAASVGHVDVAALLIKYNACVNA 814

Db 670 TPLHLVAQEGHVPVADVLIKHGVMVDATTRMGYTPHLVASHYGNIKLVKFLQHQADVNA 729

Qy 815 TDKWAFTPLHEAAOKGTOLCALLLAHGAADPTLKNQEGOTPLDL-----VS 860

Db 730 KTKLGYSLPHQAQOQGHDTIVTLLKNGASPNVSDGTYTPLAIAKRLGVIYVTDVLKVV 789

Qy 861 ADDVSALLTAAMPSPSALPSC-----YKPK 884

Db 790 TDETSFVLVSDKHRMSFPETVDEILDVSEDEBELISFKAERRDSRDVDEKELLDVFPK 849

Qy 885 VLVNGVRSPGATADALSSGSPSSSLS-----AASSLDNLSGSFSELSVVSSSGTEGASS 939

Db 850 LDQVVESPA-----PRIPCAMPETVIVIRSEEQEASKEYDEDSLIPSPATETSDN 901

Qy 940 LEKKEVPGVDPSITOFVNLGLEHLMDIFERQITLDVLVEMGHKELKEIGINAYGHRHK 999

Db 902 ISPVASPVHTGFLVSM-----VDARGSGMRGSRHN 932

Qy 1000 LIKGVE-----RLISQOGLNPVLTNTSGSTILIDLP----- 1034

Db 933 GLRVVPIPTCAAPTRITCLRVKPKQLSTPPPLAEEGLASRIIALGPTGAQFLSPVIVE 992

Qy 1035 -----DDKEFQSVSEEMOSTVREHRDGGHAGGIFNRYNLIKIOKVCN 1076

Db 993 IPHFASHGRGDRELVLVRSENGSVWKEHR-----SRYGESYLDQILN 1034

RESULT 8

SUHK

ankyrin 1, erythrocyte splice form 1 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N;Contains: ankyrin 2.2

Matches	292;	Conservative	157;	Mismatches	375;	Indels	307;	Gaps	28
Qy	105	ACRNGDVERKRLVTPKEKNSRDTAGRKSTPLHFAAGFGRKQYVEYLLQNGANVQARDG	164						
Db	52	ASKEGHVKVMVVELLHKE--IILETTTKKGNTALHIAALAGQDEVRELVVNGANVAGSQK	110						
Qy	165	GLIPLHNACSFGEAEVYNLLRHGADPNARDNNWYTPPLHEAAIKGKIDVCIVLLOHGAE	224						
Db	111	GFTPLMAAQENHLEVYVKELLENGANQNVATEDGFTPLVALQOQGHENVVAHLINTYTKG	170						
Qy	225	TI-----RNTDGRATLDLADPSAKAVLTGEYKKDELLESARSNEBKMALLTPLN	275						
Db	171	KVRLPALHIAARNDDTRTA-----AVLLQNDPNPDLV---SKTG-----FTPLH	211						
Qy	276	VNCHASDGRKS-----TPHLAAGYNRVKIVQLLLOHGADVHARDKG	317						
Db	212	IAAHYENLVNAQLLNRGASVNFPPQNGITPLHIASRRGNVIMVRLLDGGAQIETKTD	271						
Qy	318	DLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADP	377						
Db	272	ELTPLCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHLDCLVRLLOQYDAE-	330						
Qy	378	TLINCHNKSAIDLAPTPQLKERLAYEFKGSHLLQAAREADVTRIKKHLSLEMVNFKHQPT	437						
Db	331	-----ID-----DIT-----LD	337						
Qy	438	HETALHCAAASPYPKRKQICEILLRGKANINEKTEFLTPLHVASEKAHNDVVEVVVKHE	497						
Db	338	HLTPLHVA--HCGHRRVAKVLLDKGAKPNSRALNGFTPLHIACKNHRVVMELLKTG	394						
Qy	498	AKVNALDNLGQTSILHRAACGHLQTRCLLSVGCDDNIIISLQFTALQMG-----NENVO	552						
Db	395	ASIDAVTESGLTPLHVASPMGHLPIVKNLLQRGASPNVSNVKVETPLHMAARAGHTEVAK	454						
Qy	553	QLLOE-----GISLGNSEADROLLE-----AAKAG	577						
Db	455	YLLQNKAKVNAKAKDDQTPHCAARIQHTNMVKLLLENNANPNLATTAGHTPLHIAAREG	514						
Qy	578	DVETVKKLCTVQ--SVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGLVP	636						
Db	515	HVETVLALLEKEASQACMTKKG--FTPLHVAAKYQKVRVAELLERDAHPNAAGKNGLTP	572						
Qy	637	LHNACSYGHEVVAELLVKGAVVNVADLWK--FTPLHEAAAKGYEICKLLLOHGADPTKK	695						
Db	573	LHVAVHHNLDIVKLLPRGSGSPH--SPAWNGYTPPLHIAAKQNVARSLLQYGGSANAE	631						
Qy	696	NRDGNTPDL--VKDGDTDIIDLGRDAALLDAAKCGCLARVKLSSPDVNVNCRDTCGRHS	754						
Db	632	SVQGVTPPLHAAQEGHAENVALL-----LSQANGNLGNKSG--L	669						
Qy	755	TPHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNA	814						
Db	670	TPHLVAQSGHPVADVLIKHHGVMDATTRMGVYTPPLHVASHYGNIKLVKFLLOHQADVNA	729						
Qy	815	TDKWAFTPLHEAAQKGTQLCALLAHGADPTLKNQEGTDPDL-----VS	860						
Db	730	KTKLGYSPLHQAAQOQHTDIVTLLLKNGASPNVSSDGTTPPLAIKRLGYISVTDVLKVV	789						
Qy	861	ADDVSGALLTAAMPSPALPSC-----YKQ	884						
Db	790	TDTESFVLVDKGRMSFFETVDEIILDVSEDEGEELISFKAERRDRSDVDEEKELLDVFK	849						
Qy	885	VLNGVRSPGATADALSSGSPSSLS-----AASLDNLGSGFSSELSSVSSSGTEGASS	939						
Db	850	LQOVESPAL-----PRPCAMPETVIRSEBQEQASKEYDESDSLIPSPATETSDN	901						
Qy	940	LEKKEVPGVDFSIQTVPRNLGLEHLMDFERQITDLVLVEMGHKELKEIGINAYCHRRK	999						
Db	902	ISPVASPVHTGFLVSM-----VDARGSGMRGSRHN	932						

933 GLRVIPPRTCAAPTRICTRLVKPQKLSLTPPLAAEEGLASRIIALGPTGAQFLSPVIVE. 992

Db 821 TTTTITTEK---HKLNPVTWTEVL-----DVSDEGDDTWTGDBGYLRPEDLK 868
Qy 926 ----SSVSSSTEGASSLEKEVPCVDSITQFV--RNGLGLEHLMDFPERQITLDVLY 979
Db 869 ELGDDSLPSSQFLDGMNLYRLYSLEGRSDSLRSFSDRSHTLTHAS--YLRDSAVNDSDV 926
Qy 980 EMGHKELKEIGINAYGHRHKLKIGVERL 1007
Db 927 VIPSHOVSTLAKEAERNYRLSWGTENL 954

RESULT 10
S37771
Ankyrin, erythrocyte - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37771
R:Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J. Biol. Chem. 268, 9533-9540, 1993
A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found an
A:Reference number: S37771; MUID:93252825; PMID:8486543
A:Accession: S37771
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1848 <BIR>
A:Cross-references: UNIPROT:Q61302; UNIPARC:UPI0000028360; EMBL:X69063; NID:G311816; PID
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:48-80/Domain: ankyrin repeat homology <AN01>
F:81-113/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN03>
F:147-175/Domain: ankyrin repeat homology <AN04>
F:176-208/Domain: ankyrin repeat homology <AN05>
F:209-241/Domain: ankyrin repeat homology <AN06>
F:242-274/Domain: ankyrin repeat homology <AN07>
F:275-307/Domain: ankyrin repeat homology <AN08>
F:308-340/Domain: ankyrin repeat homology <AN09>
F:341-373/Domain: ankyrin repeat homology <AN10>
F:374-406/Domain: ankyrin repeat homology <AN11>
F:407-439/Domain: ankyrin repeat homology <AN12>
F:440-472/Domain: ankyrin repeat homology <AN13>
F:473-505/Domain: ankyrin repeat homology <AN14>
F:506-538/Domain: ankyrin repeat homology <AN15>
F:539-571/Domain: ankyrin repeat homology <AN16>
F:572-604/Domain: ankyrin repeat homology <AN17>
F:605-637/Domain: ankyrin repeat homology <AN18>
F:638-670/Domain: ankyrin repeat homology <AN19>
F:671-703/Domain: ankyrin repeat homology <AN20>
F:704-736/Domain: ankyrin repeat homology <AN21>
F:737-769/Domain: ankyrin repeat homology <AN22>
F:770-802/Domain: ankyrin repeat homology <AN23>

Query Match 13.6%; Score 876; DB 2; Length 1848;
Best Local Similarity 29.7%; Pred. No. 4.4e-45;
Matches 250; Conservative 132; Mismatches 281; Indels 178; Gaps 21;

Qy 105 ACRNGDVERKRLVTPKEKNSRDTAGRKSTPLHFAAGFGKDVVEYLLQNGVAVQARDGG 164
Db 56 ASKEGHVVMVVELLHKE-IILETTTKGNTALHIAALAGQDEVRELNVYGNVNAQSQK 114
Qy 165 GLIPLHNACSFQHAENVVLLRHGADPNARDNNVTPLHEAIAKIDVICVLLQGAEP 224
Db 115 GTPLYMAAQENHLEVVKFLENGANQNVATEDGFTPLAVLQQGHENVVAHLINYGTK 174
Qy 225 TI-----RNTDQRTALDLPKAVLGEYKKBLLSARSNGEKNWALLITPLN 275
Db 175 KVRLLPALHTAARNDDTRTA-----AVLLQNDPNPVL--SKTG-----FTPLH 215
Qy 276 VNCHASDGRKS-----TPLHLAGYNNRVKIVQLLQHGADVHAKDKG 317
Db 216 IAAHYENLVNAQLLNRGASVNFPTQGITPLHIASRRGNVIMVRLLDGRGAIETRTKD 275

Qy 318 DLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVECSLLSYGADP 377
Db 276 ELTPLHCAARNGHVRISILLDHGAPIQAKTKNGLSPIHMAAQGDHLDVRLLLQYNAB- 334
Qy 378 TLLNCHNKASIDLAPTPOKLERLAYEFKHSLLQAREADVTRIKKHLISLEWVNFKHPOT 437
Db 335 -----ID-----DIT-----ID 341
Qy 438 HETALHCAASPYPKRKQICELLRLKGANINEKTEFLTPLHVAASEKAHNDVVEVVKHE 497
Db 342 HLTPLHVA-----HCGHHRVAKVLLDKGAKPNRSLNGFTPLHIACKKHIRWELLKTKG 398
Qy 498 AKVNALDNLGOTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQV----GNENVOQ 553
Db 399 ASIDAVTESGLTPLHVASFMGHLPIVKNLQRGASPNVSNVKVETPLHMAABAGHTEVAK 458
Qy 554 LLOEGISLGNSEAD-----RQLE-----AAKAG 577
Db 459 YLLQNKAKANAKAKDDQDTPHCAARIGHTGMVKLLLENGASPNLATTAGHTPLHTAAREG 518
Qy 578 DVETVKLCTVQ--SVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDKGLVP 636
Db 519 HVDTALALLEKEASQACMTKKG--FTPLHVAAYKGVRLAELELLEHDAHNAAGNGLTP 576
Qy 637 LHNACSYGHEVVAELLVKHGAVNVNADLWK--FTPLHEAASKYBICILLQHGADPTKK 695
Db 577 LHVAVHNHNLDIVKLLPRGSGPH--SPAANGYVTPHIAAKNQIEVARSLQYGGSANAE 635
Qy 696 NRDGNTPDL--VKQGDTPIDQLLRGDAALLDAKKGCLARVKKLSPPDNVNCRDQGRHS 754
Db 636 SVQGVTPHLAAQEGHTEWALL-----LSQANGNLGNKSG--L 673
Qy 755 TPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGHVDVAALLIKYNACVNA 814
Db 674 TPLHLVSGEHPVPADVLIKHGVTDTATRMGYTPLHVAHYGNIKLVKFLQHQADVNA 733
Qy 815 TDKWAFTPLHEAAQKGRGTQCALIALHAGADPTLKNQEGQTPLDL-----VSADDSALL 868
Db 734 KTKLGYSPHQAAQGGHTDIVTLLKNGASPNVSSNGTTPLAIAKRLGYISVTDVLKV 793
Qy 869 T 869
Db 794 T 794

RESULT 11
I49502
Ankyrin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49502
R:White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory dome
A:Reference number: I49502; MUID:92345717; PMID:1386265
A:Accession: I49502
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1862 <RES>
A:Cross-references: UNIPROT:Q02357; UNIPARC:UPI000002921E; GB:M84756; NID:G191939; PID:1
C:Genetics:
A:Gene: Ank-1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:40-72/Domain: ankyrin repeat homology <AN01>
F:73-105/Domain: ankyrin repeat homology <AN02>
F:106-138/Domain: ankyrin repeat homology <AN03>
F:139-167/Domain: ankyrin repeat homology <AN04>
F:168-200/Domain: ankyrin repeat homology <AN05>
F:201-233/Domain: ankyrin repeat homology <AN06>
F:234-266/Domain: ankyrin repeat homology <AN07>
F:267-299/Domain: ankyrin repeat homology <AN08>
F:300-332/Domain: ankyrin repeat homology <AN09>

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F; 366-398/Domain:	ankyrrin	repeat	homology	<AN11>
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F; 432-464/Domain:	ankyrrin	repeat	homology	<AN13>
F; 465-497/Domain:	ankyrrin	repeat	homology	<AN14>
F; 498-530/Domain:	ankyrrin	repeat	homology	<AN15>
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F; 597-629/Domain:	ankyrrin	repeat	homology	<AN18>
F; 630-662/Domain:	ankyrrin	repeat	homology	<AN19>
F; 663-695/Domain:	ankyrrin	repeat	homology	<AN20>
F; 696-728/Domain:	ankyrrin	repeat	homology	<AN21>
F; 729-761/Domain:	ankyrrin	repeat	homology	<AN22>
F; 762-794/Domain:	ankyrrin	repeat	homology	<AN23>

Query Match 13.5%; Score 874; DB 2; Length 1862;
Best Local Similarity 29.7%; Pred. No. 5.9e-45;
Matches 250; Conservative 132; Mismatches 281; Indels 17

Qy	105	ACRNGDVERVKRLVTPBKVNSRDTAGRKSTPLPHFAAGFRKDVVEYLLONGANVQAORDDG	164
Db	48	ASKEGHVKMVVELLHK-E-IILETTTKKGN TALHIAALAGODEVRELVYNGYANNAOSQK	106
Qy	165	GLIPLHNACSPGHAEVUNLLRHGADPNARDWNVYTPLHEAAIKGKIDVCIVLLOHGAE	224
Db	107	GFTPLYMAAOENHLEVKFLENGANQVATEDGFTPLAVALQOQHENVVAHLINYGTKG	166
Qy	225	TI-----RNTDGR TALDPSAKAVATIGEYKDKDELLESASNGNEEKWALLPLN	275
Db	167	KVRLPALHIAARNDTRTA-----AVLQNDPNPDLV--SKTG-----FPLH	207
Qy	276	VNCHASDGRKS-----TPLHAAGYNRVKIIVOLLQHGADVHAKDKG	317
Db	208	IAAHYENLNVAAQLLLNRGASVNFPTQNGITPLHIASRRGNVIMVRLLLDRGAQIETRTKD	267
Qy	318	DLVPLHNACSYGHVEYVELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLISYGADP	377
Db	268	ELTPLHCAARNGHVRISBILLDHGAPIAKTKNGLSPLHMAAQGDHLDVCRLLHQYNAB-	326
Qy	378	TLNCHNKSATDLAPTOLKERLAYEPFGKHSLLQAAREADVTRIKKHSLEWVNFKHPQT	437
Db	327	-----ID-----DIT-----LD	333
Qy	438	HETALHCAAASPYPRKQICELLRRKGANINEKTFPLPHVASEKAHNDVVEVVKHE	497
Db	334	HLTPLHVAA---HCGHHRVAVLDKGAKPNSRALNGFTPLHIACKKHIRVWELLKKG	390
Qy	498	AKVNALDNLGOTS LHRAAVYCHLOT CRLLLSYGDPNIIISLGFTALOM-----GNENVQO	553
Db	391	ASIDAUTESGLTPLHVASFMGHLPLVKNLLQRGASPNVSNVKVETPLHMAARAGHTEVAK	450
Qy	554	LLQEGISIGNSEAD-----ROLLE-----AAKAG	577
Db	451	YLLQNKAKANAKAKDDQTPLHCAARIIGHTGMVKLLENGASPNLIATTAGHTPLHTAAREG	510
Qy	578	DVEVTKLCTVQ--SVNCRDIEGRSTPLHFAAGYNRVSVWYLLQHGADVHAKDKGLVP	636
Db	511	HVD TALALLEKASQACMTKKG--FTPLHVAAYKGVKVLAEULLLEHDAHNAAGKNGLTP	568
Qy	637	LHNAACSYGHVEABELLVKHGAVNVNADLWK--FTPLHEAAAKGKVEICKLLQHGADPTKK	695
Db	569	LHVAVHNNLDIVKLLPRGGS PH-SPAWNGVTPHLHIAAKQNOIEVARSLLYQGGSANAE	627
Qy	696	NRDGNTPLDL-VKGDGDTDIQDLIRGDAALLDAAKGKCLARVKKLSSPDNVNCRDTQGRHS	754
Db	628	SVQGVTPPLHAAOEGHTEWALL-----LSKQANGLNKGSG--L	665
Qy	755	TPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGHVDVAALTIKYNACVNA	814
Db	666	TPLHLVSGEGHVLVADVLIKGVTVDTATRRMGVYTPLHVASHYGNIKLVKFLLOHQADVNA	725
Qy	815	TDKWAFTPLHEAAQKGRTOQLCALLLHAGADPTLKNQEGOTPLDL-----VSADPVSALL	868

Db 726 KTKLGYSPLHQAQAQGHDTDIVTLLKNGASPNVSSNGTTPLATAKRLGYISVTDVLKV 785
 Qy 869 T 869
 |
 Db 786 T 786
 RESULT 12
 Tk13940
 ankyrin - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: Tk13940
 R:Dubreuil, R.R.; Yu, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
 A:Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin :
 A:Reference number: Z17820; PMID:95024098; PMID:7937942
 A:Accession: Tk13940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1549 <DUB>
 A:Cross-references: UNIPROT:Q24241; UNIPARC:UPI0000007E386; EMBL:L35601; NID:955
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0011747

Query Match	13.4%;	Score 866.5;	DB 2;	Length 1549;
Best Local Similarity	27.4%;	Pred. No. 1.3e-44;		
Matches 311;	Conservative 173;	Mismatches 492;	Indels 159;	Gaps 34
Qy	98	AARELFECRNGDVERVKRLV----	TPEKVSGRDTAGRKSTPLHFAAGFGKDKDQVVEYLQN	154
Db	38	ATISFLRAARSGDIKKWDFDLCGEIS	DINSCNANGLNA--LHLAAKQGYVDICCELLRR	95
Qy	155	GANYQARDGGGLIPLHNACSPGHABV	NVLLRLHGGADPNARDNWNVTPPLHEAAIKGKIDVC	214
Db	96	GIKIDNATKKGNTALHIASLAGQHDVI	NQILLYNANVNVQSLNGFTPLPYMAQENHDNCC	155
Qy	215	IVLLQHGAEPITRTDGTALDLA----	DPSAKAVLTGEYK--KDELLESARGSNEEK	266
Db	156	RTLIIANGANPSLSTEDGTFPLAVAN	QQQHDKIIVALLENDVRGKVRPLPALHTAAKQNDVN	215
Qy	267	MWALLTPLNVNCHASDGRKSTPLHLA	AGYNRVKIVOLLQHGADVHAKDGLVPLHNAC	326
Db	216	AAKULLQHPNADIVSKSGFTPLHIAH	YGVNDVIATLLNNKADVNYVAKHNITPLHVAC	275
Qy	327	SYGHVEVTELLVKHGACVYNMDLWQF	TPLHEAASKVRVEVCSLLLSYGADPTLLNCHN-K	385
Db	276	KWGKLSLCTLLCRGAKIDAATRDGLT	PLHCASRSGHVEVIKHLLOQNA-PILTTKYNGL	334
Qy	386	SAIDLAPTQPKERLAYBFKGHSLSLQA	AREADVTRIKKHLSLE-----MVNF	432
Db	335	SALHWAQAQGE-----HDEAAHLL	LDNKAPVDEVTVDTALHVAAHCGHVKVALLLDY	388
Qy	433	K-HPOTHE-----TALHCAAASPYPK	RKQICEILLRKGANINEKTEFLTPLHVASEKAHN	487
Db	389	KANPNARALNGFTPLHIAACK--NR	IKKVELLIKHGANIGATTESGLTPLHVASFWGCI	445
Qy	488	DVEVVVHGEAKVNALDNLGOTSLHRAA	YCQHLOTCRLLLSYGCDPNIISLQOFTAL---	544
Db	446	NIVVYLLOHGEASADLPTTGETTPLH	ARANQADIIRILLR-SAKVDAIVREGOTPLHVA	504
Qy	545	-QMGNEN-VQOLLQEGISLGNSEADR-	-QLLEBAKAGADVETVKKLTCTVOSVNCRDIEGRQ	600
Db	505	SRLGNINIMILLQHGAEINQAQNDKY	SALHTAAKEGQENIIVQVLLENGAEIN-NAVTKKG	563
Qy	601	STPLHFAAGYNRVSVVEVYLLOHGAD	VHAKDKGGLVPLHNACSYGHVEVAELLVKHAQVNV	660
Db	564	FTPLHLACKYQGNVVQILLQNGASID	FQCKNDVTPLVAVATHYNNPISVELLLKNGSSPN	623
Qy	661	VADLWKFTPLHEAAAKGYEICKLLLOH	GADPTKKNRDGNTPDL-LVKDGDITDIQDLRRG	719
Db	624	LCARNGOCAIHTACKNTYLEIAMOLLO	HGADVNIISKSGFSPLHLAAQCGNVDVMQVLLLE	683


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Db 579 RGPV-----DIEGKQVTPHVAHYNNDKVMALLLENG 613
Qy 777 ADVNAQKGLIPLHNAASYGHVDAALLIKYNACVNATDKWAFTPLHFAAQKRGRTOLCA 836
Db 614 ASAKAAAKNGVTPHLIAAKKQMEIATLLQPKADPNKSRAGTPLHLSAQEGHKEISG 673
Qy 837 LLLAHGADPTLKNQEGQTPDLVADD-----VSALLTAAMPSPSALPCYK 882
Db 674 LLIENGSDVGAKANGLUTAMHLCAQEDHVPVPAQILYNNGAELNSKTNAGYTPHLHV-ACHF 732
Qy 883 PQVLNGVR---SPGATADALSSGSPSSLSAASSLNLGSGFSELSSVSSSGTEGASS 939
Db 733 GQ-LNMVKFLVENGADVGEKTRASYTPHLHQAQQOQHNNVCVYLLE-----NGASP 781
Qy 940 LEKKEVPQVDFSTQFVRNLG---LEHLMDFPREQITLDVLVEMGHKELKEIGIN--- 992
Db 782 NEQATGQTPLSIAQ---RLGVSVWETRLVTVTITTTTVDERYKPNQPEAMNETM 838
Qy 993 -----AYGHRKLI-----KGVRLISGOOGLNPVTLNTSG--- 1024
Db 839 FSESEDEGQAABEVAHAHEKDFSDNLTQGLQDSTGVHMIHTGBQLLQRSQELENGGAIP 898
Qy 1025 ---SGTILIDLPDKFQSFQSEEMQS---TVREHRDG--GHAGGIFNRVNIILKIQVC 1075
Db 899 KING---GMSPT-EKEFAKTAIPVATSPINTSOSFGIAPRAGSISGGFQQOPLHGAG 953
Qy 1076 NKLWERYTHRRKE--VSEENHNHANERMLPHGS---PFVNAIHKGF-----DERHA 1123
Db 954 PEDNLEELVRAQHNPINAGNYDNGGVAMLENGHADNVPIGHVHTQPSFLISPLVDARGG 1013
Qy 1124 YIGMFAGIYFAENSCKSNQYVIGGGTCTCPVHKDRSCVICHRLQLFCRVTLGKFKLQ 1183
Db 1014 AMRCRHSVGRVILVPPRKASQ-----PIR-----VTCRY-LRKO--- 1046
Qy 1184 FSAKMAHSPP 1194
Db 1047 ---KLAHPPP 1053

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T42691
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C;Species: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42691
R;Blöcker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A;Reference number: 222230
A;Accession: T42691
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-791 <AAA>
A;Cross-references: UNIPROT:Q9UPA4; UNIPARC:UPI000006DC92; EMBL:AL133087
A;Experimental source: adult testis; clone DKEZp434D2328
C;Genetics:
A;Note: DKEZp434D2328.1

Query Match
Beat Local Similarity 10.2%; Score 657; DB 2; Length 791;
Matches 243; Conservative 115; Mismatches 331; Indels 172; Gaps 29;

Qy 102 LFEACRNGDSERVKRLVT-PBKVNSRDTAGRKSTPLHFAAGFGKRVVYLLQNGANVQA 160
Db 7 LHAASNGQINVKHLLNLGVEIDEINVG--NTALHIACYNGQDAVNVNELIDYGANVQ 64
Qy 161 RDCGGLPLHNACSGFH-ABVVNLLRHGADPNARDNNVYTPLEAAKKGIDVCIVLQ 219
Db 65 PNNNGFTPLHFAASTHGALELLVNGADVNIQSKDGKSPLHMTAVHGRFTRSQTLIQ 124
Qy 220 HGABFTTRNTDGTALDLPDSAKAVLTGYEYKQDELLESARSNGNEKMMALLT----- 272
Db 125 NGGEIDCVDKGNTPHVA-----ARYGHELLINTLITSGADTAK 164
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Qy 273 -----PLN---VNCHA-----SDGRK-----STP-----L 289
Db 165 CGHSMFPPLHLAALNAHSDCCRKLLSGQKYSIVLPSNEHVLVSAGFEIDTPDKFGRTCL 224
Qy 290 HLAAGYNRVKIVQLLQHQHADVHAKDKGLVPLHNACSYGHYEVTELLVHKHACVNAMD 349
Db 225 HAAAAGNVCEIKLQSSGADPHKDKCGRTPLHYAAANCHFHCIETLVTTGGANVNETDD 284
Qy 350 WQFTPLHAAAKNRVVCVSLLSYGDPTLL-NCHNKAIDLAPTPOKLER---LAYEFK 405
Db 285 WGRTHLYAAASD-----MDRNKTILGNADHNS-ELERARELKEKEATLCLEF- 332
Qy 406 GHSLLQAAREADVTRIKKLSLEWVAFKHPQTHE---TALHCAAAASPYPKPKOICELL 461
Db 333 ---LLQ-----NDANPSIRDKEGYSIHAAAAYGH---ROCLELL 367
Qy 462 RKGANINEKTKFELT--PLHVASEKAHNDVVVVVHEAKVNALDNLGQTSLHRAAYCGH 519
Db 368 ERTNSGFEESSDGNATKSPHLAAAYNGHQAELVQLSLVDLDIRDEKGRALTDLAAFKGH 427
Qy 520 LQTCRLLSYGCDPNTISLQGFALTQNGENVQQLQEGISLGNSEADROLLEAAKAGDV 579
Db 428 TECVEALIN-----QGASIFVKDNTKRTPLHASVINGHTLCRLLELLEAD--- 473
Qy 580 ETVKKLTQVSNCRDIEGRSQSTPLHFAAGYNRVSVVYLLQHGADVHAKDKGLVPLHN 639
Db 474 -----NPEADVQKDAQG--TPLMLVAAYGHIDAVSLLEKEANVDTVDILGCTALHR 524
Qy 640 ACSYGHVEAELVKGHGVVNVADLMKFTPLHFAAAAKGYEICKLLQHG---ADPTKGN 696
Db 525 GIMTGHECVQMLEGEVSLCKDSRGRTPLHYAAARGHATLSELQALSEEDCCCFKD 584
Qy 697 RDGNTPLD--LVKGDPTDIQDLR-----GD-----AALLDAKKGLCARVKLS 739
Db 585 NQGYTPLHWAACYNENNCIEVLEQKCFKFIQNPFTPLHCAIINDHG--NCASILLGAI 642
Qy 740 SPDVNCRDTOGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHV 799
Db 643 DSSIVSCRDDKGR--TPLHAAAFADHVECIQLLRHSAPVNAVDSNGKTLMAAENGQA 700
Qy 800 DVAALII-KYNACVNATDKWAFTPLHFAAQKRGRTQLCALLAHGADPTL---KNOEGQTP 855
Db 701 GAVDILVNSAQADLTVDKDKLNTPLHLACSKGHEKCALLIILDKIQDESLINEKNALQTP 760
Qy 856 LDLVSADDDVSALLTAAMPSPA 876
Db 761 LHVAARNGLKVVVEELIAKGA 781

RESULT 15
H71274
probable ankyrin - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H71274
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin,
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McMor
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71274
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-934 <COL>
A;Cross-references: UNIPROT:O83807; UNIPARC:UPI000000D32A9; GB:AE001254; GB:AE000520; NID:
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0835
C;Superfamily: syphilis spirochete probable ankyrin; ankyrin repeat homology
F;281-313/domain: ankyrin repeat homology <AN2>

Query Match
8.7%; Score 563.5; DB 1; Length 934;
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Best Local Similarity 23.8%; Pred. No. 2.2e-26; Matches 254; Conservative 159; Mismatches 373; Indels 281; Gaps 36;

859 KNTSILKTLVGFAVNKTDGAGESILHYAAKVADEKTLQGLLAMNRF 905
Search completed: December 18, 2006, 17:35:54
Job time : 46.1952 secs

QY	86	ACASAAAEAVEPAARELFEACRNGDVERVKRLVTEPEKNSRDTAGRKSTPLHFAAGFRK	145
Db	24	SCITSSSPQ-ASVDLFEMVARGDLDLTKRFGKDSVNVDRANG--DTLLH--VGVLRN	78
QY	146	D--VVEYLLQNGANYQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNMNYPLH	203
Db	79	DAHVVDFLLSMGADTEAQDASGTPLMVAVENTCFESVEMLIARDASLFSRDAQDTPLT	138
QY	204	EAAIKGKIDVICV-----LLQH-----GAETIRNTDGRTA	234
Db	139	RAIRKGTAEHLVTRKTLQKDSGKTPMHWAVRALDRDLIKHLVTLGPPPTQERDADGHTP	198
QY	235	LQADPSAKAVLTGEYKDELLESAR--SGNEEKWALITPLNVNCHASDGRKSTPLHLA	292
Db	199	LSLAYSSSDARAAEVAADLLGGELMHGSPSEFIAVLKKNYDLHFTDG--STPLHVM	256
QY	293	AGYNRVKIVQLLQHGADVHAKDKGDLVPLHNACSYGHEVTELLVKGACVNMADLMQF	352
Db	257	AKGYTGFGVQFLVDRKVNNAK-----NLSSA	283
QY	353	TPLEAASKRVEVCSLLSYGADPTLNCNKSALDL--APTPQKRLAYEFKGHSLLQ	411
Db	284	TPLEAVRAGQVDAAVLLLRSGADPNVRDASGNTCLHLVAPAP--FRVRLV-----GALLD	337
QY	412	AAREADVTRIKHLSLEWNVFKPQTHETALCAAAPYKPKQICEILLRKGANINEKT	471
Db	338	AGASVAI-----KDYGETPLHVAAR--LGMDFRPFVRLVVGAGADISERN	380
QY	472	KEFLTPLHVAEKAHNDVVVVVKEAKVNALDNLGQTSIHRAAYCGHLOTCLRLIS---	528
Db	381	KKGETPLVLTIDRDRDLTAIFYSLGADIHAEDMERGETPLTKALARG--LETVKIVVTDN	439
QY	529	-----YGDNPNIISLQGPITALQMNENVQQLQEGISIGNSEADRLLEAAKAGDVETV	582
Db	440	LYKQDVWGRDPLHVAVSRRAHLDI-----VKFLFRE-----PKQMI-----	475
QY	583	KCLTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLLQHGAD-----	625
Db	476	-----ARDTWG--NTLLHYAVANDDRVAGBFLMRGADIFSTNVHGVSPKLTALT	523
QY	626	-----VHAKDKGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLH	671
Db	524	TSGREDMLTAAVNHVADTGGNTPLHACEWKLTAINGILRKGAIEARNLQETPLF	583
QY	672	EAAAKGKYEICKLLOHGADPTKKNRDNTPDLVKOGDTDIQLLRGDAALLDAKKGC	731
Db	584	SAVKSDAAEVISILLHPQ-----GPNALVDA-----	610
QY	732	LARVKLSPPDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLL-----QHGADVNAQDKG	786
Db	611	-----RDVAG--NTVLHACVRSALRSADVLIREADARHVSLLNARNLSG	653
QY	787	LPLHNAASYGHVDVAALLIKYNACVATDKWAFPLHEAOKGRTQCLCALLAHGADPT	846
Db	654	KEPLHLAARAGVNDPTRLILLSRVVLMGDETKSALTDAVLADQEEVHMLLSAGANPV	713
QY	847	LKNQEGQTPDLVSDADDVALLTAAMPSPALPSCYKQVNLNGVRSFGATADALSSGSPSP	906
Db	714	QDMYGRTPFH-----EAVL-----CNSQSVIAALRAAGGNPFARDSYGTTT	755
QY	907	SSLSAASSLDNLSGSFSELSVVSSSGTEGASSLE---KKEVPGVDFTSQFVNLGLEH	963
Db	756	LSLALLKG--DTFVGAVVGKDPPLANS--DGQTPHLAVMENVPVQTF-----RLLLAK	805
QY	964	LMDIFEREQITLDVLVEMGHKELKEIGINAYGHRKLIK--GVERLISGOQGLNP---YLT	1019
Db	806	GYPIDKRDGMSSALVLAIKKORSDL-----CHELLAGADLFIANNVGESPALLVLS	858
QY	1020	LNTSGSGTIL-IDLSPDDKQFQSV-----EEMQSTVREHRDG	1056

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:21:50 ; Search time 248 Seconds
(without alignments)
4625.078 Million cell updates/sec

Title: US-10-616-101-4

Perfect score: 6464

Sequence: 1 RCSARRGAAGGQAGRGARV.....AYPEYLITYIMRPEGMVDG 1240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6108	94.5	1166	1	TNKS2 HUMAN
2	5760.5	89.1	1167	2	Q800E0 CHICK
3	5103.5	79.0	1327	1	TNKS1 HUMAN
4	5098	78.9	1320	2	Q5PEX9 MOUSE
5	5095.5	78.8	1327	2	Q4G0F2 HUMAN
6	5074	78.5	1266	2	Q800D9 CHICK
7	5010.5	77.5	1303	2	Q5XGK5 XENLA
8	4875.5	75.4	1212	2	Q4RG97 TETNG
9	4681.5	72.4	1055	2	Q59FX0 HUMAN
10	4285.5	66.3	976	2	Q8BX62 MOUSE
11	4156.5	64.3	1168	2	Q7PYH8 ANOGA
12	4005	62.0	1181	2	Q9VBP3 DROME
13	3997	61.8	1181	2	Q9XZ37 DROME
14	3324	51.4	1047	2	Q4S372 TETNG
15	3066	47.4	601	2	Q8BXH7 MOUSE
16	3013	46.6	589	2	Q3UES3 MOUSE
17	2063	31.9	408	2	Q5P537 MOUSE
18	1944.5	30.1	471	2	Q4FZM0 XENLA
19	906	14.0	1806	2	Q574D8 RAT
20	906	14.0	1984	2	Q574D7 RAT
21	904	14.0	1136	2	Q9N180 BOVIN
22	897	13.9	1861	2	Q7Z3G4 HUMAN
23	895	13.8	1765	2	Q4U258 MOUSE
24	895	13.8	1961	2	Q4U256 MOUSE
25	894	13.8	1861	2	Q5CZ99 HUMAN
26	893	13.8	1726	2	Q4VC68 MOUSE
27	892.5	13.8	4377	1	ANK3 HUMAN
28	891	13.8	1943	2	Q4U259 MOUSE
29	889	13.8	1940	2	Q4U257 MOUSE
30	888.5	13.7	1762	2	Q88521 RAT
31	885.5	13.7	2622	2	Q70511 RAT

32	882	13.6	4372	2	Q5VXD5 HUMAN	Q5vxd5 homo sapien
33	880.5	13.6	1863	2	Q723L5 HUMAN	Q723L5 homo sapien
34	880	13.6	1856	2	Q99407 HUMAN	Q99407 homo sapien
35	878.5	13.6	1719	2	Q13768 HUMAN	Q13768 homo sapien
36	878.5	13.6	1880	1	ANK1 HUMAN	P16157 homo sapien
37	877	13.6	1899	2	Q59FF2 HUMAN	Q59ff2 homo sapien
38	877	13.6	3924	1	ANK2 HUMAN	Q01484 homo sapien
39	876	13.6	1848	2	Q61302 MOUSE	Q61302 mus musculus
40	876	13.6	1878	2	Q3UHP2 MOUSE	Q3uhp2 mus musculus
41	876	13.6	1907	2	Q3UHP2 MOUSE	Q3uhp2 mus musculus
42	875	13.6	1950	2	Q4RT14 TETNG	Q4rt14 tetraodon n
43	875.5	13.5	4408	2	Q4RNF0 TETNG	Q4rnf0 tetraodon n
44	874	13.5	1862	1	ANK1 MOUSE	Q02357 mus musculus
45	872	13.5	1219	2	Q8C9R3 MOUSE	Q8c9r3 mus musculus

ALIGNMENTS

RESULT 1	
TNKS2 HUMAN	
ID TNKS2 HUMAN STANDARD; PRT; 1166 AA.	
AC Q9H2K2; Q9H8F2; Q9HAS4;	
DT 27-MAR-2002, integrated into UniProtKB/Swiss-Prot.	
DT 01-MAR-2001, sequence version 1.	
DT 07-MAR-2006, entry version 41.	
DE Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1-interacting ankyrin-related ADP-ribose polymerase 2) (Tankyrase-like protein) (Tankyrase-related protein).	
DE Name=TNKS2; Synonyms=PARP5B, TANK2, TNKL;	
GN Homo sapiens (Human).	
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC Homo.	
OC NCBI_TaxID=9606;	
OX [1]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Fetal brain;	
RX MEDLINE=21072550; PubMed=11205898;	
RA Monz D., Munnia A., Comtesse N., Fischer U., Steudel W.-I., Feiden W., Glass B., Meese E.U.;	
RT "Novel tankyrase-related gene detected with meningioma-specific sera."	
RL Clin. Cancer Res. 7:113-119(2001).	
RN [2]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Mammary carcinoma;	
RX MEDLINE=21190090; PubMed=11294570; DOI=10.1038/ej.gene.6363722;	
RA Kuimov A.N., Ruprash D.V., Petrov V.N., Vdovichenko K.K., Scanlan M.J., Jongeneel C.V., Lagarkova M.A., Nedospasov S.A.;	
RT "Cloning and characterization of TNKL, a member of tankyrase gene family."	
RL Genes Immun. 2:52-55(2001).	
RN [3]	
RP NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.	
RC TISSUE=Liver;	
RX MEDLINE=21264473; PubMed=11278563; DOI=10.1074/jbc.M009756200;	
RA Lyons R.J., Deane R., Lynch D.K., Ye Z.-S.J., Sanderson G.M., Eyre H.J., Sutherland G.R., Daly R.J.;	
RT "Identification of a novel human tankyrase through its interaction with the adaptor protein Grb14."	
RL J. Biol. Chem. 276:17172-17180(2001).	
RN [4]	
RP NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.	
RC TISSUE=Placenta;	
RX MEDLINE=21443728; PubMed=11454873; DOI=10.1074/jbc.M105968200;	
RA Kaminker P.G., Kim S.-H., Taylor R.D., Zebrafidian Y., Funk W.D., Morin G.B., Yaswen P., Campisi J.;	
RT "TANK2, a new TRF1-associated poly(ADP-ribose) polymerase, causes rapid induction of cell death upon overexpression."	
RL J. Biol. Chem. 276:35891-35899(2001).	
RN [5]	
RP NUCLEOTIDE SEQUENCE, FUNCTION, AND INTERACTIONS WITH TRF1 AND	

RP LNPEP/OTASE.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=21661461; PubMed=11802774; DOI=10.1042/0264-6021.3610451;
 RA Sbioio J.I., Lodish H.F., Chi N.-W.;
 RT "Tankyrase-2 oligomerizes with tankyrase-1 and binds to both TRF1
 RT (telomere-repeat-binding factor 1) and IRAP (insulin-responsive
 RT aminopeptidase).";
 RL Biochem. J. 361:451-459(2002).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA Yin Y., Gelmann E.P.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15164054; DOI=10.1038/nature02462;
 RA Deloukas P., Earthworm M.E., Grafham D.V., Rubenfield M., French L.,
 RA Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
 RA Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
 RA Taylor A., Batties J., Bird C.P., Alnough R., Almeida J.P., Camire D.,
 RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Beggule C.B., Bailey J.,
 RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
 RA Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,
 RA Carter N.P., Chapman J.C., Clark S.V., Clarke G., Clee C.M., Clegg S.,
 RA Corby N., Coulson A., Dhani P., Dutta I., Dunn M., Faulkner L.,
 RA Frankish A., Frankland J.A., Garner P., Garnett J., Gribble S.,
 RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,
 RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
 RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
 RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,
 RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,
 RA Loveland J., Lovell J., McLaren S., McIay K.E., McMurray A.,
 RA Madhugri-Mohammadi M., Matthews L., Milne S., Nickerson T.,
 RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,
 RA Pellan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
 RA Sarafidou T., Sehra H.K., Showkhen R., Skuce C.D., Smith M.,
 RA Standing L., Sycamore N., Teater J., Thorpe A., Torcaso W.,
 RA Tracey A., Fromans A., Isolas J., Wall M., Walsh J., Wang H.,
 RA Weinstock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,
 RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
 RA Siebert R., Fichtel K., Bentley D., Durbin R., Hubbard T.,
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 10.";
 RL Nature 429:375-381(2004).
 RN [8]
 RP TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Negahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirakawa K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotsuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Toshiya S., Komai F., Hara R., Takeuchi K., Arita M., Inose N.,
 RA Mueshino K., Yuuki H., Ohshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe K., Kunagai A., Takemoto M., Kawakami B.,
 RA Yanazaki M., Watanabe M., Taniguchi A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [9]
 RP FUNCTION, AND ADP-RIBOSYLATION.
 RX MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002;
 RA Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
 RT "Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2
 RT at human telomeres.";
 RL Mol. Cell. Biol. 22:332-342(2002).
 RN [10]
 CC -!- FUNCTION: May regulate vesicle trafficking and modulate the
 CC subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP
 CC activity and can modify TRF1, and thereby contribute to the
 CC regulation of telomere length.
 CC -!- CATALYTIC ACTIVITY: NAD(+) + (ADP-D-riboseyl) (n)-acceptor =
 CC nicotinamide + (ADP-D-riboseyl) (n+1)-acceptor.
 CC -!- SUBUNIT: Oligomerizes and associates with TNKS. Interacts with the
 CC cytoplasmic domain of LNPEP/Oase in SLC2A4/GLUT4-vesicles. Binds
 CC to the N-terminus of Grb14 and TRF1 with its ankyrin repeat
 CC region.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and
 CC with juxtanuclear SLC2A4/GLUT4-vesicles. Also found around the
 CC pericentriolar matrix of mitotic centrosomes. During interphase, a
 CC small fraction of TNKS2 is found in the nucleus, associated with
 CC TRF1.
 CC -!- TISSUE SPECIFICITY: Highly expressed in placenta, skeletal muscle,
 CC liver, brain, kidney, heart, thymus, spinal cord, lung, peripheral
 CC blood leukocytes, pancreas, lymph nodes, spleen, prostate, testis,
 CC ovary, small intestine, colon, mammary gland, breast and breast
 CC carcinoma, and in common-type meningioma. Highly expressed in
 CC fetal liver, heart and brain.
 CC -!- PTM: ADP-ribosylated (-auto).
 CC -!- SIMILARITY: Contains 15 ANK repeats.
 CC -!- SIMILARITY: Contains 1 PARP catalytic domain.
 CC -!- SIMILARITY: Contains 1 SAM (sterile alpha motif) domain.
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: AF305081; AAG25674.1; ALT INIT; mRNA.
 CC EMBL: AF264912; AAG44694.1; -; mRNA.
 CC EMBL: AF329696; AAK13463.1; -; mRNA.
 CC EMBL: AF342982; AAK25811.1; -; mRNA.
 CC EMBL: AF309033; AAK82330.1; -; mRNA.
 CC EMBL: AF438201; AAL40795.1; -; mRNA.
 CC EMBL: AL359707; CAC78760.1; -; Genomic DNA.
 CC EMBL: AK023746; BAB14665.1; ALT_INIT; mRNA.
 CC HSSP: P16157; IN11.
 CC Ensembl: ENSG00000107854; Homo sapiens.
 CC HGNC: HGNC:15677; TNKS2.
 CC MIM: 607128; Gene.
 CC InterPro: IPR001290; PARP.
 CC InterPro: IPR012317; PARP_catalytic.
 CC InterPro: IPR001660; SAM.
 CC InterPro: IPR011510; SAM_2.
 CC Pfam: PF00023; Ank; 17.
 CC Pfam: PF06644; PARP; 1.
 CC Pfam: PF07647; SAM_2; 1.
 CC SMART: SM00248; ANK; 15.
 CC SMART: SM00454; SAM; 1.
 CC PROSITE: PS00297; ANK_REPEAT; 1.
 CC PROSITE: PS00088; ANK_REPEAT; 15.
 CC PROSITE: PS01059; PARP_CATALYTIC; 1.
 CC PROSITE: PS0105; SAM_DOMAIN; 1.
 CC ADP-ribosylation; ANK repeat; Chromosomal protein;
 CC Glycosyltransferase; Golgi stack; NAD; Nuclear protein; Repeat;
 CC Telomere; Transferase.
 CC CHAIN 1 1166 Tankyrase 2.
 CC REPEAT 57 89 ANK 1.
 CC REPEAT 90 122 ANK 2.

FT	REPEAT	123	155	ANK 3.
FT	REPEAT	210	242	ANK 4.
Query Match				
Best Local Similarity 94.5%; Score 6108; DB 1; Length 1166;				
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	75	MSGRCCAGGGAACASAAAEEAVEPAARELFEACRNGDVERVKRLVTPPEKVNSRDITAGRKST	134	
Db	1	MSGRCCAGGGAACASAAAEEAVEPAARELFEACRNGDVERVKRLVTPPEKVNSRDITAGRKST	60	
Qy	135	PLHFAAGFRKDVVYLLQNGANVQARDGGGLPLHNACSFHAEVNVLLRHGADPNAR	194	
Db	61	PLHFAAGFRKDVVYLLQNGANVQARDGGGLPLHNACSFHAEVNVLLRHGADPNAR	120	
Qy	195	DNWNTYPLHEAAIKGKIDVICVLLQHGAEPTIRNTDGTALDADPSAKAVLTGYYKDE	254	
Db	121	DNWNTYPLHEAAIKGKIDVICVLLQHGAEPTIRNTDGTALDADPSAKAVLTGYYKDE	180	
Qy	255	LLESARSGNEEKWALLTFLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAK	314	
Db	181	LLESARSGNEEKWALLTFLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAK	240	
Qy	315	DGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYG	374	
Db	241	DGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYG	300	
Qy	375	ADPTLLNCHNSAIDLATPQLKERLAYEFKGSLLQAREADVTRIKKHSLEWVNFKH	434	
Db	301	ADPTLLNCHNSAIDLATPQLKERLAYEFKGSLLQAREADVTRIKKHSLEWVNFKH	360	
Qy	435	PQTHETALHCAAASYPKPKQICELLKRGANINEKTEFTPLHVAASEKAHNDVVEVV	494	
Db	361	PQTHETALHCAAASYPKPKQICELLKRGANINEKTEFTPLHVAASEKAHNDVVEVV	420	
Qy	495	KHEAKVNDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQNGENVQOL	554	
Db	421	KHEAKVNDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQNGENVQOL	480	
Qy	555	LOEGISLGNSEADROLLEAKAGDVETVKKLTQVSNCRDIEGQSTPLHFAAGYNNVS	614	
Db	481	LOEGISLGNSEADROLLEAKAGDVETVKKLTQVSNCRDIEGQSTPLHFAAGYNNVS	540	
Qy	615	VVEYLQHGADVHAKDGGVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAA	674	
Db	541	VVEYLQHGADVHAKDGGVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAA	600	
Qy	675	AKGYEICKLLOHGADPTKKNRDGNTPLDLVKOGDTPDQDLRGDAALLDAAKKGCLAR	734	
Db	601	AKGYEICKLLOHGADPTKKNRDGNTPLDLVKOGDTPDQDLRGDAALLDAAKKGCLAR	660	
Qy	735	VKKLSSPDNVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNA	794	
Db	661	VKKLSSPDNVNCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNA	720	
Qy	795	SYGHVDVAALIKYNACVNTDKWFTPLHEAAQKRTQOLCALLAHGADPTLKNQEGQT	854	
Db	721	SYGHVDVAALIKYNACVNTDKWFTPLHEAAQKRTQOLCALLAHGADPTLKNQEGQT	780	
Qy	855	PLDLVSADVDVSAALLTAAMPSPALPCYKQVNLVGRSPCATADALSSGSPSSLSAASS	914	
Db	781	PLDLVSADVDVSAALLTAAMPSPALPCYKQVNLVGRSPCATADALSSGSPSSLSAASS	840	
Qy	915	LDNLGSGSFSELSVSSSGTGASLEKEVPGVDFTSQFVNLGLHLMIDIFEREQIT	974	
Db	841	LDNLGSGSFSELSVSSSGTGASLEKEVPGVDFTSQFVNLGLHLMIDIFEREQIT	900	
Qy	975	LDVLVEMGHKEIKETGINAYGHRHKLIGVRELISGQQLNPYLTLNTSGSSTILIDLSP	1034	
Db	901	LDVLVEMGHKEIKETGINAYGHRHKLIGVRELISGQQLNPYLTLNTSGSSTILIDLSP	960	
Qy	1035	DDKEFQSVVEEMQSTVREHRDGHAGGIFNRYNIIKIQKVCNKKLWERYTHRRKEVSEEN	1094	

Db	961	DDKEFQSVVEEMQSTVREHRDGHAGGIFNRYNIIKIQKVCNKKLWERYTHRRKEVSEEN	1020	
Qy	1095	HNHANERMLPHGSPFVNALIHKGFDERHAYIGGFMFGAGIYFAENSSKSNQYVYGIGGGTG	1154	
Db	1021	HNHANERMLPHGSPFVNALIHKGFDERHAYIGGFMFGAGIYFAENSSKSNQYVYGIGGGTG	1080	
Qy	1155	CPVHKDRSCYICHRLQLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALEY	1214	
Db	1081	CPVHKDRSCYICHRLQLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALEY	1140	
Qy	1215	IYRGEQAYPEYLITYQIMRPEGVDG	1240	
Db	1141	IYRGEQAYPEYLITYQIMRPEGVDG	1166	
RESULT 2				
Q800E0	CHICK	PRELIMINARY;	PRT;	1167 AA.
AC	Q800E0;			
DT	01-JUN-2003,	integrated into UniProtKB/TrEMBL.		
DT	01-JUN-2003,	sequence version 1.		
DT	07-FEB-2006,	entry version 14.		
DE	Tankyrase 2.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BJ20021450;			
RA	De Rycker M., Venkatesan R.N., Wei C., Price C.M.;			
RT	"Vertebrate tankyrase domain structure and sterile alpha motif (SAM)-			
RT	mediated multimerization";			
RL	Biochem. J. 372:87-96(2003).			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	EMBL; AY142107; AAN41650.1; -, mRNA.			
DR	HSSP; Q00420; IAWC.			
DR	Ensembl; ENSGALG00000011438; Gallus gallus.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.			
DR	GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.			
DR	InterPro; IPR002110; ANK.			
DR	InterPro; IPR001290; PARP.			
DR	InterPro; IPR012317; PARP_catalytic.			
DR	InterPro; IPR001660; SAM.			
DR	InterPro; IPR011510; SAM_2.			
DR	Pfam; PF00023; Ank; 19.			
DR	Pfam; PF00644; PARP; 1.			
DR	Pfam; PF07647; SAM_2; 1.			
DR	PRINTS; PR01415; ANKYRIN.			
DR	SMART; SM00454; SAM; 1.			
DR	PROSITE; PS0297; ANK_REPEAT; 1.			
DR	PROSITE; PS0088; ANK_REPEAT; 15.			
DR	PROSITE; PS1059; PARP_CATALYTIC; 1.			
DR	PROSITE; PS0105; SAM_DOMAIN; 1.			
KW	ANK repeat; Repeat.			
SC	SEQUENCE 1167 AA; 126932 MW; 7842BF482B9229E9 CRC64;			
Query Match 89.1%; Score 5760.5; DB 2; Length 1167;				
Best Local Similarity 93.8%; Pred. No. 0;				
Matches 1095; Conservative 33; Mismatches 36; Indels 3; Gaps 2;				
Qy	75	MSGRCCAGGGAACASAA--AAEAVEPAARELFEACRNGDVERVKRLVTPPEKVNSRDTAGRK	132	
Db	1	MAARCCAGGAALAEAPCGSAVEP-AEELFEACRNGDVERVKRLVRENVSRTAGRK	59	
Qy	133	STPLHFAAGFRKDVVYLLQNGANVQARDGGGLPLHNACSFHAEVNVLLRHGADPN	192	

Db 60 SSPLHFAAGFGRKDVVEYLLQSGANVHARDGGGLIPLHNACSPGHAENVNLLPHGANPN 119
Qy 193 ARDNWNTPLHEAAIKGKIDVCIVLLQHGABPTIRNTDGRFTALDADPSAKAVLTGYKK 252
Db 120 ARDNWNTPLHEAAIKGKIDVCIVLLQHGABPTIRNTDGRFTALDADPSAKAVLTGYKK 179
Qy 253 DELLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVH 312
Db 180 DELLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVH 239
Qy 313 AKDGDVPLHNACSYGHEYTELLVKGACVNAWDLWQFTPLHEAASKRVEVCSLLS 372
Db 240 AKDGDVPLHNACSYGHEYTELLVKGACVNAWDLWQFTPLHEAASKRVEVCSLLS 299
Qy 373 YGADPTLLNCHNSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKGHSLEWVNF 432
Db 300 YGADPTLLNCHNSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKGHSLEWVNF 359
Qy 433 KHPOTHTALHCAASPYPKKQICELLRKGANINEKTEFLTPLVHASEKAHNDVVEV 492
Db 360 KHPOTHTALHCAASPYPKKQICELLRKGANINEKTEFLTPLVHASEKAHNDVVEV 419
Qy 493 VVXHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDFPNIISLQGFALQNGENNVQ 552
Db 420 VVXHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDFPNIISLQGFALQNGENNVQ 479
Qy 553 QLLQEGISLGNSEADROLLEAAKAGDVETVKKLTCTQSVNCRDIEGROSTPLHPAAGYNR 612
Db 480 QLLQEGISLGNSEADROLLEAAKAGDVETVKKLTCTQSVNCRDIEGROSTPLHPAAGYNR 539
Qy 613 VSVVEYLLQHGADVHAKDGLVPLHNACSYGHEYTELLVKGACVNAWDLWQFTPLHE 672
Db 540 VSVVEYLLQHGADVHAKDGLVPLHNACSYGHEYTELLVKGACVNAWDLWQFTPLHE 599
Qy 673 AAAGKYEICKLLQHGADPTKKNRDNPTDLVDKGDGTQDILRGDGAALLDAKKGCL 732
Db 600 AAAGKYEICKLLQHGADPTKKNRDNPTDLVDKGDGTQDILRGDGAALLDAKKGCL 659
Qy 733 ARVKKLSPDNVNCRDQTGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHN 792
Db 660 ARVKKLSPDNVNCRDQTGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHN 719
Qy 793 AASGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRQTQCALLAHAGADPTLNQEG 852
Db 720 AASGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRQTQCALLAHAGADPTLNQEG 779
Qy 853 QTPDLVSADVDVSAALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAA 912
Db 780 QTPDLVTADDVSAALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAA 839
Qy 913 SSLDNLGSGFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNIGLEHMDIFEREQ 972
Db 840 SSLDNLGSGFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNIGLEHMDIFEREQ 899
Qy 973 ITLDVLVEMGHKEIKETGINAYGRHKLIKVERLISQOGLNPLYTLNTSSGFTLIDL 1032
Db 900 ITLDVLVEMGHKEIKETGINAYGRHKLIKVERLISQOGLNPLYTLNTSSGFTLIDL 959
Qy 1033 SPDDKEFQSVSEEMQSTVREHDDGSHAGGIFNRRYNIILKIQRKCNKLUWERYTHRRKEVSE 1092
Db 960 SSEDKEFQSVSEEMQSTVREHDDGSHAGGIFNRRYNIILKIQRKCNKLUWERYTHRRKEVSE 1019
Qy 1093 ENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGCMFGAGIYFAENSCKNQYVYGIGG 1152
Db 1020 ENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGCMFGAGIYFAENSCKNQYVYGIGG 1079
Qy 1153 TGCPIVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGCHSVTGRPSVNGLALAE 1212
Db 1080 TGCPIVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGCHSVTGRPSVNGLALAE 1139
Qy 1213 YVIVIRGEQAYPEYLITVQIMRPEGVMD 1239
Db 1140 YVIVIRGEQAYPEYLITVQIVKPEATTE 1166

RESULT 3
TNKS1 HUMAN
ID TNKS1_HUMAN STANDARD; PRT; 1327 AA.
AC O95271; O95272;
DT 27-MAR-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1999, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase I) (TNKS-1) (TRF1-
DE interacting ankyrin-related ADP-ribose polymerase).
GN Name=TNKS; Synonyms=PARPSA, PARPL, TIN1, TINP1, TNKS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RX MEDLINE=99040105; PubMed=9822378; DOI=10.1126/science.282.5393.1484;
RA Smith S., Giriat I., Schmitt A., de Lange T.;
RT "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
RL Science 282:1484-1487(1998).
RN [2]
RP SUBCELLULAR LOCATION.
RX MEDLINE=99454782; PubMed=10523501;
RA Smith S., de Lange T.;
RT "Cell cycle dependent localization of the telomeric PARP, tankyrase,
RT to nuclear pore complexes and centrosomes.";
RL J. Cell Sci. 112:3649-3656(1999).
RN [3]
RP FUNCTION, AND PHOSPHORYLATION.
RX MEDLINE=20556282; PubMed=10988299; DOI=10.1074/jbc.M007635200;
RA Chi N.-W., Lodish H.F.;
RT "Tankyrase is a Golgi-associated mitogen-activated protein kinase
RT substrate that interacts with IRAP in GLUT4 vesicles.";
RL J. Biol. Chem. 275:38437-38444(2000).
RN [4]
RP FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
RX MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002;
RA Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
RT "Role for the related poly(ADP-ribose) polymerases tankyrase 1 and 2
RT at human telomeres.";
RL Mol. Cell. Biol. 22:332-342(2002).
RN [5]
RP IDENTIFICATION IN A COMPLEX WITH POT1; TERF1 AND TINF2.
RX MEDLINE=22711259; PubMed=12768206; DOI=10.1038/nature01688;
RA Leayza D., De Lange T.;
RT "POT1 as a terminal transducer of TRF1 telomere length control.";
RL Nature 424:1013-1018(2003).
CC -1- FUNCTION: May regulate vesicle trafficking and modulate the
CC subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP
CC activity and can modify TERF1, and thereby contribute to the
CC regulation of telomere length.
CC -1- CATALYTIC ACTIVITY: NAD(+) + (ADP-D-riboseyl)(n)-acceptor =
CC nicotinamide + (ADP-D-riboseyl)(n+1)-acceptor.
CC -1- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with
CC the cytoplasmic domain of LMPEP/Otase in SLC2A4/GLUT4-vesicles.
CC Binds to the N-terminus of telomeric TERF1 via the ANK repeats.
CC Found in a complex with POT1; TERF1 and TINF2.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and
CC with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is
CC also found at nuclear pore complexes and around the pericentriolar
CC matrix of mitotic centrosomes. During interphase, a small fraction
CC of TNKS is found in the nucleus, associated with TERF1.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O95271-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O95271-2; Sequence=VSP_004538, VSP_004539;
CC Note=No experimental confirmation available;

Db 1119 QSVSEEMQSTIREHRDGNAGGIENRNVIRIQKVVNKKLBRECHRQKEVSENNHHN 1178
 Qy 1100 ERMFLHSGSPFVNAIHKGFDERHAYIGMGFAGYIYFAENSCKSNQYVYGGTGCPCVHK 1159
 Db 1179 ERMFLHSGSPFINAIHKGFDERHAYIGMGFAGYIYFAENSCKSNQYVYGGTGCPTHK 1238
 Qy 1160 DRSCYICHRQLFCRVTLGKSFLOFSAMKNHSPGHHSVTCRPSVNGLALAEVYVIRGE 1219
 Db 1239 DRSCYICHRQLFCRVTLGKSFLOFSAMKNHSPGHHSVTCRPSVNGLALAEVYVIRGE 1298
 Qy 1220 QAYPEYLITQIMRPE 1235
 Db 1299 QAYPEYLITQIMRPE 1314
 RESULT 4
 Q6PPX9 MOUSE PRELIMINARY; PRT; 1320 AA.
 AC Q6PPX9
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Tnks protein.
 GN Name=Tnks.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J.J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Boas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; BC057370; AAH57370.1; -, mRNA.
 DR HSP; Q00420; IAW.
 DR Ensembl; ENSMUSG00000031529; Mus musculus.
 DR MGI; MGI:1341087; Tnks.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR001290; PARP.
 DR InterPro; IPR012317; PARP_catalytic.
 DR InterPro; IPR001660; SAM.

DR InterPro; IPR011510; SAM_2.
 DR Pfam; PF00023; Ank; 19.
 DR Pfam; PF00644; PARP; 1.
 DR Pfam; PF07647; SAM_2; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 15.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PSS0088; ANK_REPEAT; 15.
 DR PROSITE; PSS1059; PARP_CATALYTIC; 1.
 DR PROSITE; PSS0105; PARM_DOMAIN; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 1320 AA; 140944 MW; A90360DC665FFCC0 CRC64;
 Query Match 78.9%; Score 5098; DB 2; Length 1320;
 Best Local Similarity 79.2%; Pred. No. 3.6e-291;
 Matches 966; Conservative 105; Mismatches 130; Indels 18; Gaps 5;
 Qy 22 AANGTAPDPVTAGSQAAR--ALSASSP--GGALLAGPGLLLRLALLALLAVAAARIMSGR 78
 Db 102 AAVGVAPTAGGGGGGNNSSASSPTSSSSSSPSPG-----SSLAESPAAAGVST 155
 Qy 79 RCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPKVNRSRDTAGRKSTPLHF 138
 Db 156 ATLGAGAGLPGVPVAVSGALRELLEACRNGDVSRLVDAANVNADKAGRKSSPLHF 215
 Qy 139 AAGFGRKVVVYLLQNGANYOARDGGGLIPLHNACSFGHAEVNVNLLRHGHGADPNARDWN 198
 Db 216 AAGFGRKVVVHLLQMGANVHARDGGGLIPLHNACSFGHAEVNVNLLCQGGADPNARDWN 275
 Qy 199 YTPLHEAAIKGKIDVCIVLQHGAEPIRTDGTALDADPSAKAVITGEYKDELLES 258
 Db 276 YTPLHEAAIKGKIDVCIVLQHGADPNIRNTDGSALDADPSAKAVITGEYKDELLEA 335
 Qy 259 ARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGVNVKIVOLLQHGADVHAKDKGD 318
 Db 336 ARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGVNVKIVOLLQHGADVHAKDKGG 395
 Qy 319 LVPLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCVSLLSYGADPT 378
 Db 396 LVPLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCVSLLSHGADPT 455
 Qy 379 LLNCHNSATDLAPTQPKERLAYEPKHSILOAREADVTRICKHLSLEVMVFKHQTH 438
 Db 456 LVNCHGKSAYDMAPTPELRRLTYEPKHSILOAREADLAKVKKTLALEILINFKQPOSH 515
 Qy 439 ETALHCAASPYKPKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVXHEA 498
 Db 516 ETALHCAVASLHPKPKQVAVELLRLKGANVNEKNKDFMTPLHVAERAHNDVMEVLHKGA 575
 Qy 499 KVNALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDDPNIIISIQGFTALQNGENVQOLQEG 558
 Db 576 KVNALDSLGQTLHRAALAGHLQTCRLLLSYGSDDPSIISLQGFTAAQMGNEAVQOILSES 635
 Qy 559 ISLGNSEADQLLEAAKAGADVETVKKLCITQSVNCRDIEGRQSTPLHFAAGYNVSVVEY 618
 Db 636 TPRMTSDVYRLLEASKAGDLETVKQLCSPQNVCNCRDLEGRHSTPLHFAAGYNVSVVEY 695
 Qy 619 LLOHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VNVVADLWKFTPLHEAAAKGK 678
 Db 696 LLHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVRHGASVNVADLWKFTPLHEAAAKGK 755
 Qy 679 YEICKLLQHGADPTKKNRDGNTPLDLVKDGDGTDIDQLLRGDAALLDAACKGCLARVKKL 738
 Db 756 YEICKLLKHGADPTKKNRDGNTPLDLVKEGDGDIDQLLRGDAALLDAACKGCLARVQKL 815
 Qy 739 SSPDNVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGH 798
 Db 816 CTPEINCRDTQGRNSTPLHLAAGYNNLEVAEYLLHGHADVNAQDKGLIPLHNAASVGH 875
 Qy 799 VDVAAALLIKYNACVNATDKWAFPLHEAAQKGRITQLCALLLAHAGADPTLNKQEGQTPDL 858
 Db 876 VDTAALLIKYNTCVNATDKWAFPLHEAAQKGRITQLCALLLAHAGADPTLNKQEGQTPDL 935

QY	859	VSADDVSALLTAAMPSPALSCYKQVNLGVVRPGATADALSSGSPSPSSLSAASSIDLNL	918
Db	936	ATADDIRALLIDAMPPEALPTCFKPOAT-----VVSASLISPASTPSCLSAASSIDLNL	988
QY	919	SGSFSELSVVSSSGTGASSLEKK--EVPQDFSIITQFVRLNGLHLMDIFEREQITLD	976
Db	989	TGPTLTDLAVGASNAGDGAAGAEKGEVAGLDMNISOFLKGLGHLRDI FETEQTLD	1048
QY	977	VLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILIDLSRDD	1036
Db	1049	VLADMGEELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILIDLSRDD	1108
QY	1037	KEFQSVSEEMQSTVREHRDGHAGGIENRYNLIKQKCNKKLWERYTHRRKEVSEENHN	1096
Db	1109	KEYQSVSEEMQSTIREHRDGHAGGIENRYNVIQKVNKKLRERFCHQKEVSEENHN	1168
QY	1097	HANERMLFHGSPFNVAIIHKGDFERHAYIGMFGAGIYFAENSKSNQYVYIGGGTGCP	1156
Db	1169	HHRNRMFLHGSPPFNVAIIHKGDFERHAYIGMFGAGIYFAENSKSNQYVYIGGGTGCP	1228
QY	1157	VHKDRSCYI CHROLLFCRVTLGKSLFQFSAMKMAHSPGHHSVTGRPSVNGLALAEVYI	1216
Db	1229	THKDRSCYI CHRQMLFCRVTLGKSLFQFSAMKMAHSPGHHSVTGRPSVNGLALAEVYI	1288
QY	1217	RGEQAYPEYLITYQIMRPE 1235	
Db	1289	RGEQAYPEYLITYQIMRPE 1307	

RESULT 5

Q4G0F2 HUMAN

ID Q4G0F2 HUMAN PRELIMINARY; PRT; 1327 AA.

AC Q4G0F2;

DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.

DT 30-AUG-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.

DE Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase.

GN Names=TNKS;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OC NCBI_TaxID=9606;

[1]

RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Testis;

RX MSDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.2426503899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchéz A.,

RA Faney J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Testis;

RG NIH MGC Project;

RL submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.

[illegible]

Db 766 CKLLKKGADFTKNDGNTPLDLVKEGDTDIQLLRGDAALLDAKKGCLARVQKLCPT 825
Qy 742 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDV 801
Db 826 ENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLLEHGADVNAQDKGLIPLHNAASYGHVDI 885
Qy 802 AALLIKYNACVNTDKWAFTHLHAAQKGRTOLCALLLAHGADPTLNQEGQTPDLVSA 861
Db 886 AALLIKYNTCVNATDKWAFTHLHAAQKGRTOLCALLLAHGADPTLNQEGQTPDLVSA 945
Qy 862 DDVSALLTAAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSI-SAASSIDNLSGS 921
Db 946 DDIRALLIDAMPSPALPCYKPOAT-----VVSAISIPASTPSCLSAASSIDNLTGP 998
Qy 922 FSELSSVVSSGTGASSLEKK--EVPQVDPSITQFVRNLGLEHLMDFIREQITLDVLV 979
Db 999 LAGLAVGASNAGDAAGTERKEGEVAGLDWNIQSFLKSLGLEHLRDFEFETEITLDVLA 1058
Qy 980 BMGHKELKEIGINAYGHRHKLKIGVERLIISQOGLNPVLTUNTSGSTILIDLSPDKF 1039
Db 1059 DMGHEELKEIGINAYGHRHKLKIGVERLLGQOQGTNPVLTTPHCYNQGTILDLAPEDKEY 1118
Qy 1040 QSVSEEMOSTVREHRDGHAGGIENRNYLKIQKVCNKKLWERVTHRRKEVSEENHNAN 1099
Db 1119 QSVSEEMOSTIREHRDGGNAGGIENRNYIRIQKVNKKLRETRCHQKEVSEENHNHN 1178
Qy 1100 ERMFLPHGSPFVNAIHKGFDRHAYIGMFGAGIYFAENSCKSNQYVVGIGGTCPPVHK 1159
Db 1179 ERMFLPHGSPFINAIHKGFDRHAYIGMFGAGIYFAENSCKSNQYVVGIGGTCPTHK 1238
Qy 1160 DRSCYICHRQLLFCRVTLGKSLFOPSAMKMAHSPGHHSVTRGSRVNGLALEYVIYRGE 1219
Db 1239 DRSCYICHRQMLFCRVTLGKSLFQSTIKMAHAPPGHHSVTRGSRVNGLALEYVIYRGE 1298
Qy 1220 QAYPEYLITYOIMRPE 1235
Db 1299 QAYPEYLITYOIMRPE 1314
RESULT 6
ID Q800D9_CHICK PRELIMINARY; PRT; 1266 AA.
AC Q800D9;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Tankyrase 1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BJ20021450;
RA De Rycker M., Venkatesan R.N., Wei C., Price C.M.;
RT "Vertebrate tankyrase domain structure and sterile alpha motif (SAM)-
mediated multimerization.";
RL Biochem. J. 372:87-96(2003).
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CC -----
DR EMBL; AY142108; AAN41651.1; -; mRNA.
DR HSSP; P16157; IN11.
DR Ensembl; ENSGALG00000011438; Gallus gallus.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-riboseyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.

DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 19.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS0297; ANK_REPEAT; 1.
DR PROSITE; PS0088; ANK_REPEAT; 15.
DR PROSITE; PS1059; PARP_CATALYTIC; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1266 AA; 136212 MW; 14B8617EF930B6E0 CRC64;
Query Match 78.5%; Score 5074; DB 2; Length 1266;
Best Local Similarity 77.6%; Pred. No. 8.7e-290;
Matches 964; Conservative 109; Mismatches 120; Indels 50; Gaps 6;
Qy 5 RRGAGGQG-----AQRGARVGAAGHTAPDPVTAGSQAARALSSSPGGLALLAGPGLL 59
Db 49 RHLAGPEGEAPPDAERPPAPCESEGAAPGP-PPGSGSSGSSASS----- 93
Qy 60 LRLALLLAVAAARIMSGRCAGGACASAAAEAVPAA-----RELFEACRNGDVERV 114
Db 94 -----SSSSSTSSSVASSPAAESPEAAGPSGAFRELLACRNGDTRV 137
Qy 115 KRLVTPKVNRSRDTAGKSTPLHFAAGFGRKDVVYLLQNGANYQAARDGGLIPLHNACS 174
Db 138 KRLVDAGNVNAKDWAGKSTPLHFAAGFGRKDVVEHLLQTGANVHARDGGLIPLHNACS 197
Qy 175 FGAHVNNLLRHGADNADNWNYPHLHAAIKGKIDVICVILLOHGAEPTRITNDGRTA 234
Db 198 FGAHVVSLLLCQADFNARDNWNYPHLHAAIKGKIDVICVILLOHGAEPNIRNTDGKSA 257
Qy 235 LDLDAPSAKAVLTGEYKKBELLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAG 294
Db 258 LDLDAPSAEAVLTGEYKKBELLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAG 317
Qy 295 YNRVKIVQLLQHGADVHAKDGLVPLHNACSYGYEVTLELVKHGACVNAMDLDWQFTP 354
Db 318 YNRVRIVQLLQHGADVHAKDGLVPLHNACSYGYEVTLELVKHGACVNAMDLDWQFTP 377
Qy 355 LHEAASKRVEVCSLLSYGADPTLLNCHNKAIDAPTQLKRLAYEPKGHSLLOAAR 414
Db 378 LHEAASKRVEVCSLLSHGADPTLVNCHGKSAVDMAPTPELRERLTYEPKGHSLLOAAR 437
Qy 415 EADVTRIKHLSLEWNVNFKPQTHETALHCAAAASPYPKRQICELLRKGANINEKTKEF 474
Db 438 EADLAKYKKTALAEIINFQKQSHETALHCAVAAPHKRVQVTELLRKGANVNEKNKDF 497
Qy 475 LTPLHVAASEKAHNDVVEVVVYKHEAKVNALNLOQTSLHRAAYCGHLOTICRLLSYGCDPN 534
Db 498 MTLPHVAAEKAHNDVMEVLKHGAKKNALDTLQGTALHRAALAGHLQTCRLLSYGSDPS 557
Qy 535 IISLQGTALOMNENVOQLLQEGISLGNSEADQLLEAAKAGDVETVKKLCTVQSVNCR 594
Db 558 IISLQGTAAQIGNEAVQQLSESTPVRTSDVYRLLEASKAGDLETVKQLCSQPNVNCR 617
Qy 595 DIEGRQSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGYEVAELLVK 654
Db 618 DLGRHSTPLHFAAGYNNRVSVVEYLLHGHGADVHAKDKGLVPLHNACSYGYEVAELLVR 677
Qy 655 HGAVVNVADLWKFTPLHAAAAGKYEICKLLQHGADPTKKNRDNTPDLVDKGDGTDIQ 714
Db 678 HGASVNVADLWKFTPLHAAAAGKYEICKLLKHGADPTKKNRDNTPDLVDKEGDIDIQ 737
Qy 715 DLIRGDAALDAAKKGCLARVKLSSPDNVCNCRDTQGRHSTPLHLAAGYNNLEVAEYLQ 774
Db 738 DLLRGDAALDAAKKGCLARVQKLTCTPENINCRDQGRNSTPLHLAAGYNNLEVAEYLLE 797
Qy 775 HGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTHLHAAQKGRTOLC 834

Db	798	HGADVNAQDKGGLIPLHNAASYGHVIDIAALLIKYNTCVNATDKWAFPTPLHEAAQKQRTQL	857
Qy	835	CALLAHGADPTLTKNOEGQTPDLIVSADDDVSALLTAAAPPSPALPSCYKPOVLNGVRSPGA	894
Db	858	CALLAHGADPTMKNOEGQTPDLATADDIRALLIDAMPEALPTCFKLQAT-----V	910
Qy	895	TADALSGPSPSASLSAASSLDNLSGSFBSLSSVSSSGTTEGASSLEKK--EVPQVDPSI	952
Db	911	VSASLISPASTPSCLSAASSIDNLGTPLAELAVCGASNTGDGAAGTERKEGVSGLDMNI	970
Qy	953	TQVFNILGLEHLMIDIPEKEOITLDVLVEMGHKEIKEGINAYGHRKLIKGVERLISGQQ	1012
Db	971	TQPLKSLGLEHLMIDIFETEQTITLDVLADMGBHEUKEIENAYGHRKLIKGVERLISGQQ	1030
Qy	1013	GLNPYLTLNTSGSTITLIDLSPDKEFPQSVVEEQMSTVREHRDGGHAGGIFNRYNLIKIQ	1072
Db	1031	GTNPYLTFHCVSQGTILLDLAPDDKEVQSVVEEQMSTIREHRDGGNAGGIFNRYNVIRIQ	1090
Qy	1073	KVCNKKLWERYTHRRKEVSENNHNANERMLFHGSPFPVNAIHHKQPDERHAYIGGMFGAG	1132
Db	1091	KVYNKKLRERFCHQKEVSENNHNHNERMLFHGSPFPVNAIHHKQPDERHAYIGGMFGAG	1150
Qy	1133	IYFAENSSKSNQYVYGGTGCVPVKDKRSCYICHRQLLCFRVTLGKSFLOFSAMKMAHS	1192
Db	1151	IYFAENSSKSNQYVYGGTGCPTPKDKRSCYICHRQLLCFRVTLGKSFLOFSMKMAHA	1210
Qy	1193	PPGHSVTVGRPSVNGLALAEYVIYRGQAYPEYLITYQIMRPE	1235
Db	1211	PPGHSVIGRPSVNGLAYAEYVIYRGQAYPEYLITYQIVKPE	1253
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ID	Q5XGK5	XENLA	
QY	Q5XGK5	XENLA	PRELIMINARY; PRT; 1303 AA.
AC	Q5XGK5		
DT	23-NOV-2004		integrated into UniProtKB/TrEMBL.
DT	23-NOV-2004		sequence version 1.
DT	07-FEB-2006		entry version 12.
DE	LOC495279	protein.	
DE	LOC495279	protein.	
GN	GN	Name=LOC495279;	
OS	Xenopus laevis	(African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodinae; Xenopus; Xenopus.		
OX	NCBI_TaxID=8355;		
RN		[1]	
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Spleen;		
RC	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;		
RX	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,		
RA	Richardson P.;		
RA	"Genetic and genomic tools for Xenopus research: The NIH Xenopus		
RT	initiative.,"		
RL	Dev. Dyn. 225:384-391(2002).		
RN		[2]	
RN	NUCLEOTIDE SEQUENCE.		
RP	TISSUE=Spleen;		
RC	MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Beasak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		

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Db 548 DVVEVLHGAGNTLDTLGGTALHRAALGHLGTLCTRLLSFGSDASIVSLQGFATAQMG 607
Qy 548 NENYQQLQBSISLGNSEADRLLEAAKAGAVETVKKLCTVQSVNCRDIDEGRSTPLHFA 607
Db 608 NEAQQILNESTPVRTSDVYRLLEASKAGDLIVKLCSSQNVNCRDLGRHSTPLHFA 667
Qy 608 AGYNRVSVYELLOHGDVIAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKF 667
Db 668 AGYNRVSVYELLVHGGADVIAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKF 727
Qy 668 TPLHAAAKGYEICKLLHGGADPTKKNRDGNTPLDVKDGDIDQLLGRDAALLDAA 727
Db 728 TPLHAAAKGYEICKLLHGGADPTKKNRDGNTPLDVKDGDIDQLLGRDALLDAA 787
Qy 728 KKGCLARVKLSSPDVNCRDQTGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGL 787
Db 788 KKGCLARVQKLTQENINCRDQTGRNSTPLHLAAGYNNLEVAEYLLHGGADVNAQDKGGL 847
Qy 788 IPLHNAASYGHVDVAALLIKYNACVNTDKWAFPLHAAQKGTQLCALLAHGADPTL 847
Db 848 IPLHNAASYGHVDIAALLIKYNTCVNTDKWAFPLHAAQKGTQLCALLAHGADPTM 907
Qy 848 KNQSGOTPLDIVSADVDYSAALLTAAMPSPALPSCYKQVNLGVRSFGATADALSGSPSS 907
Db 908 KNQSGOTPLDLATADDIRALLIDAMPPEALPSCPKQAT-----VVSASIIISPASTPS 960
Qy 908 SLASAASLDNLGSEFSELSSVSSSGTEGASLEKK--EVPGVDFSTQTFVNLGLEHLM 965
Db 961 CLSAASISDNLGTEPLAELAVGVSNAGDGAAGTERKEGEVTCLDNMNINQFLKSLGLEHLR 1020
Qy 966 DIFEREQITDLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGS 1025
Db 1021 DIFETEQTDLVADMGEELKEIGINAYGHRHKLKIGVERLLGQOQTNPYLTFHCVSQ 1080
Qy 1026 GTILIDLSDDKEFQSVVEEEMQSVRHRDGGHAGGIFNRVNLKIOKNCKKLWEYRTH 1085
Db 1081 GTVLDDLASDKHQSVVEEEMQSVRHRDGGNAGGVNFRVNRVIRIQIKVKKLRERFCH 1140
Qy 1086 RRKEVSEENHNHNERMLFHGSPFNVAIIHKGFDERHAYIGGMFAGIYFAENSCKSNQY 1145
Db 1141 RQKEVSEENHNHNERMLFHGSPFNVAIIHKGFDERHAYIGGMFAGIYFAENSCKSNQY 1200
Qy 1146 VYIGGGTGCPVHKDRSCYICHRQLLCRVTLGKSLFQFSAMKAKHSPPGHHSVTGRPSV 1205
Db 1201 VYIGGGTGCPVHKDRSCYICHRQLLCRVTLGKSLFQFSMTKMAHAPPGHHSVIGRPSV 1260
Qy 1206 NGLALAEVVIYRGOAYPEYLITYQIMRPE 1235
Db 1261 NGLAYAEVVIYRGOAYPEYLITYQIMRPE 1290
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RESULT 8

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OARG97_TETNG
ID OARG97_TETNG PRELIMINARY; PRT; 1212 AA.
AC OARG97;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE Chromosome 12 SCAP15104, whole genome shotgun sequence. (Fragment).
GN ORFNames=STENG00034904001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Flecher C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
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RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Crenaud C., Duprat S., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier C., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellia M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolious H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RN Nature 431:946-957(2004).
RL NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
CC EMBL: CAAE01015104; CAG12585.1; -; Genomic_DNA.
CC
CC GO: GO:0005634; C:nucleus; IEA.
CC GO: GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
CC GO: GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR012317; PARP_catalytic.
CC InterPro: IPR001660; SAM_.
CC Pfam: PF00023; Ank_15.
CC Pfam: PF00644; PARP; 1.
CC Pfam: PF07647; SAM_2; 1.
CC PRINTS: PR01415; ANKYRIN.
CC SMART: SM00248; ANK; 13.
CC SMART: SM00454; SAM; 1.
CC PROSITE: PS50297; ANK_REPEAT; 1.
CC PROSITE: PS50088; ANK_REPEAT; 13.
CC PROSITE: PS51059; PARP_CATALYTIC; 1.
CC PROSITE: PS50105; SAM_DOMAIN; 1.
CC ANK repeat.
CC NON_TER 1
CC NON_TER 1212 1212
CC SEQUENCE 1212 AA; 131719 MW; 973307E7F92C219 CRC64;
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Query Match 75.4%; Score 4875.5; DB 2; Length 1212;
Best Local Similarity 75.8%; Pred. No. 4.1e-278;
Matches 925; Conservative 109; Mismatches 92; Indels 95; Gaps 9;

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Qy 82 GGGACASAAAAEVAEPAAARELFEACRNGDYERVKLVTPPEKVNSTRDTAGRKSTPLHFAAG 141
Db 7 GSGAASPTDGSISGGAFFELFEACRNGDYERVKRLV--DSVNV----- 48
Qy 142 FGRKDVVEYLLQNGANVQARDGGLPLHNACSFHAEVNVNLLRHGADPNARDNNYTP 201
Db 49 LGKTTWNTFLOTGANVHARDGGLPLHNACSFHAEVNVNLLRHGADPNARDNNYTP 108
Qy 202 LHEAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKDELLESARS 261
Db 109 LHEAAIKGKIDVCIVLLQHGADPNIRNTDGTALDLADPSAKAVLTGEYKDELLESARS 168
Qy 262 GNEEKMAILLPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDKGLVP 321
Db 169 GNEEKMAILLPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDKGLVP 228
Qy 322 LHNACSYGHVEVTELVKHKACVNMADLMQFTPLHAAASKNRVEVCSSLLLSYGADPTLLN 381
Db 229 LHNACSYGHVEVTELLKHKACVNMADLMQFTPLHAAASKNRVEVCSSLLLSYGADPTLLN 288
Qy 382 CHNKSATDLAPTQLKERLAYEPKSHLSLQAAAREADVTRIKKHLSELMVNFKHPQTHETA 441
Db 289 CHKSAVDMAPTPELKORLYTEFKGSHLSLQAAAREADMAKVKTKTIALEIIISFKHPQTHETA 348
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QY 442 L-----HCAASPPPKRKQICELLRLKGANINEKTEPLTLHVASEKAHNDVVEV 492
Db 349 LMLKVAAYFQHCASVAPPKRKQVTELLRLKGANINDKNKDPMTPLHVAEERAHNDILEV 408
QY 493 VVKHAKVNALDNLGOTSILHRAAYCHLQTCRLLLSYGCDDPHIISLQFTALQMGNNVQ 552
Db 409 LOKHGAKVNAADTLGQTLALHRAALAGHIQTCRLLLSYGDPAFVSLQFTTAQMGNEAVQ 468
QY 553 QLLQGISLGNSEADROLLEAKAGDVETV-----KKLCTV 588
Db 469 QILNENPVRNSDVDFLEAKAGDLDTQVWSLALRLVSEGMRLOKVLVSQOLCSP 528
QY 589 QSVNCRDIEGROSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEV 648
Db 529 QNVNCRDLEGRHSTPLHFAAGYNNRVVVEYLLHHGADVHAKDGLVPLHNACSYGHEV 588
QY 649 AELLVKGAVNVADLWKFTPLHEAAAKGYBEICKLLOHGADPTKQNRDGNTPLDLVKD 708
Db 589 AELLVRHGASVNVADLWKFTPLHEAAAKGYBEICKLLLKHGADPTKQNRDGNIPLDVYKD 648
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QY 769 AEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAPTPLHEAAQ 828
Db 709 AEYLLQHGADVNAQDKGLIPLHNAASYGHVDIAALLIKYNTCVNATDKWAPTPLHEAAQ 768
QY 829 KGTOLCALLAHGADPTLKNQEGQTPLD-----LVSADD 863
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QY 864 VSALLTAAMPSPALSCYKPO---VLNGVRSPGATADALSSGSPSSISAASSIDNLSG 920
Db 829 ITRALLIDAMPDPALPCFQPAQTVVSASVISPAST-----PCLSAASSIDNLAG 878
QY 921 SFSELSSVVSSSGT-----EGASSLEKK--EVPVDFFSITQFVRNLGLEHLMDFEREQIT 974
Db 879 PLTELAAAVSTGSGVADGATGSRKGEWMTLMDNISQFLKSLGLDHLRDIIFEREQIT 938
QY 975 LDVLVEMGHKEIKETGINAYGHRHLIKGVERLISGQGLNPLYTLNTSGSTIILIDLSP 1034
Db 939 LDVLADMGEELKEIGINAYGHRHLIKGVERLLGQCGANPLYTFHCASQGTIILIDLAP 998
QY 1035 DDKEFQSVSEEMQSTVREHRDGHAGGIFNRNIIKIQKVCNKLWERYTHRKEVSEEN 1094
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QY 1095 HNHNEMRLFHGSPFNATIIHKGFDERHAYIGCMFGAGIYFAENSCKNQYVYIGGGTG 1154
Db 1059 HNHNEMRLFHGSPFNATIIHKGFDERHAYIGCMFGAGIYFAENSCKNQYVYIGGGTG 1118
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Db 1119 CPVHKDRSICYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSTVGRPSVNGLAIEYV 1178
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Db 1179 IYRGEQAYPEYLITYQILKPE 1199

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Q59FX0 HUMAN PRELIMINARY; PRT; 1055 AA.
AC Q59FX0;
DT 26-APR-2005, integrated into UniProtKB/T-EMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
DE variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC
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CC -----
DR EMBL; AB209339; BAD92576.1; -; mRNA.
DR Ensemble; ENSG00000173273; Homo sapiens.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001560; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 17.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 13.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS02097; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00088; ANK_REPEAT; 13.
DR PROSITE; PS10059; PARP_CATALYTIC; 1.
DR PROSITE; PS00105; SAM_DOMAIN; 1.
KW ANK repeat.
FT NON_TER 1
SQ SEQUENCE 1055 AA; 115234 MW; 9210519D299EB805 CRC64;

Query Match 72.4%; Score 4681.5; DB 2; Length 1055;
Best Local Similarity 82.9%; Pred. No. 9e-267;
Matches 870; Conservative 94; Mismatches 76; Indels 9; Gaps 2;

QY 189 ADPNARDNNWYTPLHEAAIKGIDVICIVLLQHGAEPTIRNTDGTALDAPSAKAVLTG 248
Db 1 ADPNARDNNWYTPLHEAAIKGIDVICIVLLQHGADPNIRNTDGTALDAPSAKAVLTG 60
QY 249 EYKDELLESARSNGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIVQLLQHG 308
Db 61 EYKDELLEAARSNGNEEKIMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIVQLLQHG 120
QY 309 ADVHAKDKGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCS 368
Db 121 ADVHAKDKGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCS 180
QY 369 LLLSYGADPTLLNCHNKSALDAPTPQKERLAYEFKGHSLLOAAREADVTRIKKHSLE 428
Db 181 LLLSHGADPTLVNCHGKSAVDWAPTEPLERLTYEFKGHSLLOAAREADLAKVKKTLALE 240
QY 429 MWNFKPQTHETALHCAASPYPKRKQICELLRLKGANINEKTEPLTLHVASEKAHND 488
Db 241 IINFKPQSHETALHCAVASLHPKQVTELLRLKGANVNEKNKDFMTPLHVAEERAHND 300
QY 489 VVEVVKHAKVNALDNLGOTSILHRAAYCGHLQTCRLLLSYGCDDPHIISLQFTALQMGN 548
Db 301 VVEVVKHAKVNALDNLGOTSILHRAALAGHIQTCRLLLSYGCDDPHIISLQFTALQMGN 360
QY 549 ENVQQLQEGISLGNSEADROLLEAKAGDVETVVKLCTVQSVNCRDIEGROSTPLHFAA 608
Db 361 EAVQQLSESTPIRTSDVDYRLEEASKAGDLETVKQLCSSQNVNCRDIEGRHSTPLHFAA 420
QY 609 GYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNVNADLWKFT 668
Db 421 GYNRVSVVEYLLHHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNVNADLWKFT 480
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Qy 669 PLHEAAAGKYEICKLLOHAGADPTKKNRGNTPLDLVKOGDTDIQLIRGDAALLDAK 728
 Db 481 PLHEAAAGKYEICKLKHAGADPTKKNRGNTPLDLVKEGDDTDIQLIRGDAALLDAK 540
 Qy 729 KGCLARVKKLSPPONVNCRDQGRHSTPLHLAAGNNLEVAEYLLQHGADVNAQDKGLI 788
 Db 541 KGCLARVKKLSPPONVNCRDQGRHSTPLHLAAGNNLEVAEYLLQHGADVNAQDKGLI 600
 Qy 789 PLHNAASGYHVDVAALIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLHAADPTLK 848
 Db 601 PLHNAASGYHVDVAALIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLHAADPTMK 660
 Qy 849 NQEGOTPLDLVSADVDVALLTRAMPPEALPSCYFQVINGVRSPCATADALSSSPSPSS 908
 Db 661 NQEGOTPLDLATADDIRALLIDAMPPEALPTCFKQPAT-----VVSASLISPASTPSC 713
 Qy 909 LSAASSIDNLGSGSELSVSSVSSGTEGASLEKK--EVPQVDFSTQFVRNLGLEHMD 966
 Db 714 LSAASSIDNLGTPLAELAVGASNAGDGAAGTERKEGEVAGLDNVIQFVLSGLEHLRD 773
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 Qy 1027 TILDLSPDDKDFQSVSEEMOSTVREHRDGHAGCIGFNRNLIKQVCKKLWERTHR 1086
 Db 834 TILDLAPEDKEYOSVEEMOSTVREHRDGGNAGGIFNRVNVIRIQVVKKLERFCHR 893
 Qy 1087 RKEYSEENHNHNERMLPHGSPFFNAILHKGDFDRHAYIGMFGAGIYFAENSCKSNQYV 1146
 Db 894 QKEYSEENHNHNERMLPHGSPFFNAILHKGDFDRHAYIGMFGAGIYFAENSCKSNQYV 953
 Qy 1147 YGIGGGTGPVHKDRSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGHHSVIGTRPSVN 1206
 Db 954 YGIGGGTGPVHKDRSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGHHSVIGTRPSVN 1013
 Qy 1207 GLAAEYVIRGEQAYPEYLITYQIMRPE 1235
 Db 1014 GLAAEYVIRGEQAYPEYLITYQIMRPE 1042
 RESULT 10
 Q8BX62_MOUSE PRELIMINARY; PRT; 976 AA.
 AC Q8BX62;
 ID 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 20.
 DE 0 day neonate cerebellum cDNA, RIKEN full-length enriched library,
 DE clone: C230076f23 product: tankyrase, TRF1-interacting ankyrin-related
 DE ADP-ribose polymerase, full insert sequence.
 GN Name=tnks;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi B., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
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BA Baxsal M., Baxter L., Beisel K.W., Bereano T., Bono H., Chalk A.M.,
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 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
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 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RX RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RL "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tonari Y., Hasegawa Y., Negami A., Schonbach C., Gojobori T.,
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 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
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RL Nature 420:563-573 (2002).
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
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RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AK048860; BAC33475.1; -; mRNA.
DR HSP; F16157; IN11.
DR Ensembl; ENSMUSG00000031529; Mus.musculus.
DR MGI; MGI:1341087; Tnks.
DR GO; GO:0005634; C:nucleus; IEA.

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DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 15.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 12.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS50297; ANK REP REGION; 1.
DR PROSITE; PS50088; ANK REPEAT; 12.
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DR PROSITE; PS50105; SAM_DOMAIN; 1.
DR ANK repeat; Repeat.
KW ANK repeat; Repeat.
SQ SEQUENCE 976 AA; 106663 MW; 356B10C89C33ECF1 CRC64;

Query Match          66.3%; Score 4285.5; DB 2; Length 976;
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Matches 798; Conservative 88; Mismatches 72; Indels 15; Gaps 3;

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QY 568 ROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQHGAD 627
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DB 361 AKDKGGLVPLHNACSYGHVEVAELLVRHGASVNVNADLWKFTPLHEAAAKGYEICK 420

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DB 421 HGADPTKNRGNTPDLVKGDDTDIDQLLRGDAALLDAKKGCLARVKQLCTPENINCR 480

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QY 983 HKELKEIGINAYGHRHKLKIGVERLISQOQGLNPVLTNTSGSGTILIDLSPDDKEFQSV 1042

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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

[4]

RL NUCLEOTIDE SEQUENCE.

RN MEDLINE=22426069; PubMed=12537572;

RP Misra S., Crosby P.A., Mungall C.J., Matthews B.B., Campbell K.S.,

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RN Berkeley Drosophila Genome Project;

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RT "Drosophila melanogaster release 4 sequence.";

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RL NUCLEOTIDE SEQUENCE.

RN FlyBase;

RP Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.

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CC -----

EMBL; A5003752; AAF56487.1; -; Genomic_DNA.

DR HSP; P20749; 1K1B.

DR FlyBase; FBgn0027508; tankyrase.

DR GO; GO:0056334; C:nucleus; IEA.

DR GO; GO:0003950; F:NADP; ADP-ribosyltransferase activity; IEA.

DR GO; GO:0004871; P:protein amino acid ADP-ribosylation; IEA.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR001290; PARP.

DR InterPro; IPR012317; PARP_catalytic.

DR InterPro; IPR001660; SAM_

DR InterPro; IPR011510; SAM_2.

DR Pfam; PF00023; ANK; 17.

DR Pfam; PF00644; PARP; 1.

DR Pfam; PF07647; SAM 2; 1.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SM00248; ANK; 15.

DR SMART; SM00454; SAM; 1.

DR PROSITE; PS00297; ANK_REPEAT; 1.

DR PROSITE; PS00088; ANK_REPEAT; 14.

DR PROSITE; PS01059; PARP_CATALYTIC; 1.

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DR PROSITE; PS01059; SAM_DOMAIN; 1.

KW ANK repeat; Repeat.

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Best Local Similarity 65.3%; Pred. No. 7.9e-227;

Matches 772; Conservative 166; Mismatches 189; Indels 56; Gaps 13;

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QY 151 LLQANGVQARDGGGLPLHNACSFGHAEVNNLLRHGADPNARDNWNVTPHLEAAIKGK 210

DB 76 LNSGASIQDDEGGLHPLHNCCSFGHAEVNNLLKAGASPNVTDNWNVTPHLEAAIKGK 135

QY 211 IDVCIVLLQHGAEPTIRNTDGR TALDAPSAKAVLTGYEKDELLESARSGNEEKMAL 270

DB 136 VDVCIALIQHGANNHTIRNSEQKTPLEADATRPVLTGEYKDELLEAARSGAEDRLAL 195

QY 271 LTPLVNCHASGRKSTPLHLAGYNRVKIVQLLOHQADVHAKDGLVPLHNACSYGH 330

DB 196 LTPLVNCHASGRKSTPLHLAGYNRVKIVQLLOHQADVHAKDGLVPLHNACSYGH 255

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Qy 451 PRKQICELLRKGANINEKTEKFLPLHVASEKAHNDVVEVVVKGHEAKNALDNLQOTS 510
Db 376 GKRQKLMELLTRKGSLLNEKNKAFPLPLHLAAELLYHDVAMEVLLKQAGKVALDLSGTP 435
Qy 511 LHRAAYCHLOTCHLLSYGCDPHIISLGFTALQMGVNNVQQLLQGISLGNSEADROL 570
Db 436 LHRCA--RDEQAVRLLSYAADTNIVSLEGTAAQLASDSDS-----NPPDSETH 488
Qy 571 LEAAKAGDVEVTKLCTVQ--SVNCRDIEGROSTPLHFAAGYNRVSVVEYLQHGADVHA 628
Db 489 LEAAKAGDLDTRKIVLNNPISVNCRDLDGRHSTPLHFAAGFNRPVQVFLHEGAEVYA 548
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Db 906 LIELFEREQITDLILAEMGHDDLQGVSAVGFPRKILKGIAQLRS-----TT 953
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Db 1014 KLWERYAHRREIAEENPLQSNERNMLFHGSPFINAIIVORGDERHAYIGMGFGAGIYFAE 1073
Qy 1138 NSSKSNQVYVIGGGTGCQVHKDKSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPGHH 1197
Db 1074 HSSKSNQVYVIGGGIGCPGSHKDKSCYVCPQLLCLVALGKSLQFSAMKWAHAPGHH 1133
Qy 1198 SVTGRPSVNGLALAEVYIYRGQAYPEYLITYQIMRPEGWVDG 1240
Db 1134 SVVGRPSAGGLHFAEYVYVYRGQSYPEYLITYQIVKPDSSSG 1176
RESULT 13
ID Q9XZ37_DROME PRELIMINARY; PRT; 1181 AA.
AC Q9XZ37;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 26.
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DE Hypothetical protein.
GN Name=tankyrase; ORFNames=CC4719;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA Aqbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
RA Celniker S.E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF132196; AAD34784.1; -; mRNA.
DR HSBL; P20749; IK1B.
DR FlyBase; FBgn0027508; tankyrase.
DR GO; GO:0005834; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR003110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM_2.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 17.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM 2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PSS0088; ANK_REPEAT; 14.
DR PROSITE; PSS1059; PARP_CATALYTIC; 1.
DR PROSITE; PSS0105; SAM_DOMAIN; 1.
DR ANK repeat; Hypothetical protein; Repeat.
SQ SEQUENCE 1181 AA; 127885 MW; 4E2BF31549BBA2D9 CRC64;

Query Match 61.8%; Score 3997; DB 2; Length 1181;
Best Local Similarity 65.2%; Pred. No. 2.4e-226;
Matches 771; Conservative 166; Mismatches 190; Indels 56; Gaps 13;

Qy 91 AAEAVEPAARELPEACNGDVERVKRLVTEKYNRDTAGRKSTPLHFAAGFGRKDVVEY 150
Db 17 AVWANDP-LRELSEACKTGIAKVKLLITPQTVNARDTAGRKSTPLHFAAGYGRREVVEF 75
Qy 151 LLONGANVQARDGGLIPLHNACSFGEAEVNNLLRHGADPNARDNNYTPLEAAAIKKG 210
Db 76 LLNSGASIQACDEGLHPLNCSFGEAEVVRLLKXAGASPTTDDNNYTPLEHAASKG 135
Qy 211 IDVCIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKDELLSARSNGEKKMAL 270
Db 136 VDVCVLLALQHGANTIRNSQKTPLELADEATRPVLTGEYKDELLSARSNGEKKMAL 195
Qy 271 LTPLVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGLVPLHNACSGH 330
Db 196 LTPLVNCHASDGRSRSTPLHLAGYNRIGIVEILLANGADVHAKDGLVPLHNACSYGH 255
Qy 331 YEVTLLVKGACVNMVMDLWQFTPLHEAASKVRVEVCSLLSYGADPTLLNCHNKSALD 390
Db 256 FDVTKLLIQAGANVNDLWAFPLHEAASKSRVEVCSLLSRGADPTLLNCHSKSAIDA 315
Qy 391 APTPOLKERLAYEPKGHSLQAAAREADVTRTKHLSLEMVNFKHPQTHETALHCAASPY 450
Db 316 APTRELRIEAFYKGHCLLDACKCDVSRKULVCAEIVNFVHPYTGDTPLHLAVNSPD 375
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451 PRRKQICELLKRGANINEKTEFLTPHVAASEKAHNDVVEVVVKEAKVNALDNLGOTS 510
 376 GRRKQIMELLTRKGSILNEKNAFLTPHAAELHYDAEVLVLLKQAKVNALDSIGLQTP 435
 511 LHRAYCGLHQLCRLLLSVCGDPNIIISOGFTALQNGNENVOOLLOEGLSNGSADRLQ 570
 436 LHRCA--RDEQAVRLLSYAADTNIVSLGLTAQAQASDLVKLLK-----NPPDSETHL 488
 571 LEAAKAGDVETVVKCLQTVQ--SVNCRDIEGROSTPLHPAAGVYRVVVEVLLQHGADVHA 628
 489 LEAAKAGDLDVTRVIRVNVPIVSNCRDLGRHSTPLHPAAGVYRVVVEVLLQHGAEVTA 548
 629 KDKGGLVPLHNAACSYGHYEVALLVKGAVVNVADLWKFTPLHEAAKGYKIBCKLLQH 688
 549 ADKGLVPLHNAACSYGHYEVTELLVKGANVNVSDLWKFTPLHEAAKGYKIBCKLLKH 608
 689 GADPTKQRDGNVTPDLVKQDGTDLQDLRGDAALLDAKKGCLARVKLSSPDVNCRD 748
 609 GADPMKQRDGNVTPDLVKESDHDVAELRGPSALLDAKKGCLARVQLVTPESINCRD 668
 749 TQGRHSTPLHNAAGVYRVVVEVLLQHGADVNAQDKGGLIPLHNAASVGHVDVAALLIKY 808
 669 AQGRNSTPLHNAAGVYRVVVEVLLQHGADVNAQDKGGLIPLHNAASVGHLDIAALLIKH 728
 809 NACVNATDKWFTPLHEAAKQRTQICALLAHGADPTLKNQEGQTPDLVSDADVSALL 868
 729 KTVVNATDKWFTPLHEAAKQRTQICALLAHGADVNAQDKGGLIPLHNAASVGHLDIAALLIKH 788
 869 TAAMPSS-----ALPSCYKQVNLVGRVSPGATADALSSGSPSS--LSAASLDNLGSGF 922
 789 QDAMATSLSQAL--SASTQSLTSSSPADPATAAAGTSSSSSSAILSPPTTETVLLPTGA 847
 923 SELSSV-----VSSS-----GTEGASLEKKEVPGVD--FSITQFVNLGLEH 963
 848 SMILSVPLPLSSSTRISPAQGAERAGGSSDDL--LPDADTITNVSGPLSSQQLHH 905
 964 LMDIFEREQITLDVIVEMGHKELKIGINAYGHRHLKINGVERLISGQGLNPLYTLANTS 1023
 906 LIELEPERQITLDILAEMGHDDLKQGVSAVYGRHKLKIGIAQLS-----TT 953
 1024 GSG-----TILIDSPDKFQSVVEEMQSVREHGGHAGGIFPNRYNLIKQKVNK 1077
 954 GTGNVNLCTLLVLDLPDDKEVFAVEEEMQATIREHNDQAGGYFTRYNIRVQKQNR 1013
 1078 KLWERYTHRRKEVSENNHANERMLFHGSPFNALIHKGPERHAYIGMGAGIYAE 1137
 1014 KLWERYAHRROBIAENFLQSNRMLFHGSPFNAIVQRFDERHAYIGMGAGIYAE 1073
 1138 NSSKSNQVYVYGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHH 1197
 1074 HSKSNQVYVYGGIGGICPESHKDKSCYVCPQLLILCRVALGKSFLOYSAKMAHAPPGHH 1133
 1198 SVTGRPSVNGLALARYIVYRGQAYPEYLITYOIMRPGMVDG 1240
 1134 SVVGRPSAGGLHFAEVYVYRGQAYPEYLITYOIKPDDSSG 1176

RESULT 14
 Q4S372.TETNG
 ID Q4S372.TETNG PRELIMINARY; PRT; 1047 AA.
 AC Q4S372.
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Chromosome 4 SCFA14752, whole genome shotgun sequence. (Fragment).
 GN ORFNames=GSTENG0024768001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 RA Maucell E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
 RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Poulain J., De Berardinis V.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Crouaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; CAAS01014752; CAG04910.1; -; Genomic DNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR012317; PARP_catalytic.
 DR Pfam; PF00023; ANK; 13.
 DR Pfam; PF00644; PARP; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 9.
 DR PROSITE; PS02097; ANK_REPEAT; 1.
 DR PROSITE; PS00088; ANK_REPEAT; 10.
 DR PROSITE; PS10509; PARP_CATALYTIC; 1.
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 FT NON TER 1047 1047
 SQ SEQUENCE 1047 AA; 114477 MW; 09E9D3AE198C75E7 CRC64;
 Query Match 51.4%; Score 3324; DB 2; Length 1047;
 Best Local Similarity 60.5%; Pred. No. 9.1e-187;
 Matches 682; Conservative 73; Mismatches 135; Indels 238; Gaps 19;
 QY 248 GEYKDELLELSARGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYVNRVIVOLLQH 307
 DB 18 GEYKDELLELSARGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYVNRVIVOLLQH 77
 QY 308 GADVHAKDKGLVPLHNAACSYGHYEVTELLVK----- 339
 DB 78 GADVHAKDKGLVPLHNAACSYGHYEVTELLVKVHTHTTHTRAQTHGTCYEWTLARPLEA 137
 QY 340 -----HGACVNAAMDLMQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKAIDLAPT 393
 DB 138 ETVPQHGACVNAAMDLMQFTPLHEAASKNRVEVCSLLLSHGADPTLLNCHSKSSVDMAPT 197
 QY 394 POLKERLAYEPKSHLLOAAREADVTRIKKHLISLSEMVNFKPQTHETALHCAASPYKCR 453
 DB 198 PELKERTYEPKSHLLOAAREADVTRIKKHLISLSEMVNFKPQTHETALHCAASPYKCR 246
 QY 454 KQICELLARKGANINEKTEFLTPHVAASEKAHNDVVEVVVKEAKVNALDNLGOT 509
 DB 247 -----LHDSASRGCGGAHNDIMEVLQKKGAKVNALDNLGOT 282
 QY 510 SLHRAAYCGHLOTCLRLLSYCGDPNIIISOGFTALQNGNENVOOLLOEGLSNGSADRLQ 569
 DB 283 ALHRAAMAGHLHTCRLLILGYGADASLVLSOGFTALQNGNENVOOLLOEGLSNGSADRLQ 342

QY 570 LLEAAKAGDVETVKLLCTVQSVNCRDIEGRQSTPLHFAAGVNRVSVVEYLLQHGADVHAK 629
DB 343 LLEAAKAGDLDVTKSLCTPQVNCNRDIEGRHSTPLHFAAGVNRVSVVEYLLHGHADVHAK 402
QY 630 DKGLVPLHNACSGHYEVAELLVKGAVNVADLWKFPTLHFAAAGKGYEICKLLQHG 689
DB 403 DKGLVPLHNACSGHYEVAELLVKGASVNVADLWKFPTLHFAAAGKGYEICKLLKHG 462
QY 690 ADPTKQVRDNTPLDLVKDGTDTQDILLRGDAALLDAKKGCLARVKKLSPDNVNCRD 749
DB 463 ADPTKQVRDNTPLDLVKDGTDTQDILLRGDAALLDAKKGCLARVKKLSPDNVNCRD 522
QY 750 QGRHSTPLHAAAGVNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGVHVDVAALLIKYN 809
DB 523 QGRNSTPLHAAAGVNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGVHVDVAALLIKHN 582
QY 810 ACVNATDKWFTPLHFAAAGKRTQCALLAHGADPTLKNQEGOTPLDLVLS----- 860
DB 583 TCVNATDKWFTPLHFAAAGKRTQCALLAHGADPTLKNQEGOTPLDLTAPVVPDQR 642
QY 861 -----ADVSALLTAAMPSPALPSCYKQVNLVGRSPGATADALSGPSPS 907
DB 643 MYDVSVPSPSQAIDIRALLIDAMPDLPCLKPO-----ATVVRWSGG----- 688
QY 908 SLSNASSLDNLGSFSELSSVSSSGTEGASSLEKKEVP-----GVDFSTIQVRN 958
DB 689 --ECQHRCDRRRGLHVPVAVLPVGGQOHRQPDHAPRRPHGRHRTSGRDVVRQ--- 742
QY 959 LGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAVGRHKLKIGVERLISGQQLNPYL 1018
DB 743 -----EGGRRYRRAP-----AAGHDQPLP----- 762
QY 1019 TLNTSGSTILIDLPDKKEF-----QSVVEEMQSTVR---EHRDGGH--AGGIFN 1064
DB 763 --BESGAGTPPHL--PERADFSPCRAGHGRARRAEGDRHQRLLRPPAQADQGHREAGRTA 819
QY 1065 RYN-----ILKIQK-----VCNKKLWE-----RTHRRKEVSENNHNN 1099
DB 820 RWKVPVPLPLLRGNRDRPGSRQGVPCGGGAEEHPRAPRRRRSLQPLQHHQGV 879
QY 1100 ERMLF-----HGSPPFNATIIHKGFDERHAYIGMFGAGIYFPAENS 1139
DB 880 KAGCFRAADRDEPALTQVCFLLADSESPFINAIHKGFDERHAYIGMFGAGIYFPAENS 939
QY 1140 SKSNQYVYGGGTGCPVHKDRSCYICH-----RQLFCRVTLGKFLQPSAM 1187
DB 940 SKSNQYVYGGGTGCPVHKDRSCYVCHRSADVNGGCLCARQMLFCRVTLGKFLQPSAM 999
QY 1188 KMAHSPGHHSVTCRPSVNGLAAYVIYRGEQAYPEYLITYQIMRPE 1235
DB 1000 KMAHAPPGHHSVTCRPSVNGLAAYVIYRGEQAYPEYLITYQIVKPE 1047
RESULT 15
Q8BXH7_MOUSE
ID Q8BXH7_MOUSE PRELIMINARY; PRT; 601 AA.
AC Q8BXH7;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 18.
DE 10 days neonate cerebellum cDNA, RIKEN full-length enriched library,
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";

Methods Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Allen J.E.,
Davis M.J., Wilming L.G., Aidinis V., Attaliya R.N., Bailey T.L.,
Bansal M.B., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Crome M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
Schombach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
Sperling S., Stupka E., Suglura K., Sultana R., Takenaka Y., Taki K.,
Tamajima K., Tan S.D., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Ueda H.K., Van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
Pekuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
Kishimoto T., Kojima M., Kondo S., Konno H., Nakano K., Nimukawa N.,
Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
Science 309:1559-1563(2005).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
[4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01366;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasai K., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217951; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Scaubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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DR EMBL; AK047094; BAC32960.2; -; mRNA.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 13.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 11.
DR PROSITE; PS00088; ANK_REPEAT; 11.
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FT NON TER
SQ SEQUENCE 601 AA; 65378 MW; F13F667AD865F807 CRC64;
Query Match 47.4%; Score 3066; DB 2; Length 601;
Best Local Similarity 97.2%; Pred. No. 6.3e-172;
Matches 584; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
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Search completed: December 18, 2006, 17:34:36
Job time : 254 secs

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:34:55 ; Search time 41.423 Seconds
(without alignments)
2620.235 Million cell updates/sec

Title: US-10-616-101-4

Perfect score: 6464

Sequence: 1 RCSARRGAAGGQAGRGARV.....AYPEYLITYQIMRPGMVDG 1240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
- 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*
- 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*
- 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
- 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCFUS COMB.pep:*
- 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
- 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	6464	100.0	1240	2	US-09-696-668-4 Sequence 4, Appli
2	6464	100.0	1240	2	US-09-843-159B-4 Sequence 4, Appli
3	6108	94.5	1166	2	US-09-972-115A-6 Sequence 6, Appli
4	6053	93.6	1166	2	US-09-350-982C-5 Sequence 5, Appli
5	5877	90.9	1227	2	US-09-843-602-26 Sequence 26, Appli
6	5766	89.2	1100	2	US-09-696-668-3 Sequence 3, Appli
7	5766	89.2	1100	2	US-09-843-159B-3 Sequence 3, Appli
8	5760	89.1	1100	2	US-09-843-159B-9 Sequence 9, Appli
9	5731.5	88.7	1100	2	US-09-427-154-2 Sequence 2, Appli
10	5656	87.5	1083	2	US-09-843-159B-10 Sequence 10, Appli
11	5452	84.3	1267	2	US-09-972-115A-4 Sequence 4, Appli
12	5103.5	79.0	1327	2	US-09-196-387-2 Sequence 2, Appli
13	5103.5	79.0	1327	2	US-09-841-835-2 Sequence 2, Appli
14	5103.5	79.0	1327	2	US-09-972-115A-8 Sequence 8, Appli
15	5031.5	77.8	1333	2	US-09-972-115A-2 Sequence 2, Appli
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22	892.5	13.8	4377	2	US-09-949-016-6978 Sequence 6978, Ap
23	878.5	13.6	1719	2	US-09-949-016-6966 Sequence 6966, Ap
24	878.5	13.6	1856	2	US-09-949-016-6964 Sequence 6964, Ap
25	878.5	13.6	1880	2	US-09-949-016-5876 Sequence 5876, Ap
26	878.5	13.6	1881	2	US-09-949-016-6965 Sequence 6965, Ap

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33	878.5	13.6	1883	2	US-09-949-016-9016	Sequence 9016, Ap
34	878.5	13.6	1883	2	US-09-949-016-9017	Sequence 9017, Ap
35	877	13.6	1839	1	US-09-172-977-4	Sequence 4, Appli
36	877	13.6	1839	2	US-09-404-108-4	Sequence 4, Appli
37	877	13.6	3924	2	US-09-538-092-1246	Sequence 1246, Ap
38	874	13.5	160	2	US-09-972-115A-20	Sequence 20, Appli
39	858	13.3	843	1	US-09-172-977-3	Sequence 3, Appli
40	858	13.3	843	2	US-09-404-108-3	Sequence 3, Appli
41	835	12.9	1745	1	US-09-031-485-33	Sequence 33, Appli
42	835	12.9	1745	1	US-08-847-429A-33	Sequence 33, Appli
43	835	12.9	1745	2	US-09-065-474-33	Sequence 33, Appli
44	835	12.9	1745	2	US-09-557-034-33	Sequence 33, Appli
45	834.5	12.9	199	2	US-09-270-767-45196	Sequence 45196, A

ALIGNMENTS

RESULT 1
US-09-696-668-4
; Sequence 4, Application US/09696668
; Patent No. 6617102

GENERAL INFORMATION:

; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ososovkaya, Valeria
; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS (US-09-696-668-4)
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-696-668-4

Query Match	100.0%	Score 6464;	DB 2;	Length 1240;
Best Local Similarity	100.0%	Pred. No. 0;		
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RESULT 2

US-09-843-159B-4
; Sequence 4, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty

; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
; FILE REFERENCES: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-159B-4

Query Match 100.0%; Score 6464; DB 2; Length 1240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RCSARRGAAGGQGAQRGARVGAAGHTAPDPVTAGSQAARALSASSPGGLALLAGPGLLL 60
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Db 1201 GRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGWVG 1240

RESULT 3

US-09-972-115A-6
; Sequence 6, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-6

Query Match 94.5%; Score 6108; DB 2; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 75 MSGRCAGGACASAAAEEVPAARELPEACRNGDVERVKRLVTPEKVNSRDTAGRKST 134
Db 1 MSGRCAGGACASAAAEEVPAARELPEACRNGDVERVKRLVTPEKVNSRDTAGRKST 60
Qy 135 PLHFAAGFRKDVVEYLLQNGANVQARDGGGLIPLHNACSFGEAEVNNLLLEHGADPNAR 194
Db 61 PLHFAAGFRKDVVEYLLQNGANVQARDGGGLIPLHNACSFGEAEVNNLLLEHGADPNAR 120
Qy 195 DNWNTPLHEAAIKGIDVICVILLQHGAEPTIRNTDGTALDLDAPSAAVLITGSKDE 254
Db 121 DNWNTPLHEAAIKGIDVICVILLQHGAEPTIRNTDGTALDLDAPSAAVLITGSKDE 180

RESULT 4

US-09-350-982C-5
; Sequence 5, Application US/09350982C
; Patent No. 6455290

Qy 255 LLESARSNGEENKMAALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLLOHGADVHAK 314
Db 181 LLESARSNGEENKMAALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLLOHGADVHAK 240
Qy 315 DKGLDVLPHNACSYGHYEVTELLVKGHCACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 374
Db 241 DKGLDVLPHNACSYGHYEVTELLVKGHCACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 300
Qy 375 ADPTLLMCHNKSADLAPTQPKERLAYEFKXGHSLLQAAAREADVTRIKKHLSELVNFKH 434
Db 301 ADPTLLMCHNKSADLAPTQPKERLAYEFKXGHSLLQAAAREADVTRIKKHLSELVNFKH 360
Qy 435 POTHETALHCAASAPYPRKQICELLRLKGANINEKTEKFEPLTLHVASEKAHNDVVEVV 494
Db 361 POTHETALHCAASAPYPRKQICELLRLKGANINEKTEKFEPLTLHVASEKAHNDVVEVV 420
Qy 495 KHEAKVNALNLGOTSJLHRAAYCGHLOTCLLLSYGCDPNTIISLOGFTALQMGNEVQOL 554
Db 421 KHEAKVNALNLGOTSJLHRAAYCGHLOTCLLLSYGCDPNTIISLOGFTALQMGNEVQOL 480
Qy 555 LQEGISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV 614
Db 481 LQEGISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV 540
Qy 615 VVEYLLQHGADVHAKDKGLVPLHNACSYGHYEVAELLVKHGA VNVNADLWKFTPLHEAA 674
Db 541 VVEYLLQHGADVHAKDKGLVPLHNACSYGHYEVAELLVKHGA VNVNADLWKFTPLHEAA 600
Qy 675 AKGYEICKLLQHGADPTKKNRDGNTPLDVKDGDITDQLLRGDAALLDAKKGCLAR 734
Db 601 AKGYEICKLLQHGADPTKKNRDGNTPLDVKDGDITDQLLRGDAALLDAKKGCLAR 660
Qy 735 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNA 794
Db 661 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNA 720
Qy 795 SYGHVDVAALLIKYNACVNAATDKWAFPLHEAAQKGRTOCALILAAGADPTLKNQEGOT 854
Db 721 SYGHVDVAALLIKYNACVNAATDKWAFPLHEAAQKGRTOCALILAAGADPTLKNQEGOT 780
Qy 855 PLDLVSADDDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALS SGPSPSSLSAASS 914
Db 781 PLDLVSADDDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALS SGPSPSSLSAASS 840
Qy 915 LDNLSSGSELSVSSVSSSGTEGASSLEKKEVPGVDFSIITQFVRLNGLHLMDFPEREQT 974
Db 841 LDNLSSGSELSVSSVSSSGTEGASSLEKKEVPGVDFSIITQFVRLNGLHLMDFPEREQT 900
Qy 975 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTLLIDLSP 1034
Db 901 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTLLIDLSP 960
Qy 1035 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTIKIQVCNKKLWERYTHRRKEVSEEN 1094
Db 961 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTIKIQVCNKKLWERYTHRRKEVSEEN 1020
Qy 1095 HNHNANERMLFHGSPFVNAILHKGDFDERHAYTGGMFGAGIYFAENSSKSNQVYIGGGTG 1154
Db 1021 HNHNANERMLFHGSPFVNAILHKGDFDERHAYTGGMFGAGIYFAENSSKSNQVYIGGGTG 1080
Qy 1155 CPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMQMAHSPPGHHSVTGRPSVNGLALAEYV 1214
Db 1081 CPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMQMAHSPPGHHSVTGRPSVNGLALAEYV 1140
Qy 1215 IYRGEQAYPEYLITYQIMRPEGWVG 1240
Db 1141 IYRGEQAYPEYLITYQIMRPEGWVG 1166

GENERAL INFORMATION:
; APPLICANT: Bertheisen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Iacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Relat
; TITLE OF INVENTION: Same
; FILE REFERENCE: PHM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (1102)..(1102)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (2650)..(2650)
; OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-5

Query Match 93.6%; Score 6053; DB 2; Length 1166;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1157; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 75 MSGRCAGGGNACASAAAAEVEPAARELPEACRNGDVERVKRLVTPKVNSTRDAGRKST 134
Db 1 MSGRCAGGGNACASAAAAEVEPAARELPEACRNGDVERVKRLVTPKVNSTRDAGRKST 60

Qy 135 PLHFAAGFRKDVVEYLLQNGANVQARDGGLIPLHNACSFGEAEVNNLLRHGADPNAR 194
Db 61 PLHFAAGFRKDVVEYLLQNGANVQARDGGLIPLHNACSFGEAEVNNLLRHGADPNAR 120

Qy 195 DNWNTPLHEAAIKGKIDVCIVLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKDE 254
Db 121 DNWNTPLHEAAIKGKIDVCIVLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKDE 180

Qy 255 LLESARGNEEKMWALLTPLNVNCHASDGRKSTPLHLAGNVRKIYVOLLQHGADYHAK 314
Db 181 LLESARGNEEKMWALLTPLNVNCHASDGRKSTPLHLAGNVRKIYVOLLQHGADYHAK 240

Qy 315 DKGLDVLPHNACSYGHEVTELLVKHGACVNAMDWQFTPLHEAASKNRVEVCSLLLSYG 374
Db 241 DKGLDVLPHNACSYGHEVTELLVKHGACVNAMDWQFTPLHEAASKNRVEVCSLLLSYG 300

Qy 375 ADPTLLCHNKSAIDLAPTQPKERLAYEFKGSLLQAAREADVTRIKGHLSELMVNFKH 434
Db 301 ADPTLLCHNKSAIDLAPTQPKERLAYEFKGSLLQAAREADVTRIKGHLSELMVNFKH 360

Qy 435 POTHETALHCAASAPYKPKQICELLIRKGANINEKTEPLTPLHVASEKANDVVEVV 494
Db 361 POTHETALHCAASAPYKPKQICELLIRKGANINEKTEPLTPLHVASEKANDVVEVV 420

Qy 495 KHEAKVNALDNLGQTSLSHRAAYCGHLOTGCRLLLSYGCDPNIISLQGTALQMGNEVQOL 554
Db 421 KHEAKVNALDNLGQTSLSHRAAYCGHLOTGCRLLLSYGCDPNIISLQGTALQMGNEVQOL 480

Qy 555 LQEGISLGNSEADRLLEAAKAGDVETVKKLCVTVQSVNCRDIEGRQSTPLHFAAGYNRVS 614
Db 481 LQEGISLGNSEADRLLEAAKAGDVETVKKLCVTVQSVNCRDIEGRQSTPLHFAAGYNRVS 540

Qy 615 VVEYLLQHGADYHAKDKGGLVPLHNACSYGHEVTELLVKHGACVNAMDWQFTPLHEAA 674
Db 541 VVEYLLQHGADYHAKDKGGLVPLHNACSYGHEVTELLVKHGACVNAMDWQFTPLHEAA 600

Qy 675 AKGYEICKLLOHGADPTKKNRGNTPDLVKDGDGTDIQLLRGDAALLDAAKKGCLAR 734
Db 601 AKGYEICKLLOHGADPTKKNRGNTPDLVKDGDGTDIQLLRGDAALLDAAKKGCLAR 660

Qy 735 VKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAA 794
Db 661 VKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAA 720

Qy 795 SYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 854
Db 721 SYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 780

Qy 855 PLDLVSADVDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSSLSAASS 914
Db 781 PLDLVSADVDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSSLSAASS 840

Qy 915 LDNLSSGSFSELSSVSSSGTEGASSLEKKEVPGVDIFSITQFVRNLGLEHLMDFEREQIT 974
Db 841 LDNLSSGSFSELSSVSSSGTEGASSLEKKEVPGVDIFSITQFVRNLGLEHLMDFEREQIT 900

Qy 975 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPNYTLTNTSGSTLIDLSP 1034
Db 901 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPNYTLTNTSGSTLIDLSP 960

Qy 1035 DKKEFQSVBEEMQSTVREHRDGGHAGGIFNRYNLIKIQKVCNKKLMERYTHRRKEVSEEN 1094
Db 961 DKKEFQSVBEEMQSTVREHRDGGHAGGIFNRYNLIKIQKVCNKKLMERYTHRRKEVSEEN 1020

Qy 1095 HNHANERMLFHGSPFFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYVIGGGTG 1154
Db 1021 HNHANERMLFHGSPFFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYVIGGGTG 1080

Qy 1155 CPVHKDRCVICHROLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYV 1214
Db 1081 CPVHKDRCVICHROLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYV 1140

Qy 1215 IYRGEQAYPEYLITYQIMRPEGMVDG 1240
Db 1141 IYRGEQAYPEYLITYQIMRPEGMVDG 1166

RESULT 5
US-09-849-602-26
; Sequence 26, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105 (JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-26

Query Match 90.9%; Score 5877; DB 2; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1148; Conservative 8; Mismatches 47; Indels 50; Gaps 5;

Qy 12 QGAQRGARVGAA-----HGTAPDPVFTAGSQAARALSASSPGGLALLIAGPGLL 59
Db 1 QGAQRGARVGAAAGMLRRSGDSREPSGPGPVERVSGGPRPPARGAGAPAPVAGAVAG----- 56

Qy 60 LRLALLLAVAAARIMSGRCAGG-----GACASAAAAEVEPAARELFEACRN 108
Db 57 -----CGGGDHVGSPLRRRRSGSLRDAAAEVPEPAARELFEACRN 96

Qy 109 GDVERVKRLVTPKVNSTRDAGRKSTPLHFAAGFRKDVVEYLLQNGANVQARDGGLIP 168
Db 109 GDVERVKRLVTPKVNSTRDAGRKSTPLHFAAGFRKDVVEYLLQNGANVQARDGGLIP 168

Db 97 GDVERVKRLVTPKVNRTAGKSTPLHFAAGFGKRVVYLLQNGANVQARDGGLIP 156
Qy 169 LHNACSFHAEVNNLLRHGADPNARDNNYTPLEAAIKGKIDVICIIVLQHGAPTRN 228
Db 157 LHNACSFHAEVNNLLRHGADPNARDNNYTPLEAAIKGKIDVICIIVLQHGAPTRN 216
Qy 229 TDGRTALDADPSAKAVLTGKIDELLESARSNGNEKMMALLTPLNVNCHASDGRKSTP 288
Db 217 TDGRTALDADPSAKAVLTGKIDELLESARSNGNEKMMALLTPLNVNCHASDGRKSTP 276
Qy 289 LHLAGYNNRVKIVOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNM 348
Db 277 LHLAGYNNRVKIVOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNM 336
Qy 349 LMQFTPLHAAAKNVEVCSLLSYGADPTLNCNKSAIDLAPTPOLKERLAYEFKHS 408
Db 337 LMQFTPLHAAAKNVEVCSLLSYGADPTLNCNKSAIDLAPTPOLKERLAYEFKHS 396
Qy 409 LIQAAAREADVTRIKKHLSEVMNFKHPQTHETALHCAASPPYKPKQICELLLRKANIN 468
Db 397 LIQAAAREADVTRIKKHLSEVMNFKHPQTHETALHCAASPPYKPKQICELLLRKANIN 456
Qy 469 ERTKFEFLPLHVASEKANDVVEVVVYVHAKVNALDNLGQTSLHRAAYCGHLQTCRLLS 528
Db 457 ERTKFEFLPLHVASEKANDVVEVVVYVHAKVNALDNLGQTSLHRAAYCGHLQTCRLLS 516
Qy 529 YGCDPNIIISLOQFTALQMGNEVQOLLEGIISLGNSEADROLLEAAKAGDVETVKLCV 588
Db 517 YGCDPNIIISLOQFTALQMGNEVQOLLEGIISLGNSEADROLLEAAKAGDVETVKLCV 576
Qy 589 QSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEV 648
Db 577 QSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEV 636
Qy 649 ABLLVKGAVNVNADLWFKPTPLHAAAAGKYBI CKLLQHGADPTKQORDGNTPLDLVKD 708
Db 637 ABLLVKGAVNVNADLWFKPTPLHAAAAGKYBI CKLLQHGADPTKQORDGNTPLDLVKD 696
Qy 709 GDTDIDQLLGDAAALDAKGLARVKLSPPDNVNCRDTCGRHSTPLHLAGYNNLEV 768
Db 697 GDTDIDQLLGDAAALDAKGLARVKLSPPDNVNCRDTCGRHSTPLHLAGYNNLEV 756
Qy 769 ABYLLQHGADVNAQDKGGLIPLHNAASYGHVDVVAALLIKYNACVNATDKWAPTPLHAAQ 828
Db 757 ABYLLQHGADVNAQDKGGLIPLHNAASYGHVDVVAALLIKYNACVNATDKWAPTPLHAAQ 816
Qy 829 KGRTOCALLAHGADPTLKNQEGQTPDLVSADVSALLTAAMPSPALPSYKPKQVING 888
Db 817 KGRTOCALLAHGADPTLKNQEGQTPDLVSADVSALLTAAMPSPALPSYKPKQVING 876
Qy 889 VRSPGATADALSSGSPSSLSAASLNLSCSFELSSVSSSGTEGASSLEKKEVPQV 948
Db 877 VRSPGATADALSSGSPSSLSAASLNLSCSFELSSVSSSGTEGASSLEKKEVPQV 936
Qy 949 DFSITQFVNGLGHLMDIFEREQITLVDLVEMGHKELKEIGINAYGHRHKLKIGVERLI 1008
Db 937 DFSITQFVNGLGHLMDIFEREQITLVDLVEMGHKELKEIGINAYGHRHKLKIGVERLI 996
Qy 1009 SQCGGLNPNYLTNTSGGTILIDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNI 1068
Db 997 SQCGGLNPNYLTNTSGGTILIDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNI 1056
Qy 1069 LKIQKVCNKKLWERTHRRKEVSENNHANERMLFHGSPFFNALIHKGFDRHAYIGM 1128
Db 1057 LKIQKVCNKKLWERTHRRKEVSENNHANERMLFHGSPFFNALIHKGFDRHAYIGM 1116
Qy 1129 FCAGIYFAENSSKSNQYVYIGGGTGCPVHK--DRSCYICHRQLLCFRTVLTKGSFLQFSAM 1187
Db 1117 FCAGIYFAENSSKSNQYVYIGGGTGQVFTKTDLTFTATAALL--PGNLGKVFPAVQCN 1174
Qy 1188 KMAHSPGHHSTGRPSVNGLALAEVYIYRGQAYPEYLITYQIMRPEGMVDG 1240
Db 1175 ENGTSPGHHSTGRPSVNGLALAEVYIYRGQAYPEYLITYQIMRPEGMVDG 1227

RESULT 6
US-09-696-668-3
; Sequence 3, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Osbovska, Valeria
; TITLE OF INVENTION: TANKRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS (C
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-696-668-3
Query Match 89.2%; Score 5766; DB 2; Length 1100;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1099; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 141 GFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNY 200
Db 1 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNY 60
Qy 201 PLHAAIKGKIDVICIIVLQHGABTIRNTDORTALDADPSAKAVLTGEEKDELLESAR 260
Db 61 PLHAAIKGKIDVICIIVLQHGABTIRNTDORTALDADPSAKAVLTGEEKDELLESAR 120
Qy 261 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 320
Db 121 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVOLLQHGADVHAKDGLV 180
Qy 321 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHAAASKNRVEVCSLLSYGADPTLL 380
Db 181 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHAAASKNRVEVCSLLSYGADPTLL 240
Qy 381 NCHNKSADLAPTQPKERLAYEFKHSLLQAAREADVTRIKKHLSEVMNFKHPQTHET 440
Db 241 NCHNKSADLAPTQPKERLAYEFKHSLLQAAREADVTRIKKHLSEVMNFKHPQTHET 300
Qy 441 ALHCAASPPYKPKQICELLARKGANINEKTEFLTPLVASEKAHNDVVEVVVHKA 500
Db 301 ALHCAASPPYKPKQICELLARKGANINEKTEFLTPLVASEKAHNDVVEVVVHKA 360
Qy 501 NALNMGTSLHRAAYCGHLQTCRLLSYGCDDPNIIISLOQFTALQMGNEVQOLLEGIS 560
Db 361 NALNMGTSLHRAAYCGHLQTCRLLSYGCDDPNIIISLOQFTALQMGNEVQOLLEGIS 420
Qy 561 LGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 620
Db 421 LGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Qy 621 QHGADVHAKDGLVPLHNACSYGHEVVAELLVKHGAVNVNADLWKFPLHAAAKGYE 680
Db 481 QHGADVHAKDGLVPLHNACSYGHEVVAELLVKHGAVNVNADLWKFPLHAAAKGYE 540
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQDLRGDAALLDAAKKGCLARVKLSS 740
Db 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQDLRGDAALLDAAKKGCLARVKLSS 600
Qy 741 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

QY 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOICALLLAHAGADPTLKNQSGOTPLDLVS 860
DB 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOICALLLAHAGADPTLKNQSGOTPLDLVS 720
QY 861 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSSG 920
DB 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
QY 921 SFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFPEREQITLDVLVE 980
DB 781 SFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFPEREQITLDVLVE 840
QY 981 MGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTINTSGSTLIDLSPPDKKEFQ 1040
DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTINTSGSTLIDLSPPDKKEFQ 900
QY 1041 SVEEEMQSTVREHRDGHAGGIFNRYNLIKQKVCNKKLMERYTHRRKEVSEENHNHANE 1100
DB 901 SVEEEMQSTVREHRDGHAGGIFNRYNLIKQKVCNKKLMERYTHRRKEVSEENHNHANE 960
QY 1101 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGGTGCPVHKD 1160
DB 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGGTGCPVHKD 1020
QY 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1080
QY 1221 AYPEYLITYQIMRPEGMDVG 1240
DB 1081 AYPEYLITYQIMRPEGMDVG 1100

RESULT 7

US-09-843-159B-3

; Sequence 3, Application US/09843159B

; Patent No. 6887675

; GENERAL INFORMATION:

; APPLICANT: Luo, Yin

; APPLICANT: Chan, Evan

; APPLICANT: Xu, Xiang

; APPLICANT: Huang, Betty

; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods

; FILE REFERENCE: A-68292-2/RMS/DHR

; CURRENT APPLICATION NUMBER: US/09/843,159B

; CURRENT FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: US 09/596,668

; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 09/427,154

; PRIOR FILING DATE: 1999-10-25

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1100

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-843-159B-3

Query Match

Best Local Similarity 89.2%; Score 5766; DB 2; Length 1100;

Matches 1099; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 141 GFGKDVVEYLLQNGANVQARDGGILPLHNACSFGEAEVNNLLRHGADPNARDNWNVT 200

DB 1 GFGKDVVEYLLQNGASVQARDGGILPLHNACSFGEAEVNNLLRHGADPNARDNWNVT 60

QY 201 PLHEAAIKGKDVCIVLLQHGAEPTIRNTDGRALDLADPPSAKAVLTGKYKDELLESAR 260

DB 61 PLHEAAIKGKDVCIVLLQHGAEPTIRNTDGRALDLADPPSAKAVLTGKYKDELLESAR 120

QY 261 SGNEEKMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDKGLV 320

DB 121 SGNEEKMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDKGLV 180
QY 321 PLHNACSYGHYEVTELLVKHGACVNMADLWQFTPLHEAAKSRVEVCSLLLSYGADPTLL 380
DB 181 PLHNACSYGHYEVTELLVKHGACVNMADLWQFTPLHEAAKSRVEVCSLLLSYGADPTLL 240
QY 381 NCHNKSADLADPTPOLKERLAYEFKGHSLQAREADVTRI KKHLSLEWMVNFKHPQTHET 440
DB 241 NCHNKSADLADPTPOLKERLAYEFKGHSLQAREADVTRI KKHLSLEWMVNFKHPQTHET 300
QY 441 ALHCAAAAPYPRKQICELLRLKGANINEKTKFEFLTPLHVASEKANDVVEVVVKGHEAKV 500
DB 301 ALHCAAAAPYPRKQICELLRLKGANINEKTKFEFLTPLHVASEKANDVVEVVVKGHEAKV 360
QY 501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDBNIIISLOGFTALQNGNENVOQLQEGIS 560
DB 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDBNIIISLOGFTALQNGNENVOQLQEGIS 420
QY 561 LGNSEADROLLEAAKAGADVETVKKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 620
DB 421 LGNSEADROLLEAAKAGADVETVKKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
QY 621 QHGADVHAKDKGGLVPLHNACSYGHYEVAEELLVKHGAVNVNADLWKFTPLHEAAAKGYE 680
DB 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAEELLVKHGAVNVNADLWKFTPLHEAAAKGYE 540
QY 681 ICKLLLOHGADPTKNRDGNTPLDLVKDGTDTQDLRLGDAALLDAKKGCLARVKLSS 740
DB 541 ICKLLLOHGADPTKNRDGNTPLDLVKDGTDTQDLRLGDAALLDAKKGCLARVKLSS 600
QY 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800
DB 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
QY 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOICALLLAHAGADPTLKNQSGOTPLDLVS 860
DB 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOICALLLAHAGADPTLKNQSGOTPLDLVS 720
QY 861 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSSG 920
DB 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
QY 921 SFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFPEREQITLDVLVE 980
DB 781 SFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFPEREQITLDVLVE 840
QY 981 MGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTINTSGSTLIDLSPPDKKEFQ 1040
DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPYLTINTSGSTLIDLSPPDKKEFQ 900
QY 1041 SVEEEMQSTVREHRDGHAGGIFNRYNLIKQKVCNKKLMERYTHRRKEVSEENHNHANE 1100
DB 901 SVEEEMQSTVREHRDGHAGGIFNRYNLIKQKVCNKKLMERYTHRRKEVSEENHNHANE 960
QY 1101 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGGTGCPVHKD 1160
DB 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGGTGCPVHKD 1020
QY 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1080
QY 1221 AYPEYLITYQIMRPEGMDVG 1240
DB 1081 AYPEYLITYQIMRPEGMDVG 1100

RESULT 8

US-09-843-159B-9

; Sequence 9, Application US/09843159B

; Patent No. 6887675

; GENERAL INFORMATION:

; APPLICANT: Luo, Yin

APPLICANT: Chan, Evan
APPLICANT: Xu, Xiang
APPLICANT: Huang, Betty
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
FILE REFERENCE: A-68292-2/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/843,159B
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/696,668
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 09/427,154
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 1100
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic mutant
US-09-843-159B-9

Query Match 89.1%; Score 5760; DB 2; Length 1100;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1098; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 141 GFGKDVVEYLLQNGANVOARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 200
DB 1 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60

QY 201 PLHEAAIKGIDVCIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 260
DB 61 PLHEAAIKGIDVCIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120

QY 261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDKGLV 320
DB 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDKGLV 180

QY 321 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 380
DB 181 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240

QY 381 NCHNKSADLAPTOLKERLAYEFKSHLSLQAAAREADVTRIKKHLSELVNFKPQTHET 440
DB 241 NCHNKSADLAPTOLKERLAYEFKSHLSLQAAAREADVTRIKKHLSELVNFKPQTHET 300

QY 441 ALHCAASPYPKRKQICELLLRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 500
DB 301 ALHCAASPYPKRKQICELLLRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 360

QY 501 NALDNLGOTSLHRAAYCGHLOTCRLLLSYGCDDPNIISLQGTALQNGENVVOLLQEGIS 560
DB 361 NALDNLGOTSLHRAAYCGHLOTCRLLLSYGCDDPNIISLQGTALQNGENVVOLLQEGIS 420

QY 561 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
DB 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480

QY 621 QHGADVHAKDKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEV 680
DB 481 QHGADVHAKDKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEV 540

QY 681 ICKLLQHGADPTKKNRDGNTPLDVKQDGTDIQDLRGDAALLDAKGCCLARVKKLSS 740
DB 541 ICKLLQHGADPTKKNRDGNTPLDVKQDGTDIQDLRGDAALLDAKGCCLARVKKLSS 600

QY 741 PNVNCRDTQGRHSPTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800
DB 601 PNVNCRDTQGRHSPTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660

QY 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOLCALLAHGADPTLKNQEGQTPDLIVS 860
DB 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOLCALLAHGADPTLKNQEGQTPDLIVS 720

QY 861 ADDVSALLTAAMPESALPSCYKPOVLNGVRSPGATADALSSGSPSSSLSAASLDNLGSG 920
DB 721 ADDVSALLTAAMPESALPSCYKPOVLNGVRSPGATADALSSGSPSSSLSAASLDNLGSG 780

QY 921 SFSLSVSSVSSGTEGASSLEKKEVPGVDFSIITQFVRNLGLEHLMDFERQITLDVLVE 980
DB 781 SFSLSVSSVSSGTEGASSLEKKEVPGVDFSIITQFVRNLGLEHLMDFERQITLDVLVE 840

QY 981 MGHEKELKEIGINAYGHRHKLKGVERLISGQGLNPNLYTLNTSGSTLIDLSPPDKKEFQ 1040
DB 841 MGHEKELKEIGINAYGHRHKLKGVERLISGQGLNPNLYTLNTSGSTLIDLSPPDKKEFQ 900

QY 1041 SVEEMOSTVREHRDGGHAGGIFNRYNLIKTKQCNKKLWERYTHRRKEVESENNHANE 1100
DB 901 SVEEMOSTVREHRDGGHAGGIFNRYNLIKTKQCNKKLWERYTHRRKEVESENNHANE 960

QY 1101 RMLFHGSPFNVAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGTCPCVHKD 1160
DB 961 RMLFHGSPFNVAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGTCPCVHKD 1020

QY 1161 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPPGHHSVTGRPSVNGIHLAEYVYIRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPPGHHSVTGRPSVNGIHLAEYVYIRGEQ 1080

QY 1221 AYPEYLITYQIMRPEGWVDG 1240
DB 1081 AYPEYLITYQIMRPEGWVDG 1100

RESULT 9
US-09-427-154-2
Sequence 2, Application US/09427154
Patent No. 6589725
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Xu, Xiang
APPLICANT: Huang, Betty
TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: A-68292-DJB/RMS/DAV
CURRENT APPLICATION NUMBER: US/09/427,154
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1100
TYPE: PRT
ORGANISM: Homo sapiens
US-09-427-154-2

Query Match 88.7%; Score 5731.5; DB 2; Length 1100;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1095; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 141 GFGKDVVEYLLQNGANVOARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 200
DB 1 GFGKDVVEYLLQNGANVOARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60

QY 201 PLHEAAIKGIDVCIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 260
DB 61 PLHEAAIKGIDVCIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120

QY 261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDKGLV 320
DB 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDKGLV 180

QY 321 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 380
DB 181 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240

QY 381 NCHNKSADLAPTOLKERLAYEFKSHLSLQAAAREADVTRIKKHLSELVNFKPQTHET 440

Db 241 NCHNKSALDLAPTQPKERLAYEFKSHLLQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Qy 441 ALHCAAASPPKQKQICELLRLKGANINEKTEPLTPLHVAASEKAHNDVVEVVVHKAHV 500
Db 301 ALHCAAASPPKQKQICELLRLKGANINEKTEPLTPLHVAASEKAHNDVVEVVVHKAHV 360
Qy 501 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDPNIISLQGFALOMGNENVOQLQEGIS 560
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDPNIISLQGFALOMGNENVOQLQEGIS 420
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
Db 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Qy 621 QHGADVHAKDGGGLVPLHNAACSYGHEVAELLVKGAVVNVADLWKFTPLHEAAAKGYE 680
Db 481 QHGADVHAKDGGGLVPLHNAACSYGHEVAELLVKGAVVNVADLWKFTPLHEAAAKGYE 540
Qy 681 ICKLLQHGADPTKKNRDGNTPLDVKGDDTDIQLLGRDAALLDAKKGCLARVKLSS 740
Db 541 ICKLLQHGADPTKKNRDGNTPLDVKGDDTDIHYLLRGDAALLDAKKGCLARVKLSS 600
Qy 741 PDNVNCRDTQGRHSTPLHNAAGYNRVSVVEYLLVKGAVVNVADLWKFTPLHEAAAKGYE 800
Db 601 PDNVNCRDTQGRHSTPLHNAAGYNRVSVVEYLLVKGAVVNVADLWKFTPLHEAAAKGYE 660
Qy 801 VAALLIKYNACVNDKWAFTPLHNAAGYNRVSVVEYLLVKGAVVNVADLWKFTPLHEAAAKGYE 860
Db 661 VAALLIKYNACVNDKWAFTPLHNAAGYNRVSVVEYLLVKGAVVNVADLWKFTPLHEAAAKGYE 720
Qy 861 ADDVSALLTAAMPSPALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASLDNLG 920
Db 721 ADDVSALLTAAMPSPALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASLDNLG 780
Qy 921 SFSELSSVSSSGTEGASSLEKKEVPVDFSIQFVRLNGLHLMDFEREQITLDVLVE 980
Db 781 SFSELSSVSSSGTEGASSLEKKEVPVDFSIQFVRLNGLHLMDFEREQITLDVLVE 840
Qy 981 MGHEKELKEIGNAYGHRHKLKGVRLISGQGLNPYLTMTSGSGTILDLSPDDKEFQ 1040
Db 841 MGHEKELKEIGNAYGHRHKLKGVRLISGQGLNPYLTMTSGSGTILDLSPDDKEFQ 900
Qy 1041 SVEEMOSTVREHDDGGHAGGIFNRYNLTKQCNKKLMERYTHRRKEVSEENHNHANE 1100
Db 901 SVEEMOSTVREHDDGGHAGGIFNRYNLTKQCNKKLMERYTHRRKEVSEENHNHANE 960
Qy 1101 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCPVHKD 1160
Db 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCPVHKD 1020
Qy 1161 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGHHSVTRGPRSVNGLALAEYVYIRGEQ 1220
Db 1021 -SCYICHRQLLFCRVTLGKSLQFSAMKMAHSPGHHSVTRGPRSVNGLALAEYVYIRGEQ 1079
Qy 1221 AYPEYLITYQIMRPEGWVDG 1240
Db 1080 AYPEYLITYQIMRPEGWVDG 1099

RESULT 10
US-09-843-159B-10
; Sequence 10, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DRH
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668

; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-09-843-159B-10

Query Match 87.5%; Score 5656; DB 2; Length 1083;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1079; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 141 GFRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVNVNLLRHHGADPNARDNNY 200
Db 1 GFRKDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNVNLLRHHGADPNARDNNY 60
Qy 201 PLHEAAIKGKIDVICIVLLOHGAEPITIRNTDGTALDLADPSAKAVLTGEYKKBELLESAR 260
Db 61 PLHEAAIKGKIDVICIVLLOHGAEPITIRNTDGTALDLADPSAKAVLTGEYKKBELLESAR 120
Qy 261 SGNEEKRMALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVOLLLOHGAADVHAKDGLV 320
Db 121 SGNEEKRMALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVOLLLOHGAADVHAKDGLV 180
Qy 321 PLHNACSYGHEVTELLVKGACVNAAMDLMQFTPLHEAASKNRVEVCSSLISYGADPTLL 380
Db 181 PLHNACSYGHEVTELLVKGACVNAAMDLMQFTPLHEAASKNRVEVCSSLISYGADPTLL 240
Qy 381 NCHNKSALDLAPTQPKERLAYEFKSHLLQAAREADVTRIKKHLSELMVNFKHPQTHET 440
Db 241 NCHNKSALDLAPTQPKERLAYEFKSHLLQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Qy 441 ALHCAAASPPKQKQICELLRLKGANINEKTEPLTPLHVAASEKAHNDVVEVVVHKAHV 500
Db 301 ALHCAAASPPKQKQICELLRLKGANINEKTEPLTPLHVAASEKAHNDVVEVVVHKAHV 360
Qy 501 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDPNIISLQGFALOMGNENVOQLQEGIS 560
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDPNIISLQGFALOMGNENVOQLQEGIS 420
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
Db 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Qy 621 QHGADVHAKDGGGLVPLHNAACSYGHEVAELLVKGAVVNVADLWKFTPLHEAAAKGYE 680
Db 481 QHGADVHAKDGGGLVPLHNAACSYGHEVAELLVKGAVVNVADLWKFTPLHEAAAKGYE 540
Qy 681 ICKLLQHGADPTKKNRDGNTPLDVKGDDTDIQLLGRDAALLDAKKGCLARVKLSS 740
Db 541 ICKLLQHGADPTKKNRDGNTPLDVKGDDTDIQLLGRDAALLDAKKGCLARVKLSS 600
Qy 741 PDNVNCRDTQGRHSTPLHNAAGYNRVSVVEYLLVKGAVVNVADLWKFTPLHEAAAKGYE 800
Db 601 PDNVNCRDTQGRHSTPLHNAAGYNRVSVVEYLLVKGAVVNVADLWKFTPLHEAAAKGYE 660
Qy 801 VAALLIKYNACVNDKWAFTPLHNAAGYNRVSVVEYLLVKGAVVNVADLWKFTPLHEAAAKGYE 860
Db 661 VAALLIKYNACVNDKWAFTPLHNAAGYNRVSVVEYLLVKGAVVNVADLWKFTPLHEAAAKGYE 720
Qy 861 ADDVSALLTAAMPSPALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASLDNLG 920
Db 721 ADDVSALLTAAMPSPALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASLDNLG 780
Qy 921 SFSELSSVSSSGTEGASSLEKKEVPVDFSIQFVRLNGLHLMDFEREQITLDVLVE 980
Db 781 SFSELSSVSSSGTEGASSLEKKEVPVDFSIQFVRLNGLHLMDFEREQITLDVLVE 840

Qy	981	MGHKELKEIGINAYGHRHKL	KGVERLI	SCQOGLNPYLT	TLNTSGSGTIL	DLSPDDKEFQ	1040
Db	841	MGHKELKEIGINAYGHRHKL	IKGVERLISQOQGLNPYLT	TLNTSGSGTIL	DLSPDDKEFQ		900
Qy	1041	SVSEEMQSTVREHRDGHAGGI	FNRYNLIK	QKVCNKKLWERY	THRRKEVSEENHNHANE	1100	
Db	901	SVSEEMQSTVREHRDGHAGGI	FNRYNLIK	QKVCNKKLWERY	THRRKEVSEENHNHANE	960	
Qy	1101	RMLFHGSPFVNAIIHKGFDERHAYI	IGMFGAGIYFAENS	SKSNQYVYIGGGTGCPVHKD	1160		
Db	961	RMLFHGSPFVNAIIHKGFDERHAYI	IGMFGAGIYFAENS	SKSNQYVYIGGGTGCPVHKD	1020		
Qy	1161	RSCYICHRQLLFCRVTLGKSFLO	FSAMKMAHSPGHHSVTGRPSVNG	LALAEVYIRGEQ	1220		
Db	1021	RSCYICHRQLLFCRVTLGKSFLO	FSAMKMAHSPGHHSVTGRPSVNG	LALAEVYIRGEQ	1080		
Qy	1221	A	1221				
Db	1081	A	1081				

RESULT 11
US-09-972-115A-4
; Sequence 4, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: The 'Xaa' at location 1 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (42)..(42)
; OTHER INFORMATION: The
; NAME/KEY: misc feature
; LOCATION: (98)..(98)
; OTHER INFORMATION: The 'Xaa' at location 98 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (110)..(110)
; OTHER INFORMATION: The
; NAME/KEY: misc feature
; LOCATION: (114)..(114)
; OTHER INFORMATION: The 'Xaa' at location 110 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (126)..(126)
; OTHER INFORMATION: The
; NAME/KEY: misc feature
; LOCATION: (139)..(139)
; OTHER INFORMATION: The 'Xaa' at location 139 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: The
; NAME/KEY: misc feature
; LOCATION: (153)..(153)
; OTHER INFORMATION: The
; NAME/KEY: misc feature

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; NAME/KEY: misc feature
; LOCATION: (787)..(787)
; OTHER INFORMATION: The 'Xaa' at location 787 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (788)..(788)
; OTHER INFORMATION: The 'Xaa' at location 788 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (789)..(789)
; OTHER INFORMATION: The 'Xaa' at location 789 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (790)..(790)
; OTHER INFORMATION: The 'Xaa' at location 790 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (791)..(791)
; OTHER INFORMATION: The 'Xaa' at location 791 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (792)..(792)
; OTHER INFORMATION: The 'Xaa' at location 792 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (793)..(793)
; OTHER INFORMATION: The 'Xaa' at location 793 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (794)..(794)
; OTHER INFORMATION: The 'Xaa' at location 794 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (795)..(795)
; OTHER INFORMATION: The 'Xaa' at location 795 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (796)..(796)
; OTHER INFORMATION: The 'Xaa' at location 796 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (797)..(797)
; OTHER INFORMATION: The 'Xaa' at location 797 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (798)..(798)
; OTHER INFORMATION: The 'Xaa' at location 798 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (799)..(799)
; OTHER INFORMATION: The 'Xaa' at location 799 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (800)..(800)
; OTHER INFORMATION: The 'Xaa' at location 800 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (801)..(801)
; OTHER INFORMATION: The 'Xaa' at location 801 stands for Lys, Asn, Arg, Ser, Thr, Ile

```

```

; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (802)..(802)

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Query Match 84.3%; Score 5452; DB 2; Length 1267;

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Best Local Similarity 86.2%; Pred. No. 0;
Matches 1072; Conservative 6; Mismatches 161; Indels 4; Gaps 2;

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Qy 1 RCSARGAAGCGAQRGARVGAAGHTAPDPVTAGSQARALSASSPGGLALLLAGPGLLL 60

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Db 26 RCLRRRGAGCGAHRXGARGRGHTAPDPVTAGSQARALSASSPGGLALLLAGPGLLL 85

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Qy 61 RLIALALLAANAARIMSGRRRCAGGAACASAAAEEVPAARELFEACNGDVERKRLVTP 120

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Db 86 RLIALALLAANAARIMSGRRRCAGGAACASAAAEEVPAARELFEACNGDVERKRLVTP 145

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Qy 121 EKNSRDTAGRKSTPLHFAAGFRKDVVEYLLONGANVQARDGGLIPLHNACSFHGAEV 180

```

```

Db 146 EKNSRDXAGRKSTPLHFAAGFRKDLXXVLLTNGANXQXDYGGLIPLHNACSFYAXX 205

```

```

Qy 181 VNLLRHGADPNARDNNWYTPLEHAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDADP 240

```

```

Db 206 IXLLXHXAPNARDNNWYTPXXEAAIKGKIXKICIVLLQHGAEPTIRNTDGTALDADP 265

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Qy 241 SAKAVLTGEYKDELLSARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNVKI 300

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Db 266 SAKAVLTGEYKDELLSARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNVKI 325

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Qy 301 VOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 360

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Db 326 VOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 385

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Qy 361 KNRVEVCSLLSYGADPTLLNCHNKSADLAPTQPKERLAYEFKGHSLLOAREADVTR 420

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Db 386 KNRVEVCSLLSYGADPTLLNCHNKSADLAPTQPKERLAYEFKGHSLLOAREADVTR 445

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Qy 421 IKKHLSEMVNFKHPQTHALHCAAAAPYKPKQICELLIRKGANINEKTEFLTPHV 480

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Db 446 IKKHLSEMVNFKHPQTHALHCAAAAPYKPKQICELLIRKGANINEKTEFLTPHV 505

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Qy 481 ASEKANDVVEVVKHAKVNALDNLGTSLSHRAAYCGHLQTCRLLLSYGCDPNIISQ 540

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Db 506 ASEKANDVVEVVKHAKVNALDNLGTSLSHRAAYCGHLQTCRLLLSYGCDPNIISQ 565

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Qy 541 FTALQMGNEVQQLQSGISLGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 600

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Db 566 FTALQMGNEVQQLQSGISLGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 625

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Qy 601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVAELLVKHGAVN 660

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Db 626 STPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVAELLVKHGAVN 685

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Qy 661 VADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGD 720

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Db 686 VADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGD 745

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Qy 721 AALLDAAKGCGLARVKLSLSPDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADV 780

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Db 746 AVLLDAAKGCGLARVKLSLSPDNVNCRDTCGRHSTPLHL-AGXXXXXXXKXXXXXXX 804

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Qy 781 AQDKGGGLPLHNAASYGHVDVAALLIKYNACVNTDKWAFPLHEAAKGRGTQLCALLA 840

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Db 805 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 864

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Qy 841 HGADPTLKNQEGQTFPLDLVSADVDVALLTAAMPSPALPCYKPOVLNGVRSPGATADALS 900

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Db 865 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 924

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Qy 901 SGPSPPSSLSAASLDNLGSGFSELSSVSSSGTEGASSLEKKEVPGVDFPSITQFVRNLG 960

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Db 925 SGPSPPSSLSAASLDNLGSGFSELSSVSSSGTEGASSLEKKEVPGVDFPSITQFVRNLG 984

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QY 961 LEHLMDFPERQITLDVLMGHEKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTL 1020
 DB 985 LEHLMDFPERQITLDVLMGHEKELKEIXINAYGHRHKLKISFERLISGQGLNPLYTL 1044
 QY 1021 NTSGSGTILDLSPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKIOKVCNK--- 1077
 DB 1045 NTSGSGTILDLSPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKIOKVCNRAKI 1104
 QY 1078 KLWERYTHRRKEVSEENHNANERMLFHGSPFVNALIHKGDFERHAYIGMFGAGIYPAE 1137
 DB 1105 RHEERYTHRRKEVSEENHNANERMLFHGSPFVNALIHKGDFERHAYIGMFGAGIYPAE 1164
 QY 1138 NSKSNQYVYIGGGTGPVHKDRSCYIICHRQLLFCRVTLGKSFLOFSAMKHAHSPGHH 1197
 DB 1165 NSKSNQYVYIGGGTGPVHKDRSCYIICHRQLLFCRVTLGKSFLOFSAMKHAHSPGHH 1224
 QY 1198 SVTGRPSVNGLAELAEVYVYRGQAYPEYLITQIMRPEGWVDG 1240
 DB 1225 SVTGRPSVNGLAELAEVYVYRGQAYPEYLITQIMRPEGWVDG 1267

RESULT 12

US-09-196-387-2

; Sequence 2, Application US/09196387

; Patent No. 6277613

; GENERAL INFORMATION:

; APPLICANT: de Lange, Titia

; APPLICANT: Smith, Susan

; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

; TITLE OF INVENTION: OF USE THEREOF

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Klauber & Jackson

; STREET: 411 Hackensack Avenue, 4th Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/196,387

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/095,225

; FILING DATE: June 10, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5800

; TELEFAX: 201-343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1327 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

US-09-196-387-2

Query Match

Best Local Similarity 79.0%; Score 5103.5; DB 2; Length 1327;

Matches 963; Conservative 110; Mismatches 128; Indels 15; Gaps 3;

QY

22 AAHGTAPEVPTAGSQAARALSASSPGGLALLAGPLLRLALLLAVAAARIMSGRCA 81

DB 112 SAAGVAPNPAGSGSNSSPSSSSPTSSSSSSSPG-----SSLAESPAAAGVSTAPL 165
 QY 82 GGAACASAAAFAVEPAARELFEACRNGDVERVKLVTPKYNRSDTAGRKSTPLHFAAG 141
 DB 166 GPAAAGPGTGPVPAVGALRELEACRNGDVSVRKLVDAANYNAMKAGKSSPLHFAAG 225
 QY 142 FORKDVVEYLQNGANVOARDGGGLPLHNACSFHAEVNNLLRHGADPNARDNNWYTP 201
 DB 226 FORKDVVEHLLQNGANVHARDGGGLPLHNACSFHAEVNNLLRHGADPNARDNNWYTP 285
 QY 202 LHEAAIKGKIDVICIVLQHGAEPTIRNTDGRTPALDAPSAKAVLTGYKODELESARS 261
 DB 286 LHEAAIKGKIDVICIVLQHGADPNIRNTDGSALDAPSAKAVLTGYKODELEAARS 345
 QY 262 GNEEKWALLPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLOHGDVHAKDGLVP 321
 DB 346 GNEEKWALLPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLOHGDVHAKDGLVP 405
 QY 322 LHNACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLSYGADPTLN 381
 DB 406 LHNACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLSHGADPTLN 465
 QY 382 CHNKAIDLAPTPOLKERYLAFEFKSHSLQAAREADVTRI KHL SLEWVNFKHPQTHETA 441
 DB 466 CHKSAVDMAPTELRERLTYEFKSHSLQAAREADVTRI KHL SLEWVNFKHPQTHETA 525
 QY 442 LHCAASPYPRKQICELLKRGANINEKTEFLPLHVASEKAHNDVVEVVKHAKVN 501
 DB 526 LHCAVASLHPRKQVTELLRKGANVNEKNDFMTPLHVAERAHNDVNEVLHKGAKVN 585
 QY 502 ALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDDNIIISLOGFTALOMGNENVOQLLEGISL 561
 DB 586 ALDTLQOTLHRAALAGHLQTCRLLLSYGSDDPSIISLOGFTAAQMGNEAVQOILSESTPI 645
 QY 562 GNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLQ 621
 DB 646 RTSDVDVRLLEASKAGDLETVKQLCSSQNVNCRDIEGRHSTPLHFAAGYNNRVSVVEYLH 705
 QY 622 HGADVHAKGGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTEPLHFAAAGKGYEI 681
 DB 706 HGADVHAKGGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTEPLHFAAAGKGYEI 765
 QY 682 CKLLLOHGADPTKQRDGNTPDLVDGDGTDIQLLRGDAALLDAKKGCLARVKLSPP 741
 DB 766 CKLLLOHGADPTKQRDGNTPDLVDGDGTDIQLLRGDAALLDAKKGCLARVKLCTP 825
 QY 742 DVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDV 801
 DB 826 ENINCRDTQGRNSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDI 885
 QY 802 AALLIKYNACVNAWKWAFTEPLHFAAAGKQRTQCALLAHGADPTLKQEGOTPLDLVSA 861
 DB 886 AALLIKYNTCVNADKWAFTEPLHFAAAGKQRTQCALLAHGADPTLKQEGOTPLDLATA 945
 QY 862 DVVSALLTAAMPSPALPSCYKPOVLNGVRSFGATADALSPPSSPSSLSAASLNDLSGS 921
 DB 946 DDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTFSCISAASINDLTGP 998
 QY 922 FSELSSVSVSSGTEGASLEKK--EVPGVDFSIOTFVRNLGLEHLMDFPERQITLDVLA 979
 DB 999 LAELAVGASNAGDAAGTERKSGVAGLDWNISQFLKSLGLEHLRDFIETEQTLDVLA 1058
 QY 980 EMGHKEKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTILDLSPDDKEF 1039
 DB 1059 DMGHEELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTILDLSPDDKEF 1118
 QY 1040 QSVREEMOSTVREHRDGGHAGGIFNRYNLIKIOKVCNKLWERYTHRRKEVSEENHNAN 1099
 DB 1119 QSVREEMOSTVREHRDGGHAGGIFNRYNLIKIOKVCNKLWERYTHRRKEVSEENHNAN 1178
 QY 1100 ERMFLFHGSPFVNALIHKGDFERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGPVHK 1159

Db 1179 ERMFLHSGSPFINAIIHKGFDERHAYIGMGAGIYFAENSSKSNQYVYVIGGGTGPCTHK 1238
Qy 1160 DRSCYICHRQLLCFRVTLGKSFLOFSAMQWHAHPPGHHSTVGRPSVNGLAIAEYVYRGE 1219
Db 1239 DRSCYICHRQMLFCRVTLGKSFLOFSAMQWHAHPPGHHSTVGRPSVNGLAIAEYVYRGE 1298
Qy 1220 QAYPEYLITYQIMRPE 1235
Db 1299 QAYPEYLITYQIMKPE 1314

RESULT 13
US-09-841-835-2
; Sequence 2, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841.835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-841-835-2

Query Match 79.0%; Score 5103.5; DB 2; Length 1327;
Best Local Similarity 79.2%; Pred. No. 0;
Matches 963; Conservative 110; Mismatches 128; Indels 15; Gaps 3;
Qy 22 AAHGTAPDPVYTAGQAARLASASPGGLALLAGPGLLRLLALLALLAAARIMSGRCA 81
Db 112 SAAGVAPNPAGSGNNSPSSSSPTSSSSSPSPG-----SSLASPEAAGVSTAPL 165
Qy 82 GGGACASAAAEVPAARELPACRNGDVERVRLVTPPEKVSRODTAGRKSTELHFAAG 141
Db 166 GPGAGGFGTGVPAVSGALRELLACRNGDSVRVRLVDAANVNNAKDWAGRKSPHFAAG 225
Qy 142 FGRKDVVEYLLQNGANQVARDGGGLIPLHNACSFGEAEVNVNLLLRHGADPNARDNNYTP 201
Db 226 FGRKDVVEYLLQMGANVHARDGGGLIPLHNACSFGEAEVNVNLLLRHGADPNARDNNYTP 285

Qy 202 LHEAAIKGKIDVICVILLOHGAEPTRINTDGRALTADPSAKAVLTGCEYKDELLESARS 261
Db 286 LHEAAIKGKIDVICVILLOHGAEPTRINTDGRALTADPSAKAVLTGCEYKDELLESARS 345
Qy 262 GNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIYVQLLQHGADVHAKDKGLVP 321
Db 346 GNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIYVQLLQHGADVHAKDKGLVP 405
Qy 322 LHNACSYGHEVTELLVKGHCANVMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLN 381
Db 406 LHNACSYGHEVTELLVKGHCANVMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLN 465
Qy 382 CHNKSALDAPTQLKRLAYEPKSHLSLQAAAEADVTRIKKHLSLSEMVNFKPQTHETA 441
Db 466 CHGKSAVDMAPTPELRERLTYPFKGSHLSLQAAAEADVTRIKKHLSLSEMVNFKPQTHETA 525
Qy 442 LHCAAAAPYPRKQICELLIRKGANINEKTKFELTPLHVAASEKAHNDVVEVWVKEAKVN 501
Db 526 LHCAVASLHPKRVQVTELLLRKGANVNEKNKDPMTPLHVAERAHNDVMEVHLKHGAKVN 585
Qy 502 ALDNLGQTSLHRAAYCCHLQTCRLLLSYGCDPNIISLQGFALQMGNEVQOQLQEGISL 561
Db 586 ALDTLQGTALHRAALAGHLQTCRLLLSYGCSPSIIISLQGFALQMGNEVQOQLQEGISL 645
Qy 562 GNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYLLQ 621
Db 646 RTSVDYRLLLEASKAGDLETVKQLCSSQNVNCRDLGRHSTPLHFAAGYNRVSVVYLLH 705
Qy 622 HGADVHAKDKGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGYEI 681
Db 706 HGADVHAKDKGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGYEI 765
Qy 682 CKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQQDLRGDAALLDAAKGCGLARVKLSPP 741
Db 766 CKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQQDLRGDAALLDAAKGCGLARVKLSPP 825
Qy 742 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDV 801
Db 826 ENTNCRDTQGRNSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDI 885
Qy 802 AALLIKYNACVNATDKWAFPLHEAAQKGTQCALILAHGADPTLKNQSGQTPLDLVSA 861
Db 886 AALLIKYNACVNATDKWAFPLHEAAQKGTQCALILAHGADPTLKNQSGQTPLDLVSA 945
Qy 862 DVYSALLTAAMPSPSALPSCYKPVNLNGVSPGATADALSSGSPSSPSLSAASSLDNLSGS 921
Db 946 DDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTPSCLSAASSIDNLTGP 998
Qy 922 FSELSSVSSSGTEGASSLEKK--EYVGVDFSTQFVYRNGLGLEHMDIIFEREQITLDVLV 979
Db 999 LAELAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSLGLEHLRDIIFETEITLDVLA 1058
Qy 980 EMGHKELKEIGINAYGHRHKLIIKGVERLISGQQLNPFYLTNTSGSGTITLIDLSPDKKEF 1039
Db 1059 DMGHEELKEIGINAYGHRHKLIIKGVERLISGQQLNPFYLTNTSGSGTITLIDLAPDEKEY 1118
Qy 1040 QSVVEEMQSTVREHRDGGHAGGIFNRYNIIKIQKVCNKKLWERYTHRRKEVSEENHNAN 1099
Db 1119 QSVVEEMQSTIREHRDGGNAGGIFNRYNIIKIQKVCNKKLWERYTHRRKEVSEENHNAN 1178
Qy 1100 ERMFLHSGSPFINAIIHKGFDERHAYIGMGAGIYFAENSSKSNQYVYVIGGGTGPCTHK 1159
Db 1179 ERMFLHSGSPFINAIIHKGFDERHAYIGMGAGIYFAENSSKSNQYVYVIGGGTGPCTHK 1238
Qy 1160 DRSCYICHRQLLCFRVTLGKSFLOFSAMQWHAHPPGHHSTVGRPSVNGLAIAEYVYRGE 1219
Db 1239 DRSCYICHRQMLFCRVTLGKSFLOFSAMQWHAHPPGHHSTVGRPSVNGLAIAEYVYRGE 1298
Qy 1220 QAYPEYLITYQIMRPE 1235
Db 1299 QAYPEYLITYQIMKPE 1314

RESULT 14
US-09-972-115A-8
; Sequence 8, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-8
Query Match 79.0%; Score 5103.5; DB 2; Length 1327;
Best Local Similarity 79.2%; Pred. No. 0;
Matches 963; Conservative 110; Mismatches 128; Indels. 15; Gaps 3;
QY 22 AAHTGAPDPVTTAGSQAARALSASSPGGALLLAGFLLRLALLLAVAAARIMSGRCA 81
DB 112 SAAGVAPNPAGSGSNSSPSSSSPTSSSSSSPSSG-----SSLAESPAAAGVSTAPL 165
QY 82 GCGAACASAAABAVPAARELFACRNGDVERKLVTPTEKNSRDTAGRKSTPLHFAAG 141
DB 166 GPGAAGPGTGVPVAVSGALRELEACRNGDVSVKRLVDAANVAKMDMAGKSSPLHFAAG 225
QY 142 FGRKDVVEYLLQNGANVQARDGGILPLHNACSFHAEVNVLLLRHGDAPNARDNNWYTP 201
DB 226 FGRKDVVEYLLQNGANVHARDGGILPLHNACSFHAEVNVLLLRHGDAPNARDNNWYTP 285
QY 202 LHEAAIKGKIDVICVILLQHGABPTIRNTDRTALDLPADPSAKAVLTGEYKDDLELSARS 261
DB 286 LHEAAIKGKIDVICVILLQHGADPNIRNTDGSALDLADPSAKAVLTGEYKDDLELSARS 345
QY 262 GNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGLVP 321
DB 346 GNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGLVP 405
QY 322 LHNACSYGHYEYVELLVKHGACVNAWDLWQFTPLHEAASKNREVCSSLSSHGADPTLVN 381
DB 406 LHNACSYGHYEYVELLVKHGACVNAWDLWQFTPLHEAASKNREVCSSLSSHGADPTLVN 465
QY 382 CHNKSAIDLAPTQPKERLAYBFKSHLSLQAAREADVTIRIKKHSLEWMVNFKHPOTHETA 441
DB 466 CHGKSAVDNAPTPELERLTIFYFKSHLSLQAAREADLAKVKTALALEINFQPOSHETA 525
QY 442 LHCAASAPYKPKQICELLRLKGANINEKTEKFLPLHVASAKANDVVEVVVKGHEAKVN 501
DB 526 LHCAVASLHPKPKQVTELLRLKGANVNEKNKDFMTPLHVAERAHNDVMEVLHKGAKVN 585
QY 502 ALDNLGQTSIHPAAVCGHLOTCELLLSYCCDNNIISLOGFTALONGNENVOQLLOGLSL 561
DB 586 ALDNLGQTSIHPAAVCGHLOTCELLLSYCCDNNIISLOGFTALONGNENVOQLLOGLSL 645
QY 562 GNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLQ 621
DB 646 RTSDVDYRLLEASAKGDLTETVQKLCSSQNVNCRDLEGRHSTPLHFAAGYNRVSVVEYLH 705
QY 622 HGADVHAKDGLVPLHNAACSYGHYEVAELLVKGAVNVADLWKFTPLHEAAAKGKVEI 681
DB 706 HGADVHAKDGLVPLHNAACSYGHYEVAELLVKGAVNVADLWKFTPLHEAAAKGKVEI 765

QY 682 CKLLIQHGDPTKKNRDGNTPDLVLKGDGTDTQDILLRGDAALLDAKKGCLARVKLSSP 741
DB 766 CKLLIQHGDPTKKNRDGNTPDLVLKGDGTDTQDILLRGDAALLDAKKGCLARVKLCTP 825
QY 742 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGHVDV 801
DB 826 ENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGHVDI 885
QY 802 AALLIKYNACVNATDKWAFTPLHEAAQGRQTCALLAHAGADPTLKNQEGQTPDLDLVA 861
DB 886 AALLIKYNACVNATDKWAFTPLHEAAQGRQTCALLAHAGADPTLKNQEGQTPDLDLVA 945
QY 862 DDVSALLTAAMPSPSALPSCYKQVNLGVSPCATADALSSGSPSSLSAASLNLGSG 921
DB 946 DDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTFSCLSAASSIDNLGTP 998
QY 922 FSELSSVVSSSGTEGASSLEKK--BVPQVDFPSITQFVNILGLEHMDIFEREQITLDVLV 979
DB 999 LAELAVGASNAGDGAAGTERKEGEVAGLDNWNISQFLKSLGLEHLRDIETEQITLDVLA 1058
QY 980 EMGHKELKEIGINAYGHRHKLKGVRLISGOOGLNPVLTNTSGTGTLIDLSPPDKKEF 1039
DB 1059 DMGHEELKEIGINAYGHRHKLKGVRLISGOOGLNPVLTNTSGTGTLIDLSPPDKKEF 1118
QY 1040 OSVEEEMOSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNHAN 1099
DB 1119 OSVEEEMOSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNHAN 1178
QY 1100 ERMLPHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGPVHK 1159
DB 1179 ERMLPHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGPVHK 1238
QY 1160 DRSCYIHRQLLFCRVTIGKSLQFSAKMAHSPGHSVTPGRPSVNGLALEYVYRGE 1219
DB 1239 DRSCYIHRQLLFCRVTIGKSLQFSAKMAHSPGHSVTPGRPSVNGLALEYVYRGE 1298
QY 1220 QAYPEYLITYQIMRPE 1235
DB 1299 QAYPEYLITYQIMRPE 1314
RESULT 15
US-09-972-115A-2
; Sequence 2, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1333
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: The 'Xaa' at location 1 stands for Lys, Asn, Arg, Ser, Thr, Ile,
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
; NAME/KEY: misc feature
; LOCATION: (2)..(2)

[illegible]

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; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; NAME/KEY: Tyr, Trp, Cys, or Phe.
; LOCATION: (32)..(32)
; OTHER INFORMATION: The 'Xaa' at location 32 stands for Lys, Asn, Arg, Ser, Thr, Ile,
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: The 'Xaa' at location 33 stands for Lys, Asn, Arg, Ser, Thr, Ile,
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: The 'Xaa' at location 34 stands for Lys, Asn, Arg, Ser, Thr, Ile,
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (35)..(35)
; OTHER INFORMATION: The 'Xaa' at location 35 stands for Lys, Asn, Arg, Ser, Thr, Ile,
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (36)..(36)
; OTHER INFORMATION: The 'Xaa' at location 36 stands for Lys, Asn, Arg, Ser, Thr, Ile,

Query Match          77.8%; Score 5031.5; DB 2; Length 1333;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 983; Conservative 7; Mismatches 135; Indels 9; Gaps 2;

QY 116 RLVTPEKVNSTRAGKSTPLHFAAGFGKQVVEVLLQNGANVQARDGGLIPLHNACSF 175
DB 116 RLVTPEKVNSTRAGKSTPLHFAAGFGKQVVEVLLQNGANVQARDGGLIPLHNACSF 259

QY 176 GHAEVNVLLRHGADPNARDNNYTPLEHAAIKGKIDVICVILLQHGAEPTIRNTDGTAL 235
DB 176 GHAEVNVLLRHGADPNARDNNYTPLEHAAIKGKIDVICVILLQHGAEPTIRNTDGTAL 319

QY 236 DLADPSAKAVLTGEYKDOELLESASGNEEKVMALLTPLNVNCHASDGRKSTPLHLAAGY 295
DB 236 DLADPSAKAVLTGEYKDOELLESASGNEEKVMALLTPLNVNCHASDGRKSTPLHLAAGY 379

QY 296 NRKIVQLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVHKHACVNAAMDLMQFTPL 355
DB 296 NRKIVQLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVHKHACVNAAMDLMQFTPL 439

QY 356 HEAAKSNRVEVCSLLSYGADPTLNCNKSIAIDLAPTQPKERLAYEFKHSLLQAAARE 415
DB 356 HEAAKSNRVEVCSLLSYGADPTLNCNKSIAIDLAPTQPKERLAYEFKHSLLQAAARE 499

QY 416 ADVTEIKHLSLEMVNFKHPOTHETALHCAASPYKPKQICELLARKGANINEKTEPL 475
DB 416 ADVTEIKHLSLEMVNFKHPOTHETALHCAASPYKPKQICELLARKGANINEKTEPL 559

QY 476 TPLHVASEKAHNDVVEVVKHAKVNALDNLGQTSILHRAAYCGHLQTCRLLLSYGCDPNI 535
DB 476 TPLHVASEKAHNDVVEVVKHAKVNALDNLGQTSILHRAAYCGHLQTCRLLLSYGCDPNI 619

QY 536 ISLQGFALQMGNEVQQLQEGISLGNSEADROLLEAAKAGDVETVKKLCVTQSVNCRD 595
DB 536 ISLQGFALQMGNEVQQLQEGISLGNSEADROLLEAAKAGDVETVKKLCVTQSVNCRD 679

QY 596 IEGROSTPLHFAAGNVRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVHKH 655
DB 596 IEGROSTPLHFAAGNVRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVHKH 739

QY 656 GAVNVADLWKFTPLHFAAGNVRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVHKH 715
DB 656 GAVNVADLWKFTPLHFAAGNVRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVHKH 799

QY 716 LIRGDAALLDRAKKGCLARVKKLSPPDNVNCRDQTQGRHSTPLHLA--AGYNNLEVAEYLL 773
DB 716 LIRGDAALLDRAKKGCLARVKKLSPPDNVNCRDQTQGRHSTPLHLA--AGYNNLEVAEYLL 859

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QY 774 QHGADVNAQDKGGLIPLHNAASYGHVDAVALLIKYNACVNATDKWATPLHEAAQKGRTO 833
DB 860 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 919
QY 834 LCALLLAHAGADPTLKNQEGOTPLDLVSAADDVSALLTAAMPSPSALPSCYKQVNLGVRSPG 893
DB 920 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 979
QY 894 ATADALSSGSPSPSSLSAASSLDNLSSGFSSELSSVSSSGTSEGASSLEKKEVPGVDFSI 953
DB 980 ATADALSSGSPSPSSLSAASSLDNLSSGFSSELSSVSSSGTSEGASSLEKKEVPGVDFSI 1039
QY 954 QFVRNLGLEHLMDFERQITLIDLVENGHKELKEIGINAYGHRHKLKIGVERLISGOOG 1013
DB 1040 QFVRNLGLEHLMDFERQITLIDLVENGHKELKEIXINAYGHRHKLKIGVERLISGOOG 1099
QY 1014 LNPYLTLNTSGGTILIDLSPDDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIOK 1073
DB 1100 LNPYLTLNTSGGTILIDLSPDDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIOK 1159
QY 1074 VCNK-----KLWERYTHRRKEYSEENHNANERMLFHGSPFVNAIHKGFDERHAYIG 1126
DB 1160 VCNKXXXXXAKIRHEERYTHRRKEYSEENHNANERMLFHGSPFVNAIHKGFDERHAYIG 1219
QY 1127 GMFGAGIYFAENSCKSNQYVYGIGGTCPCPVHKDSCYICHRQLLFCRVTLGKSLQFSA 1186
DB 1220 GMFGAGIYFAENSCKSNQYVYGIGGTCPCPVHKDSCYICHRQLLFCRVTLGKSLQFSA 1279
QY 1187 MKMAHSPGHSVTCRPSVNGLALAEYVYIRGEQAYPEYLITYQIMRPEGMVDG 1240
DB 1280 MKMAHSPGHSVTCRPSVNGLALAEYVYIRGEQAYPEYLITYQIMRPEGMVDG 1333

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Search completed: December 18, 2006, 17:37:14
Job time : 46.423 secs.

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:55:21 ; Search time 40.3471 Seconds
(without alignments)
2975.278 Million cell updates/sec

Title: US-10-616-101-4

Perfect score: 6464

Sequence: 1 RCSARRGAAGGAGGARGARV.....AYPEYLITYQIMRPEGMDG 1240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 381649 seqs, 96809478 residues

Total number of hits satisfying chosen parameters: 381649

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	878.5	13.6	1880	7	US-11-050-875-628
2	878.5	13.6	1881	7	US-11-050-875-629
3	877	13.6	1330	7	US-11-293-697-3237
4	714.5	11.1	919	7	US-11-293-697-4122
5	527	8.2	743	7	US-11-371-354-56501
6	505.5	7.8	685	6	US-10-533-519-1308
7	478	7.4	765	7	US-11-375-615-56
8	465	7.2	765	7	US-11-317-329-3
9	465	7.2	765	7	US-11-317-329-34
10	465	7.2	765	7	US-11-317-329-35
11	465	7.2	765	7	US-11-317-329-36
12	465	7.2	765	7	US-11-317-329-37
13	465	7.2	765	7	US-11-317-329-38
14	465	7.2	765	7	US-11-317-329-39
15	465	7.2	765	7	US-11-317-329-40
16	465	7.2	765	7	US-11-317-329-41
17	465	7.2	765	7	US-11-317-329-42
18	465	7.2	765	7	US-11-317-329-43
19	465	7.2	765	7	US-11-317-329-44
20	462	7.1	1061	7	US-11-397-222-4
21	432	6.7	616	7	US-11-371-354-59433
22	411.5	6.4	1050	7	US-11-371-354-65355
23	408.5	6.3	435	7	US-11-371-354-13702
24	408.5	6.3	435	7	US-11-371-354-78380
25	398.5	6.2	1719	7	US-11-344-932-378

ALIGNMENTS

RESULT 1
US-11-050-875-628
; Sequence 628, Application US/11050875
; Publication No. US20060263786A1

; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1001
; CURRENT APPLICATION NUMBER: US/11/050.875
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1583
; SEQ ID NO 628
; LENGTH: 1880
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-050-875-628

Query Match	13.6%	Score	878.5	DB	7	Length	1880
Best Local Similarity	25.8%	Pred. No.	1.4e-47				
Matches	292	Conservative	157	Mismatches	375	Indels	307
Gaps	28						
QY	105	ACRNDGVERKRLVTP	PEKVNRSRTAGKSTPLHFAAGFGRKDVVEYLLQNGANVOARDG	164			
Db	51	ASKEGHVKNVVELLHKE	-IILETTTKGNTALHIAALAGQDEVVRELNVYGANVNAQSK	109			
QY	165	GLIPLHNACSGHAEVNVLLRHGADPNARDNNWYTPHLEAAIKGIDVICVILLOHGAEP	224				
Db	110	GFTPLYMAAQENHLEVKFKLENGANQVATEDGFTPLAVALQQGHENVAHLINYGTGK	169				
QY	225	TI-----RNTDGR TALDLP	SAKAVLTGVEYKDKDELLESARSGNEEKWALLTPLN	275			
Db	170	KVRLPALHIAARNDDRTA	-----AVLLQNDPNPDLV--SKTG-----FTPLH	210			
QY	276	VNCHASDGRKS-	-----TFLHLAGYNRVKIVQLLQHQADVHAKDKG	317			
Db	211	IAAHVENLVAQLLLNRGASVNFPTQNGITPLHIAARRGNVIMVRLLLDRGAQIETTKD	270				
QY	318	DLVPLHNACSGHVEVTELLVKHGCACVNDLWFTPLHLEAAKRVKVEVCSILLISYGADP	377				
Db	271	ELTFLHCAARNGHVRISILLDHGAPIQAKTKNGLSPIHMAAQGDHLDVCRLLLYDAE-	329				
QY	378	TLLCHNKSATDLAPTQPKERLAEVFKGSLQAAREADVTRIKCHLSLEWVNFKHQPT	437				
Db	330	-----ID-----DIT-----	-----LD	336			
QY	438	HETALHCAAAFPYPRKQICELLRKGANINEKTKFTPLHVASSEKAHNDVVEVVKHE	497				


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Db      337  HLTPHVA---HCGHHRVAKVLLDKGAKPNRSLNGFTPLHIAACKNHNVRVMEILLKTG 393
Qy      498  AKVNALDNLGOTS LHRAAVYCGHLCQTRLLSYGCDPNIIISLGFTALQMG-----NENVQ 552
Db      394  ASIDAVTESGLTPLHVASFMGHLPIVKNLLQKGASPNVSNVKVETPLHMAARAGHTEVAK 453
Qy      553  QLLQE-----GISLGNSEADROLLE-----AAKAG 577
Db      454  YLLQNKAKVNAKADDTQPLHCAARIGHNTNMVLLKENNANPNLATTAGHTPLHIAAREG 513
Qy      578  DVETVKLCTVQ-SVNCRDIEGRQSTPLHFAAGYNRVSVVYLLQHGADVHAKDKGLVP 636
Db      514  HVEITVLALEKEAQACMTKKG--FTPLHVAAGTKVRVAELLERDAHPNAAGNGLTP 571
Qy      637  LHNACSYGHYEVABELLVKHGAVNVADLWK-FTPLHEAAAKGYEICKLLQHGADPTKK 695
Db      572  LHVAVHNNLDIVKLLPRGGSHP-SPAWNGYTPHIAAKQNVQEVARSLLQYGSANAE 630
Qy      696  NRDGNTPDL-LVKDGTDIQDLIRGDAALLDAKKGCLARVKKLSPPDNVNCRTQGRHS 754
Db      631  SVQGVTPHLAAQEGHAEVALL-----LSQANGNLKSG--L 668
Qy      755  TPLHLAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVDVAALLIKYNACVNA 814
Db      669  TPLHVAQEGHPVADVLIKHGVMDATTRNGYTPHVAHYGNIKLVKFLQHQADVNA 728
Qy      815  TDKWAFTPLHAAQKGRTOCALLLAHGADPTLKNQEGQTPDL-----VS 860
Db      729  KTKLGYSPHQAQOQHTDIVTLKNGASPNVSSDGTTPLAIAKRLGYISVTDVLKVV 788
Qy      861  ADDVSALLTAAMPSPALPSC-----YKQ 884
Db      789  TDTSFVLVSDKHMSFPETVDEILDVSEDEGBELISFKAERRDRSDVBEKELLDVFK 848
Qy      885  VLNGVRSPGATADALSSGSPSSLS-----AASSLNLSSFSFELSSVSSSGTEGASS 939
Db      849  LDQVVEPAI-----PRIPCAMPETVIRSEEQASKEYDEDSLISSPATETSDN 900
Qy      940  LEKKEVPGVDSITQFVRNLGLEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHK 999
Db      901  ISPVASPVHTGFLVSM-----VDARGSGMRGSRHN 931
Qy      1000  LIKGE-----RLISGQQLNPLYTLNTSGSTILIDLSP----- 1034
Db      932  GLRWIPPTCAAPTRITCLVKPKLSTPPPLAEEGLASRIIALGTGAQFLSPVIVE 991
Qy      1035  -----DKKEFQSEEEQSTVREHRCGHAGGIFNRYNLIKQVCN 1076
Db      992  IPFHASHGRGDRDELVLRSNGSVKKEH-----SRYGESYLDQILN 1033

RESULT 2
US-11-050-875-629
; Sequence 629, Application US/11050875
; Publication No. US20060263786A1
; GENERAL INFORMATION:
; APPLICANT: Comugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 1847.1001
; CURRENT APPLICATION NUMBER: US/11/050.875
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1583
; SEQ ID NO 629
; LENGTH: 1881
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-875-629

Query Match 13.6%; Score 878.5; DB 7; Length 1881;
Best Local Similarity 25.8%; Pred. No. 1.4e-47;
Matches 292; Conservative 157; Mismatches 375; Indels 307; Gaps 28;

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Qy      105  ACRGDVERVKRLVTPKVNRSRTAGRKSTPLHFAAGFRKQVVVEYLLQNGANVQARDG 164
Db      52  ASKEGHYKVMVVELLHKE-IILEFTTKGNTALHIAALAGQDEVVRELVNYNGANNAOSQK 110
Qy      165  GLTPLHNACSFGEAEVNNLLRHGADPNARDNNWYTPLEHAAIKGKIDVCITVLLQHGAE 224
Db      111  GFTPLYNAAQENHLEVVVKFLENGANQVATEDGFTPLAVALQOQHENVVAHLNLYGK 170
Qy      225  TI-----RNTDGRATLDLADPSAKAVLTGYKKDELLESARSNGEEOOMALLTPLN 275
Db      171  KVRPLPALHIAARNDTRTA-----AVLLQNDPNPDL--SKTG-----FTPLH 211
Qy      276  VNCHASGRKS-----TPLHLAGYNRVKIVOLLQHGADVHAKDKG 317
Db      212  IAAHYENLANVAQLLNRGASVNFPPQNGITPLHIAASRRGNVIMVRLLLDRAQLETTKD 271
Qy      318  DLVPLHNACSYGHYEVTELLVKGACVNAWDLWQFTPLHEAASKNRVEVCSLLSYGADP 377
Db      272  ELTPLHCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHLDVRLLLQYDAE- 330
Qy      378  TLLNCHNKSAIDLAFTPOLKERLAYEPKSHSLLOAAREADVTRIKKLSLEMVNPKHPQT 437
Db      331  -----ID-----DIT-----LD 337
Qy      438  HETALHCAASPYPKRQICELLIRKCANINEKTEFLTPHVASSEKAHNDVVEVVKHE 497
Db      338  HLTPHVA---HCGHHRVAKVLLDKGAKPNRSLNGFTPLHIAACKNHNVRVMEILLKTG 394
Qy      498  AKVNALDNLGOTS LHRAAVYCGHLCQTRLLSYGCDPNIIISLGFTALQMG-----NENVQ 552
Db      395  ASIDAVTESGLTPLHVASFMGHLPIVKNLLQKGASPNVSNVKVETPLHMAARAGHTEVAK 454
Qy      553  QLLQE-----GISLGNSEADROLLE-----AAKAG 577
Db      455  YLLQNKAKVNAKADDTQPLHCAARIGHNTNMVLLKENNANPNLATTAGHTPLHIAAREG 514
Qy      578  DVETVKLCTVQ-SVNCRDIEGRQSTPLHFAAGYNRVSVVYLLQHGADVHAKDKGLVP 636
Db      515  HVEITVLALEKEAQACMTKKG--FTPLHVAAGTKVRVAELLERDAHPNAAGNGLTP 572
Qy      637  LHNACSYGHYEVABELLVKHGAVNVADLWK-FTPLHEAAAKGYEICKLLQHGADPTKK 695
Db      573  LHVAVHNNLDIVKLLPRGGSHP-SPAWNGYTPHIAAKQNVQEVARSLLQYGSANAE 631
Qy      696  NRDGNTPDL-LVKDGTDIQDLIRGDAALLDAKKGCLARVKKLSPPDNVNCRTQGRHS 754
Db      632  SVQGVTPHLAAQEGHAEVALL-----LSQANGNLKSG--L 669
Qy      755  TPLHLAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVDVAALLIKYNACVNA 814
Db      670  TPLHVAQEGHPVADVLIKHGVMDATTRNGYTPHVAHYGNIKLVKFLQHQADVNA 729
Qy      815  TDKWAFTPLHAAQKGRTOCALLLAHGADPTLKNQEGQTPDL-----VS 860
Db      730  KTKLGYSPHQAQOQHTDIVTLKNGASPNVSSDGTTPLAIAKRLGYISVTDVLKVV 789
Qy      861  ADDVSALLTAAMPSPALPSC-----YKQ 884
Db      790  TDTSFVLVSDKHMSFPETVDEILDVSEDEGBELISFKAERRDRSDVBEKELLDVFK 849
Qy      885  VLNGVRSPGATADALSSGSPSSLS-----AASSLNLSSFSFELSSVSSSGTEGASS 939
Db      850  LDQVVEPAI-----PRIPCAMPETVIRSEEQASKEYDEDSLISSPATETSDN 901
Qy      940  LEKKEVPGVDSITQFVRNLGLEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHK 999
Db      902  ISPVASPVHTGFLVSM-----VDARGSGMRGSRHN 932
Qy      1000  LIKGE-----RLISGQQLNPLYTLNTSGSTILIDLSP----- 1034
Db      933  GLRWIPPTCAAPTRITCLVKPKLSTPPPLAEEGLASRIIALGTGAQFLSPVIVE 992
Qy      1035  -----DKKEFQSEEEQSTVREHRCGHAGGIFNRYNLIKQVCN 1076

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Db 993 IPHFASHGRGDRVLVLRSENGSVWKEHR-----SKYGESYLDQILN 1034

RESULT 3

US-11-293-697-3237
; Sequence 3237, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3237
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3237

Query Match 13.6%; Score 877; DB 7; Length 1330;
Best Local Similarity 29.7%; Pred. No. 9.9e-48;
Matches 293; Conservative 137; Mismatches 402; Indels 156; Gaps 23;
QY 105 ACNNGDVER-VKRLVTPKNSRDTRAGKSTPLHFAAGRGKDVVEYLQNGANVOARD 163
Db 17 AARAGNLKRVVEYLKGGIDINTCNQNLNA--LHLAAKEGHVGLVQELLRGSSVDSATK 74
QY 164 GGLIPLHNACSGHARVNLRLRHGADPNARDNWNYPPLHAAIKGIDVICVILHOGAE 223
Db 75 KNTALHIALASQAQAEVVKVLEKGEINAINAQSONGFTPLYMAQENHIDVVKYLLNGAN 134
QY 224 PTRINTDGR-----ALDLADPSAKAVLTGEYKDEL-----LESARSGNEEKMAILLPLN 275
Db 135 QSTATDGTFTPLVALQOQHNOQVAILLENDYKGVRLPALHIAARKDTSKSAALLQ-- 192
QY 276 VNCHASDGRKS-----TPLHLAGYNRVKIVQLLHOGADVHAKDGLVPLHN 324
Db 193 -NDHNADVQSKMNVNRTTESGFTPLHIAAHYGNVNVATLLNRGAADVFTARNGITPLHV 251
QY 325 ACSGYHYETELLVKGACVNAWDLWQFTPLHAAKSNRVEVCSLLSYGADPTLLNCHN 384
Db 252 ASKRGNTNWKLLDRGGQIDAKTRDGLTPLHCAARSQHDQVVELLGERGA-PLIARTKN 310
QY 385 KSAIDLAPTQPKERLAYEFKGHSLLOQAAREADVTRIKKHSLEWVNFKHP-----QTHE 439
Db 311 -----GLSPLHMAAQGDHVECVGHL-----LOHKAPVDDVTLDYL 345
QY 440 TALHCAASAPYPRKQICELLURKGANINEKTEFTPLHVAASEKANDNVVVKHAEK 499
Db 346 TALHVA-----HCGHYRVTKLLDXRPNARALNGFTPLHIAACKNRIKVMELLVKYGA 402
QY 500 VNALNLGTSLHRAAYCHLOTCLLLSYGCDPNIIISLOGTALQMN-----ENVQOL 554
Db 403 IQAITESGLTPTHVAFMGHMINVILLQNGASPDVTNIRGETALHMAARAGQVEVRL 462
QY 555 LOEGI-----SLGNSEADROLLE-----AAKAGDV 579
Db 463 LRNALVDARAREEQTPHIAISRLGKTEIVQLLQHMHPDAATTNRYTPLHISREGV 522
QY 580 ETWKLLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHN 639
Db 523 DVASVLLLEAGAHSATK-KGFTPLHVAAYKYSGLDVAKLLQRRAAADSAGKNGLTPLHV 581
QY 640 ACSGYHYEVAELLVKGAVNVVADLWKFPTPLHAAKAGKYICKLLQHGADPTKNRDG 699
Db 582 AAHYDNQKVALLEKSGASPHATAKNGYTPHIAAKNQMQIASTLLNAGYAEINVTQOG 641
QY 700 NTPDLIV-KDGTDTIQDLRLGDAALLDAKGLARVKVLSPPDNVNCRDTCGRHSTPLH 758

Db 642 VTPLHLASQEGHTDMVTLLLDKGANIHMSTKSGL-----TSLH 679
QY 759 LAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYCHVDVAALLIKYNACVNATDKW 818
Db 680 LAAQEDKVNVDILTCKGDAQDAHTKLGTYPLIVACHYGNVNVNPLFKQGANVNAKTGN 739
QY 819 AFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL-----VSADDVSALITAA 872
Db 740 GYTPHLQAQQOQHTHIIINVLLQHGAKPNATTANGNTALAIKRLGVISVVDILKVVEEV 799
QY 873 PPSALPCYKPOVLNGVRSPGATDALSSGSPSSLSAASSLDNLSSGFSSEL----- 925
Db 800 TTTTITITEK-----HKLNVPTMTTEVL-----DVSDEGDDTWTGDEYLRPEDLK 847
QY 926 -----SSVVSSSGTEGASSLEKEVPGVDFSIQFV--RNLSGLEHMDIFEREQITLDVLV 979
Db 848 ELGDDSLPSSQFLDGMNYLRYLSLEGGRSDSRFSFSDRSHTLSHAS--YLRDSAVMDDSV 905
QY 980 EMGHKELKEIGINAYGHRHKLKIGVERL 1007
Db 906 VIPSHOVSTLAKEAERNSYRLSWGTEENL 933

RESULT 4

US-11-293-697-4122
; Sequence 4122, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4122
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4122

Query Match 11.1%; Score 714.5; DB 7; Length 919;
Best Local Similarity 28.7%; Pred. No. 1.6e-37;
Matches 246; Conservative 109; Mismatches 287; Indels 215; Gaps 27;
QY 121 EKVNSRDTRAGKSTPLHFAAGRGKDVVEYLQNGANVOARDGGLIPLHNACSGHAEV 180
Db 7 EDVNTLDS--EKRTPLHVAAPFLGDAEIIELLLSGARVNAKDNMMLTPLHRAVSRSEA 64
QY 181 VNLLRHGADPNARD--NWNYPPLHAAIKGIDVICVILHOGAEPTIRNTRDGTALDLAD 239
Db 65 VQVLTKHSADVARDKNMQ--TPLHVA----- 90
QY 240 PSKAVLTGEYKOBELLESARSGNEEKMAILLPLNVNCHASDGRKSTPLHLAGYNRVK 299
Db 91 -ANKAV-----KCAEVIPLLSVNVSDRGRTALHHAALNGHVE 129
QY 300 IVQLLQHGADVHAKDGLVPLHNACSGYHYEVTELVVGHGACVNAWDLWQFTPLHAA 359
Db 130 MNVLLAKGANINAFDKORRALHWAAYMGHLDVVALINHGAEVTKDKKGYTPLHAA 189
QY 360 SKNRVEVCSLLSYGADPTLLNCHNKSIAIDAPTQPKERLAYEPKHSLLQAREADV 419
Db 190 SNGQINVVKVLLNLGVEIDENVYNTALHIA-----CYN-----GQDAVNV 231
QY 420 RIKKHSLEWVNFKHPQTHE-TALHCAASAPYPRKQIC-ELLLRKGANINEKTEFTLP 477
Db 232 ELIDY-----GANVNPQNVNGFTPLHFAAASHT---GALCLELLVNVNGADVNIQSKGKSP 284
QY 478 LHVASEKAHNDVVEVVKHAKVNALDNLGQTSLHRAAYCGLHQTCLLLSYGCDPNIIIS 537

Db 285 LHMTAVHGRFTRSTLQNGEIDCVKDGNTPLHVAARYGHELLINTLTSGADTAKG 344
Qy 538 LQGTALQMGNNVQQLQOEGISIGNSEADQQLLEAAKAGDVETVKLCTVQSVNCRDIE 597
Db 345 IHSMPPLHLAALN-----AHSDDCKRL--SSGFIDTPDKF----- 379
Qy 598 GROSFTPLHFAAGYVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA 657
Db 380 GR--TCLHAAAAGGNVCEIKLQSSGADFHKKDKCGRTPLHYAAAANCHFHCIETLVTTGA 437
Qy 658 VNVADLWKFTPLHEAAA-----KGYEIC-KLLQHG 689
Db 438 NVNETDWRGTALHYAAAADMORNTKILGNHNDNSBELERARELKEKATLCLFBLOND 497
Qy 690 ADPTKQNRD-----NTPLDLVK-DG----- 709
Db 498 ANPSIRDKEGYNSHYAAAAYGHRQCLELLERTNSGFEESSDGSATKSPHLAAYNHGHQA 557
Qy 710 -----DTDIQDLRGDAALDAAKKGCLARVVKLSSP-----DNVNCRDTOGRH 753
Db 558 LEVLQSLVDLDIRD-EGRTALDLAFAFKGHTCEVEALINFGASIFVKDNVTKR----- 610
Qy 754 STPLHLAAGYNNLVAEYLLQHGAD---VNAODKGLIPLHNAASYGHVDVAALLIKYN 809
Db 611 -TPLH-ASVINGHTLCURLLELIDNPENAVDVDAKAGOTPLMLAVAGHIDAVSLLLEKE 668
Qy 810 ACVNATDKWFTPLHEAAKQRTQCALLLAHAGADPTLKQSGOTPLDLVSADD-----VS 865
Db 669 ANVDVILGCTALHRGIMTGHBCVQMLLEQEVSLCKDSRGRTPLHYAAAARGHATWLS 728
Qy 866 ALLTAAMPSPSALPCYK 882
Db 729 ELLQWAL--SEEDCCFK 743

RESULT 5

US-11-371-354-56501
; Sequence 56501, Application US/11371354
; Publication No. US2006027594A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; PRIOR FILING DATE: 2006-03-07
; PRIOR FILING DATE: 2006-07-04
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 56501
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-56501
Query Match 8.2%; Score 527; DB 7; Length 743;
Best Local Similarity 24.0%; Pred. No. 1.3e-25;
Matches 201; Conservative 98; Mismatches 238; Indels 302; Gaps 19;

Qy 143 GRXDVVEYLLQNGANVOARDGGLIPLHNA-----CSFGHAEVNVNLLLRHGADPNARDNW 197
Db 2 GHREIVEHLLDHGAENVHEDVDGRTALSVAAALCPVASKGHASVSVSLIDRGAEVHDCDKD 61
Qy 198 NYTPLHEAAIKGIDVCIVLLOHGAEBTIRNTDGTALDLDADPSAKAVLTGEYKKBELLE 257
Db 62 GMTPLLVAAVEGHVDVVDLLEGGAD--VDHTD----- 92
Qy 258 SARSGNEEKWALLTPLNNVCHASDGRKSTPLHLAAGYNNVKIVVOLLQHGADVHAKDKG 317
Db 93 -----NNGR--TPLLAAASMGHASVNVNTLLFWGAAVDSIDSE 127
Qy 318 DLVPLHNACSYGHYEYVTELLVKGACVNAVDLQWFTPLHEAASKNRVEVCSLLLSYGADP 377
Db 128 GRTVLSIASAGNVVVVTTLLDRGLDENHRDDAGTTPPLHMAA----- 169
Qy 378 TLLNCHNKAIDLAPTQLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMNVNFKHPQT 437
Db 170 -----PEGHRL----- 175
Qy 438 HETALHCAAAAPYKPKQICELLRLKGANINEKTEPLTPLHVASEKAHNDVVEVVVKE 497
Db 176 -----ICEALIEOGARTNEIDNDGRIPFILASQEGHYDCVQILLENK 217
Qy 498 AKYNALDNLGOTSILHRAAYCGHLQTCCELLLSYCDPNIIISLOGFTALQMGNNVQQLQOE 557
Db 218 SNIDQRYDGRNALRVAALLEGHRDIEVLLFSHGAD----- 252
Qy 558 GISLGNSEADQQLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVVE 617
Db 253 -----VNCKDADGRPT--LYILALENQLTMAE 277
Qy 618 YLLQHGADVHAKKGGLVPLHNACSYGHYEVAELLVKHGAVNVVADLWKFTPLHEAAK 677
Db 278 YFLENGANVEASDAEGRTALHVSQWGHMEMVQVLIAYHADVNAADNEKRSALQSAWQ 337
Qy 678 KYEICKLLQHGADPTKKNRDNTPDLVDKGDITDIDLLRGDAALDAAKKGCLARVKK 737
Db 338 HVKVVQQLLIEHG-----AVVD----- 353
Qy 738 LSSPDNVNCRDTCQRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYG 797
Db 354 -----HTCQGATACIAAQEGHIDVQVLLHGHADPNHADQFGRMTAMVAAKNG 403
Qy 798 HVDVAALLIKYNACVATDKWFTPLHEAAKQRTQCALLLAHAGADPTLK-NOEGQTPL 856
Db 404 HSQIIKLLKEYGA--SSLNGCSPSPVHTMEQKPLQSLSSKV-----QSLTIKSNSSGST-- 455
Qy 857 DLVSADDVSALLTAAMPSPSALPCYKQVLENGVRSFGATADALSSGSPSSSL--SAASS 914
Db 456 ---GGGD-----MQPS-----LRGL--PNGPHTAFSSPSPSPSTVDROKSS 492
Qy 915 LDNLSGSFSLSVSSSGTEGASSLEKKEVPGVDFSIQTQFVRNLGLEHLMDFEREQI 973
Db 493 LSNNSLKSSKNLSRLTTSSTATAQT-----VPIDSFNLSFTTEQIQHSLPRSRRSQSI 546

RESULT 6

US-10-533-519-1308
; Sequence 1308, Application US/10533519
; Publication No. US20060263774A1
; GENERAL INFORMATION:
; APPLICANT: CLARK, HILARY
; APPLICANT: SCHOENFELD, JILL
; APPLICANT: VANLOOKEREN, MENNO
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1984R1 US
; CURRENT APPLICATION NUMBER: US/10/533,519

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; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/34312
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/423,394
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2517
; SEQ ID NO 1308
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-533-519-1308

```

Query Match	7.8%; Score 505.5; DB 6; Length 685;
Best Local Similarity	24.0%; Pred. No. 2.8e-24;
Matches	195; Conservative 92; Mismatches 264; Indels 263; Gaps 19;
QY	104 EACRNGDVERVKGILVTPKEVNSRDTAGRKSTPLHFAAGFRGKOVVEYLLQNGANVQARD 163
DB	2 EASQEGHLELVKYLLA--SGANVNIATTATGDTALTATYACENGHTVDADVLLQAGADLQKED 60
QY	164 -----GGLIPLHNACSFGRHAENVNLLLRHGADPN-ARDNWNVYPLH 203
DB	61 MKTILSGIDPAKQHESEGRPTLMAKARAGHLCTVPLISKGANVRATANNDHTVVS 120
QY	204 EAAIKGKIDYICVILLOHGAEPTRINTDGRAL-----DLADPSA 242
DB	121 LACAGGHILAVELLAHGADPTHRLKDGSTMLTEAAKGHTNVVSYLLDPNNVLVSPTT 180
QY	243 KAVLTGEYKDELLESARGBE-----EKWALLTPLNVN-----CHASDGRKST 287
DB	181 DVSQLPSPSQDQSEPDRTSQENSPALLGVQKAVSTRVPTGSMSSQTTTCLTPESCQ 240
QY	288 PLHLAAG----YNRVKIVQLLQHGADVHAKOKDLVPLHNACSYGHYVETLLVKHGA 342
DB	241 TSNVASQSPVPVPSVDV-----DAHTESNHD-TALTLCAGGHEELVSLIARDA 290
QY	343 CVNAMDLQWQTPLHEAASKNRVECSLLLSYGADPTLLNCHNKSALIDLAPTQLKERLAY 402
DB	291 KIEHRDKKGTPLILAATAGHVGVEILLDKGD-----324
QY	403 EFKGHSLLQARADVTRI KKHLSLEMVNFKHQPTHETALHCAASYPYKPKQICEILLR 462
DB	325 -----IEAQSE-----RTKDTPLSLACSG--GRQEVVDLLLA 354
QY	463 KGANINEKTEFTPLHVASEKAHNDVVEVVVKHEAKVNL--DNLGQTSILHRAAYCGHL 520
DB	355 RGANKKHRNVSDYTPLSLQASGGYVNIKIILLNAGAEINSGTQSLGISPLMLAAMNGHV 414
QY	521 QTCRLLSYGCDPNIISLQGFALTQMGNNVQQLQEGISLGNSEADRLLEAAKAGDVE 580
DB	415 PAVKLLLDWGS DIN-----428
QY	581 TVKXKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGLVPLHNA 640
DB	429 -----AQIETNRNTALTACFCQRAEWSLLDRKANVEHRAKTTGLTPLMEA 475
QY	641 CSYGHVEVAELLVKHGAVNVVADI--WKFTPLHEAAKGYEKYCKLLQHQGADPTKQRD 698
DB	476 ASGGYAEVGRVLLDKGADVNAAPPVPS SRDTALTITAADKHGYKFCELLIHRGAHIDVENKK 535
QY	699 GNTPLDLVKDGDITDIQDLLRGDAALLDAKKGCLARVKKLLSSPDNVNCRDTQGRHSTPLH 758
DB	536 GNTPLMLASNG-----546
QY	759 LAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIK-----807
DB	547 -----GHFDVVQLLVQAGADVDAADNRKIITPLMSAFRKGHVQVYLKVEVNFPPSDIEC 601
QY	808 --YNACVNAITDKWAFPTPLHSAQ---KGRQTOLCA 836
DB	602 MRYIATII--TDKELLKKKCHOCVETIVKAKDQOAAA 633

RESULT 7
US-11-375-615-56
Sequence 56, Application US/11375615
Publication No. US20060198974A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY D.
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: MARTINEZ, RICARDO
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
TITLE OF INVENTION: ENZYMES
FILE REFERENCE: 038602/1366
CURRENT APPLICATION NUMBER: US/11/375,615
CURRENT FILING DATE: 2006-03-15
PRIOR APPLICATION NUMBER: US/10/182,243
PRIOR FILING DATE: 2003-07-07
PRIOR APPLICATION NUMBER: PCT/US01/02337
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 765
TYPE: PRT
ORGANISM: Homo sapiens
US-11-375-615-56

[illegible]

Db 708 LKVLVEAGAQLDVQDGVSCITPLQLALRSRKQIGMSFL--EGKPSVATLGGSKP 759

RESULT 8

US-11-317-329-3

Sequence 3, Application US/11317329

Publication No. US20060105413A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR FILING DATE: US/10/128,174

PRIOR FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 765

TYPE: PRT

ORGANISM: Homo sapiens

US-11-317-329-3

Query Match 7.2%, Score 465; DB 7; Length 765;

Best Local Similarity 30.1%; Pred. No. 1.3e-21;

Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP---TPOLKERLAYEFKSHLSLQAAREADVTRIKKHSLEWMNFKHPQTHET 440

Db 338 KRALQLSDRKNLVPRDELCIYENKVTPQLQFLVAQGSVEQVRLLLA-----HEV 386

Qy 441 ALHCAAASPYPKRKQICELLRLKGANINEKTEPLTLHVASEKAKHNDVVEVVVKEAKV 500

Db 387 DVDCQTASGY-----TPLLIAAQDQDPLCALLAHGADA 421

Qy 501 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDPNIISLOGFTALQMGNNVQQLQEGIS 560

Db 422 NRVEDGWAFLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN-----471

Qy 561 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGNVRVSVVEYLL 620

Db 472 --NFENVARLLVSRQA-----DPNLEAEGK--TPLHVAAYFGHVSILVKLLT 514

Qy 561 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGNVRVSVVEYLL 620

Db 472 --NFENVARLLVSRQA-----DPNLEAEGK--TPLHVAAYFGHVSILVKLLT 514

Qy 621 QHGAADVHAKDKGLVPLHNACSYGHEVAELLVKHGAVNVVADLWKFTPLHEAAAKGYE 680

Db 515 SOGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574

Qy 681 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDTIQDLRLGDAALLDAAKKGCLARVKKLSS 740

Db 575 ICKMLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLA 613

Qy 741 PDVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800

Db 614 ESHANMAGALGANVWTPHLAARHGEAEVVSALLQCGADPNAAEQSGWTPHLAVQRTFL 673

Qy 801 VAALLIKYNACVNATDKWFTPLHEAAKQRTOLCALLLAHGAADPTLKNQEGTFLDL 858

Db 674 SVINLLEHHANVHARNKVGWTPAHLAALKGNATILKVLVEAGAQLDVQDGVSCITPLQL 731

RESULT 9

US-11-317-329-34

Sequence 34, Application US/11317329

Publication No. US20060105413A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR FILING DATE: US/10/128,174

; PRIOR FILING DATE: 2002-04-23

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 34

; LENGTH: 765

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-317-329-34

Query Match 7.2%, Score 465; DB 7; Length 765;

Best Local Similarity 30.1%; Pred. No. 1.3e-21;

Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP---TPOLKERLAYEFKSHLSLQAAREADVTRIKKHSLEWMNFKHPQTHET 440

Db 338 KRALQLSDRKNLVPRDELCIYENKVTPQLQFLVAQGSVEQVRLLLA-----HEV 386

Qy 441 ALHCAAASPYPKRKQICELLRLKGANINEKTEPLTLHVASEKAKHNDVVEVVVKEAKV 500

Db 387 DVDCQTASGY-----TPLLIAAQDQDPLCALLAHGADA 421

Qy 501 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDPNIISLOGFTALQMGNNVQQLQEGIS 560

Db 422 NRVEDGWAFLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN-----471

Qy 561 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGNVRVSVVEYLL 620

Db 472 --NFENVARLLVSRQA-----DPNLEAEGK--TPLHVAAYFGHVSILVKLLT 514

Qy 621 QHGAADVHAKDKGLVPLHNACSYGHEVAELLVKHGAVNVVADLWKFTPLHEAAAKGYE 680

Db 515 SOGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574

Qy 681 ICKLLLOHGADPTKKNRDGNTPLDLVKDGTDTIQDLRLGDAALLDAAKKGCLARVKKLSS 740

Db 575 ICKMLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLA 613

Qy 741 PDVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800

Db 614 ESHANMAGALGANVWTPHLAARHGEAEVVSALLQCGADPNAAEQSGWTPHLAVQRTFL 673

Qy 801 VAALLIKYNACVNATDKWFTPLHEAAKQRTOLCALLLAHGAADPTLKNQEGTFLDL 858

Db 674 SVINLLEHHANVHARNKVGWTPAHLAALKGNATILKVLVEAGAQLDVQDGVSCITPLQL 731

RESULT 10

US-11-317-329-35

Sequence 35, Application US/11317329

Publication No. US20060105413A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR FILING DATE: US/10/128,174

PRIOR FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 35

LENGTH: 765

TYPE: PRT

ORGANISM: Homo sapiens

US-11-317-329-35

Query Match 7.2%, Score 465; DB 7; Length 765;

Best Local Similarity 30.1%; Pred. No. 1.3e-21;

Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP---TPOLKERLAYEFKSHLSLQAAREADVTRIKKHSLEWMNFKHPQTHET 440

Db 338 KRALQLSRKNLVRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 441 ALHCAAAASPYPKPKQICELLRLKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 500
Db 387 DVDCQTASG-----TPLLIAAQOQDPLCALLAHGADA 421
Qy 501 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDPNIIISLQGTALQMGNEVVOQLLEQGIS 560
Db 422 NRVEDGWAFLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN-----471
Qy 561 LGNSEADRLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 620
Db 472 --NFENVARLLVSROA-----DNLREAEGK--TPLHVAAYFGHVSIVKLTL 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAAKGYE 680
Db 574 SQAELDAQORNLRTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGLHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 740
Db 575 ICKMLRYGASLELPTHQGTWTPHL-----AYKGHL-EIHLHA 613
Qy 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGAALGAVNWTPLHLAARHGEEAVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNTDKWFTPLHEAAKAGRTQLCALLLAHAGADPTLKNQSGQTPDL 858
Db 674 SVINLEHNVHARNKVGWTPAHLAALKGNATAILKVLVEAGAQLDVQDQVSGCTPLQL 731

RESULT 11
US-11-317-329-36
; Sequence 36, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-36

Query Match 7.2%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP----TPOLKERLAYEFKSHLSLQARADVTTRIKKLSLEWVNFKHPQTHET 440
Db 338 KRALQLSRKNLVRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 441 ALHCAAAASPYPKPKQICELLRLKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 500
Db 387 DVDCQTASG-----TPLLIAAQOQDPLCALLAHGADA 421
Qy 501 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDPNIIISLQGTALQMGNEVVOQLLEQGIS 560
Db 422 NRVEDGWAFLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN-----471
Qy 561 LGNSEADRLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 620
Db 472 --NFENVARLLVSROA-----DNLREAEGK--TPLHVAAYFGHVSIVKLTL 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAAKGYE 680
Db 574 SQAELDAQORNLRTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGLHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 740
Db 575 ICKMLRYGASLELPTHQGTWTPHL-----AYKGHL-EIHLHA 613
Qy 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGAALGAVNWTPLHLAARHGEEAVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNTDKWFTPLHEAAKAGRTQLCALLLAHAGADPTLKNQSGQTPDL 858
Db 674 SVINLEHNVHARNKVGWTPAHLAALKGNATAILKVLVEAGAQLDVQDQVSGCTPLQL 731

Db 515 SQAELDAQORNLRTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGLHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 740
Db 575 ICKMLRYGASLELPTHQGTWTPHL-----AYKGHL-EIHLHA 613
Qy 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGAALGAVNWTPLHLAARHGEEAVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNTDKWFTPLHEAAKAGRTQLCALLLAHAGADPTLKNQSGQTPDL 858
Db 674 SVINLEHNVHARNKVGWTPAHLAALKGNATAILKVLVEAGAQLDVQDQVSGCTPLQL 731

RESULT 12
US-11-317-329-37
; Sequence 37, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 37
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-37

Query Match 7.2%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP----TPOLKERLAYEFKSHLSLQARADVTTRIKKLSLEWVNFKHPQTHET 440
Db 338 KRALQLSRKNLVRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 441 ALHCAAAASPYPKPKQICELLRLKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 500
Db 387 DVDCQTASG-----TPLLIAAQOQDPLCALLAHGADA 421
Qy 501 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDPNIIISLQGTALQMGNEVVOQLLEQGIS 560
Db 422 NRVEDGWAFLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN-----471
Qy 561 LGNSEADRLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 620
Db 472 --NFENVARLLVSROA-----DNLREAEGK--TPLHVAAYFGHVSIVKLTL 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAAKGYE 680
Db 574 SQAELDAQORNLRTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGLHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAKKGCLARVKKLSS 740
Db 575 ICKMLRYGASLELPTHQGTWTPHL-----AYKGHL-EIHLHA 613
Qy 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGAALGAVNWTPLHLAARHGEEAVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNTDKWFTPLHEAAKAGRTQLCALLLAHAGADPTLKNQSGQTPDL 858
Db 674 SVINLEHNVHARNKVGWTPAHLAALKGNATAILKVLVEAGAQLDVQDQVSGCTPLQL 731


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RESULT 13
US-11-317-329-38
; Sequence 38, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-38

Query Match          7.2%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP-----TPOLKERLAYEFKGHSLLQAAREADVTRIKKGLSLEMVNFKHPQTHET 440
Db 338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
Qy 441 ALHCAASAPYPRKRQICELLRKGANINEKTEFELPLHVASEKAHNDVVEVVVKEAKV 500
Db 387 DVDCQTASGY-----TELLIAAQDQDPDLCALLAHGADA 421
Qy 501 NALDNLGQTSIHRAAVCGHLOTCTRLLSYCGDPNIISLQGTALQMGNNVQQLQEGIS 560
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVWEYLL 620
Db 472 --NFENVARLLVSRQA-----DPNLRBAEGK--TPLHVAAYFGHVSILVKLLT 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVVADLWKFTPLHEAAAKGYE 680
Db 515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 681 ICKLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKLSS 740
Db 575 ICKMLLYGASLELPTHQGWTPHLH-----AAYKGHL--EIIHLLA 613
Qy 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGALGAVNWTPLHLAARHGEAEVVSALLQCGADPNAAEQSGWTPHLAVQVSTFL 673
Qy 801 VAALLIKYCNATDKWFTPLHEAAQKGTQICALLLAHAGADPTLKNQEGQTFPLDL 858
Db 674 SVINLLEHNVHARNKVGWTPAHLAALKGNITALKVLVEAGAQLDVQDGVSCSTPLQL 731

RESULT 14
US-11-317-329-39
; Sequence 39, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-39

Query Match          7.2%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP-----TPOLKERLAYEFKGHSLLQAAREADVTRIKKGLSLEMVNFKHPQTHET 440
Db 338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
Qy 441 ALHCAASAPYPRKRQICELLRKGANINEKTEFELPLHVASEKAHNDVVEVVVKEAKV 500
Db 387 DVDCQTASGY-----TELLIAAQDQDPDLCALLAHGADA 421
Qy 501 NALDNLGQTSIHRAAVCGHLOTCTRLLSYCGDPNIISLQGTALQMGNNVQQLQEGIS 560
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVWEYLL 620
Db 472 --NFENVARLLVSRQA-----DPNLRBAEGK--TPLHVAAYFGHVSILVKLLT 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVVADLWKFTPLHEAAAKGYE 680
Db 515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 681 ICKLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKLSS 740
Db 575 ICKMLLYGASLELPTHQGWTPHLH-----AAYKGHL--EIIHLLA 613
Qy 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGALGAVNWTPLHLAARHGEAEVVSALLQCGADPNAAEQSGWTPHLAVQVSTFL 673
Qy 801 VAALLIKYCNATDKWFTPLHEAAQKGTQICALLLAHAGADPTLKNQEGQTFPLDL 858
Db 674 SVINLLEHNVHARNKVGWTPAHLAALKGNITALKVLVEAGAQLDVQDGVSCSTPLQL 731

RESULT 15
US-11-317-329-40
; Sequence 40, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-40

Query Match          7.2%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP-----TPOLKERLAYEFKGHSLLQAAREADVTRIKKGLSLEMVNFKHPQTHET 440
Db 338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
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